BLAST score	315
E value	7.0e-52
Match length	119
% identity	90
NCBI Description	(AL021635) predicted protein [Arabidopsis thaliana]

Seq. No.	156999
Seq. ID	LIB3176-063-P1-K1-G5
Method	BLASTX
NCBI GI	g4587519
BLAST score	682
E value	5.0e-72
Match length	142
% identity	96
NCBI Description	(AC007060) Strong similarity to F19I3.7 gi_3033380 putative coatomer epsilon subunit from Arabidopsis thaliana BAC gb_AC004238. ESTs gb_Z17908, gb_AA728673, gb_N96555, gb_H76335, gb_AA712463, gb_W43247, gb_T45611, g

Seq. No.	157000
Seq. ID	LIB3176-063-P1-K1-G6
Method	BLASTX
NCBI GI	g3334124
BLAST score	536
E value	6.0e-55
Match length	119
% identity	91
NCBI Description	ATP SYNTHASE DELTA CHAIN, MITOCHONDRIAL PRECURSOR (OLIGOMYCIN SENSITIVITY CONFERRAL PROTEIN) (OSCP) >gi_1655482_dbj_BAA13600_ (D88375) delta subunit of mitochondrial F1-ATPase [Arabidopsis thaliana]

Seq. No.	157001
Seq. ID	LIB3176-063-P1-K1-G9
Method	BLASTX
NCBI GI	g3128228
BLAST score	436
E value	2.0e-43
Match length	101
% identity	83
NCBI Description	(AC004077) putative ribosomal protein L18A [Arabidopsis thaliana] >gi_3337376 (AC004481) putative ribosomal protein L18A [Arabidopsis thaliana]

Seq. No.	157002
Seq. ID	LIB3176-063-P1-K1-H1
Method	BLASTX
NCBI GI	g1732570
BLAST score	122
E value	5.0e-45
Match length	130
% identity	77
NCBI Description	(U72153) beta-glucosidase [Arabidopsis thaliana]

Seq. No.	157003
Seq. ID	LIB3176-063-P1-K1-H2
Method	BLASTX

NCBI GI	g99004
BLAST score	188
E value	4.0e-14
Match length	144
% identity	33
NCBI Description	famA protein - Streptomyces purpurascens >gi_47381_emb_CAA43934_ (X61931) FAS domain [Streptomyces purpurascens]

Seq. No.	157004
Seq. ID	LIB3176-063-P1-K1-H3
Method	BLASTX
NCBI GI	g114335
BLAST score	668
E value	2.0e-70
Match length	142
% identity	92
NCBI Description	PLASMA MEMBRANE ATPASE 2 (PROTON PUMP) >gi_67973_pir__PXMUP2 H+-transporting ATPase (EC 3.6.1.35) type 2, plasma membrane - Arabidopsis thaliana >gi_166629 (J05570) H+-ATPase [Arabidopsis thaliana]

Seq. No.	157005
Seq. ID	LIB3176-063-P1-K1-H4
Method	BLASTN
NCBI GI	g2642152
BLAST score	248
E value	1.0e-137
Match length	276
% identity	98
NCBI Description	Arabidopsis thaliana chromosome II BAC T5I7 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	157006
Seq. ID	LIB3176-063-P1-K1-H6
Method	BLASTX
NCBI GI	g2586125
BLAST score	477
E value	5.0e-48
Match length	99
% identity	97
NCBI Description	(U89512) b-keto acyl reductase [Arabidopsis thaliana]

Seq. No.	157007
Seq. ID	LIB3176-064-P1-K1-A1
Method	BLASTN
NCBI GI	g4589439
BLAST score	175
E value	1.0e-93
Match length	356
% identity	98
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MQM1, complete sequence

Seq. No.	157008
Seq. ID	LIB3176-064-P1-K1-A10
Method	BLASTX

NCBI GI	g2181186
BLAST score	178
E value	1.0e-13
Match length	45
% identity	78
NCBI Description	(X97323) outward rectifying potassium channel KCO1 [Arabidopsis thaliana] >gi_2230761_emb_CAA69158_ (Y07825) kco1 [Arabidopsis thaliana]

Seq. No.	157009
Seq. ID	LIB3176-064-P1-K1-A4
Method	BLASTX
NCBI GI	g1518540
BLAST score	661
E value	2.0e-69
Match length	140
% identity	94
NCBI Description	(U53418) UDP-glucose dehydrogenase [Glycine max]

Seq. No.	157010
Seq. ID	LIB3176-064-P1-K1-A5
Method	BLASTX
NCBI GI	g4416320
BLAST score	71
E value	3.0e-23
Match length	152
% identity	40
NCBI Description	(AF105998) methylenetetrahydrofolate reductase; MTHFR [Mus musculus]

Seq. No.	157011
Seq. ID	LIB3176-064-P1-K1-A6
Method	BLASTX
NCBI GI	g1363489
BLAST score	633
E value	3.0e-66
Match length	130
% identity	93
NCBI Description	thioglucosidase (EC 3.2.3.1) 3D precursor - Arabidopsis thaliana >gi_984052_emb_CAA61592_ (X89413) thioglucoside glucohydrolase [Arabidopsis thaliana]

Seq. No.	157012
Seq. ID	LIB3176-064-P1-K1-A7
Method	BLASTN
NCBI GI	g3985955
BLAST score	62
E value	2.0e-26
Match length	183
% identity	90
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MTH16, complete sequence [Arabidopsis thaliana]

Seq. No.	157013
Seq. ID	LIB3176-064-P1-K1-A9
Method	BLASTN
NCBI GI	g4468801

BLAST score	59
E value	8.0e-25
Match length	187
% identity	85
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F6G17 (ESSA project)

Seq. No.	157014
Seq. ID	LIB3176-064-P1-K1-B1
Method	BLASTX
NCBI GI	g115385
BLAST score	298
E value	3.0e-27
Match length	65
% identity	92
NCBI Description	CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR (CAB-4) (LHCP) >gi_166646 (M63931) light-harvesting chlorophyll a/b binding protein [Arabidopsis thaliana]

Seq. No.	157015
Seq. ID	LIB3176-064-P1-K1-B10
Method	BLASTX
NCBI GI	g1732570
BLAST score	155
E value	2.0e-19
Match length	97
% identity	59
NCBI Description	(U72153) beta-glucosidase [Arabidopsis thaliana]

Seq. No.	157016
Seq. ID	LIB3176-064-P1-K1-B2
Method	BLASTX
NCBI GI	g3123264
BLAST score	373
E value	4.0e-36
Match length	82
% identity	90
NCBI Description	60S RIBOSOMAL PROTEIN L27 >gi_2244857_emb_CAB10279_ (Z97337) hypothetical protein [Arabidopsis thaliana]

Seq. No.	157017
Seq. ID	LIB3176-064-P1-K1-B4
Method	BLASTN
NCBI GI	g3236234
BLAST score	240
E value	1.0e-132
Match length	425
% identity	96
NCBI Description	Arabidopsis thaliana chromosome II BAC F13M22 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	157018
Seq. ID	LIB3176-064-P1-K1-B5
Method	BLASTN
NCBI GI	g995618
BLAST score	302
E value	1.0e-169

Match length	417
% identity	93
NCBI Description	A.thaliana mRNA for lectin-like protein

Seq. No.	157019
Seq. ID	LIB3176-064-P1-K1-B6
Method	BLASTX
NCBI GI	g4455223
BLAST score	309
E value	3.0e-29
Match length	104
% identity	73
NCBI Description	(AL035440) putative DNA binding protein [Arabidopsis thaliana]

Seq. No.	157020
Seq. ID	LIB3176-064-P1-K1-B7
Method	BLASTN
NCBI GI	g166631
BLAST score	184
E value	3.0e-99
Match length	233
% identity	94
NCBI Description	A.thaliana chloroplast ATP synthase gamma subunit (atpC1) gene, complete cds

Seq. No.	157021
Seq. ID	LIB3176-064-P1-K1-C1
Method	BLASTX
NCBI GI	g2827002
BLAST score	287
E value	5.0e-26
Match length	83
% identity	71
NCBI Description	(AF005993) HSP70 [Triticum aestivum]

Seq. No.	157022
Seq. ID	LIB3176-064-P1-K1-C12
Method	BLASTX
NCBI GI	g2499480
BLAST score	169
E value	2.0e-12
Match length	46
% identity	63
NCBI Description	PET112-LIKE PROTEIN >gi_1354211 (U49790) PET112-like protein [Bacillus subtilis]

Seq. No.	157023
Seq. ID	LIB3176-064-P1-K1-C2
Method	BLASTN
NCBI GI	g4510323
BLAST score	260
E value	1.0e-144
Match length	291
% identity	98
NCBI Description	Arabidopsis thaliana BAC T7B11 from chromosome IV near 10 cM, complete sequence

Docket No. 10004.0005

Seq. No.	157024
Seq. ID	LIB3176-064-P1-K1-C3
Method	BLASTX
NCBI GI	g232031
BLAST score	231
E value	1.0e-19
Match length	72
% identity	58
NCBI Description	ELONGATION FACTOR 1 BETA' >gi_322851_pir__S29224 translation elongation factor eEF-1 beta' chain - rice >gi_218161_dbj_BAA02253_ (D12821) elongation factor 1 beta' [Oryza sativa]

Seq. No.	157025
Seq. ID	LIB3176-064-P1-K1-C6
Method	BLASTN
NCBI GI	g4582444
BLAST score	231
E value	1.0e-127
Match length	363
% identity	91
NCBI Description	Arabidopsis thaliana chromosome II BAC T9H9 genomic sequence, complete sequence

Seq. No.	157026
Seq. ID	LIB3176-064-P1-K1-D10
Method	BLASTX
NCBI GI	g99771
BLAST score	50
E value	3.0e-42
Match length	125
% identity	78
NCBI Description	ubiquitin 81-aa extension protein 1 - Arabidopsis thaliana >gi_166934 (J05539) ubiquitin extension protein (UBQ5) [Arabidopsis thaliana]

Seq. No.	157027
Seq. ID	LIB3176-064-P1-K1-D11
Method	BLASTX
NCBI GI	g4567260
BLAST score	308
E value	2.0e-28
Match length	97
% identity	67
NCBI Description	(AC006841) putative NADPH dependent mannose 6-phosphate reductase [Arabidopsis thaliana] >gi_4582440_gb_AAD24825.1_AC007142_3 (AC007142) putative NADPH-dependent mannose-6-phosphate reductase [Arabidopsis thaliana]

Seq. No.	157028
Seq. ID	LIB3176-064-P1-K1-D12
Method	BLASTX
NCBI GI	g2062161
BLAST score	144
E value	6.0e-12

Match length	116
% identity	46
NCBI Description	(AC001645) jasmonate inducible protein isolog [Arabidopsis thaliana]

Seq. No.	157029
Seq. ID	LIB3176-064-P1-K1-D2
Method	BLASTX
NCBI GI	g3834325
BLAST score	369
E value	2.0e-35
Match length	92
% identity	93
NCBI Description	(AC005679) Strong similarity to gb_AF067141 gamma-glutamyl hydrolase from Arabidopsis thaliana. ESTs gb_R83955, gb_T45062, gb_T22220, gb_AA586207, gb_AI099851 and gb_AI00672 come from this gene. [Arabidopsis thaliana]

Seq. No.	157030
Seq. ID	LIB3176-064-P1-K1-D3
Method	BLASTX
NCBI GI	g4558679
BLAST score	691
E value	5.0e-73
Match length	144
% identity	95
NCBI Description	(AC006586) 40S Ribosomal protein S16 [Arabidopsis thaliana]

Seq. No.	157031
Seq. ID	LIB3176-064-P1-K1-D4
Method	BLASTX
NCBI GI	g4454036
BLAST score	603
E value	9.0e-63
Match length	128
% identity	89
NCBI Description	(AL035394) putative major latex protein [Arabidopsis thaliana]

Seq. No.	157032
Seq. ID	LIB3176-064-P1-K1-D5
Method	BLASTN
NCBI GI	g16371
BLAST score	35
E value	2.0e-10
Match length	71
% identity	87
NCBI Description	A.thaliana gene (LHCP AB 180) for chlorophyll a/b binding protein

Seq. No.	157033
Seq. ID	LIB3176-064-P1-K1-D7
Method	BLASTX
NCBI GI	g2252841
BLAST score	182
E value	4.0e-18
Match length	110

% identity	44
NCBI Description	(AF013293) No definition line found [Arabidopsis thaliana]

Seq. No.	157034
Seq. ID	LIB3176-064-P1-K1-D8
Method	BLASTN
NCBI GI	g3176695
BLAST score	60
E value	2.0e-25
Match length	133
% identity	90
NCBI Description	Arabidopsis thaliana chromosome I BAC F14J9 genomic sequence contains phyA marker, complete sequence [Arabidopsis thaliana]

Seq. No.	157035
Seq. ID	LIB3176-064-P1-K1-E1
Method	BLASTX
NCBI GI	g1657621
BLAST score	778
E value	3.0e-83
Match length	158
% identity	95
NCBI Description	(U72505) G6p [Arabidopsis thaliana] >gi_3068711 (AF049236) putative acyl-coA dehydrogenase [Arabidopsis thaliana]

Seq. No.	157036
Seq. ID	LIB3176-064-P1-K1-E10
Method	BLASTN
NCBI GI	g3883123
BLAST score	146
E value	2.0e-76
Match length	378
% identity	85
NCBI Description	Arabidopsis thaliana arabinogalactan-protein (AGP3) mRNA, complete cds

Seq. No.	157037
Seq. ID	LIB3176-064-P1-K1-E12
Method	BLASTX
NCBI GI	g465602
BLAST score	210
E value	8.0e-17
Match length	84
% identity	52
NCBI Description	HYPOTHETICAL 32.9 KD PROTEIN IN NFO-FRUA INTERGENIC REGION >gi_405885 (U00007) yeiN [Escherichia coli] >gi_1788490 (AE000306) orf, hypothetical protein [Escherichia coli] >gi_744200_prf__2014253BL yeiN gene [Escherichia coli]

Seq. No.	157038
Seq. ID	LIB3176-064-P1-K1-E2
Method	BLASTX
NCBI GI	g3249100
BLAST score	442
E value	9.0e-46
Match length	122

% identity	79
NCBI Description	(AC003114) Match to calreticulin (AtCRTL) mRNA gb_U27698 and DNA gb_U66344. ESTs gb_T45719, gb_T22451, gb_H36323 and gb_AA042519 come from this gene. [Arabidopsis thaliana]
Seq. No.	157039
Seq. ID	LIB3176-064-P1-K1-E4
Method	BLASTX
NCBI GI	g3128228
BLAST score	77
E value	1.0e-71
Match length	146
% identity	95
NCBI Description	(AC004077) putative ribosomal protein L18A [Arabidopsis thaliana] >gi_3337376 (AC004481) putative ribosomal protein L18A [Arabidopsis thaliana]
Seq. No.	157040
Seq. ID	LIB3176-064-P1-K1-E5
Method	BLASTX
NCBI GI	g124226
BLAST score	62
E value	8.0e-26
Match length	88
% identity	72
NCBI Description	INITIATION FACTOR 5A-2 (EIF-5A) (EIF-4D) >gi_100278_pir__S21059 translation initiation factor eIF-5A.2 - curled-leaved tobacco >gi_19702_emb_CAA45104_ (X63542) eukaryotic initiation factor 5A (2) [Nicotiana plumbaginifolia]
Seq. No.	157041
Seq. ID	LIB3176-064-P1-K1-E6
Method	BLASTN
NCBI GI	g3702735
BLAST score	128
E value	9.0e-66
Match length	164
% identity	95
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MQL5, complete sequence [Arabidopsis thaliana]
Seq. No.	157042
Seq. ID	LIB3176-064-P1-K1-E7
Method	BLASTX
NCBI GI	g115767
BLAST score	246
E value	2.0e-55
Match length	122
% identity	81
NCBI Description	CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR (CAB-165/180) (LHCP) >gi_81603_pir__A29280 chlorophyll a/b-binding protein ab165 - Arabidopsis thaliana >gi_16368_emb_CAA27540_ (X03907) chlorophyll a/b binding protein (LHCP AB 65) [Arabidopsis thaliana] >gi_16372_emb_CAA27541_ (X03908) chlorophyll a/b binding protein (LHCP AB 180) [Arabidopsis thaliana]

Seq. No.	157043
Seq. ID	LIB3176-064-P1-K1-F10
Method	BLASTX
NCBI GI	g2062164
BLAST score	300
E value	8.0e-28
Match length	113
% identity	67
NCBI Description	(AC001645) jasmonate inducible protein isolog [Arabidopsis thaliana]

Seq. No.	157044
Seq. ID	LIB3176-064-P1-K1-F2
Method	BLASTX
NCBI GI	g1707012
BLAST score	383
E value	7.0e-37
Match length	79
% identity	94
NCBI Description	(U78721) tyrosyl-tRNA synthetase isolog [Arabidopsis thaliana]

Seq. No.	157045
Seq. ID	LIB3176-064-P1-K1-F3
Method	BLASTX
NCBI GI	g3914442
BLAST score	487
E value	4.0e-49
Match length	145
% identity	68
NCBI Description	PHOTOSYSTEM I REACTION CENTRE SUBUNIT VI PRECURSOR (LIGHT-HARVESTING COMPLEX I 11 KD PROTEIN) (PSI-H) >gi_1916350 (U92504) PSI-H subunit [Brassica rapa]

Seq. No.	157046
Seq. ID	LIB3176-064-P1-K1-F4
Method	BLASTX
NCBI GI	g1350930
BLAST score	566
E value	2.0e-58
Match length	118
% identity	96
NCBI Description	40S RIBOSOMAL PROTEIN S13

Seq. No.	157047
Seq. ID	LIB3176-064-P1-K1-F6
Method	BLASTN
NCBI GI	g3337347
BLAST score	55
E value	3.0e-22
Match length	99
% identity	89
NCBI Description	Arabidopsis thaliana chromosome II BAC F13P17 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	157048

Seq. ID	LIB3176-064-P1-K1-F8
Method	BLASTX
NCBI GI	g3549670
BLAST score	519
E value	7.0e-53
Match length	104
% identity	98
NCBI Description	(AL031394) putative protein [Arabidopsis thaliana]

Seq. No.	157049
Seq. ID	LIB3176-064-P1-K1-G1
Method	BLASTN
NCBI GI	g4206764
BLAST score	101
E value	1.0e-49
Match length	257
% identity	85
NCBI Description	Arabidopsis thaliana putative type 1 membrane protein (PMP) mRNA, complete cds

Seq. No.	157050
Seq. ID	LIB3176-064-P1-K1-G10
Method	BLASTX
NCBI GI	g4584527
BLAST score	62
E value	7.0e-61
Match length	142
% identity	90
NCBI Description	(AL049607) putative protein [Arabidopsis thaliana]

Seq. No.	157051
Seq. ID	LIB3176-064-P1-K1-G2
Method	BLASTX
NCBI GI	g2245037
BLAST score	154
E value	1.0e-10
Match length	74
% identity	46
NCBI Description	(Z97342) nuclear antigen homolog [Arabidopsis thaliana]

Seq. No.	157052
Seq. ID	LIB3176-064-P1-K1-G5
Method	BLASTN
NCBI GI	g4587641
BLAST score	235
E value	1.0e-129
Match length	429
% identity	98
NCBI Description	Arabidopsis thaliana chromosome I BAC F20D21 genomic sequence, complete sequence

Seq. No.	157053
Seq. ID	LIB3176-064-P1-K1-G6
Method	BLASTN
NCBI GI	g4589434
BLAST score	265
E value	1.0e-147

Match length	460
% identity	98
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MNJ7, complete sequence

Seq. No.	157054
Seq. ID	LIB3176-064-P1-K1-G7
Method	BLASTX
NCBI GI	g2829889
BLAST score	401
E value	1.0e-43
Match length	98
% identity	89
NCBI Description	(AC002396) Hypothetical protein [Arabidopsis thaliana]

Seq. No.	157055
Seq. ID	LIB3176-064-P1-K1-G8
Method	BLASTX
NCBI GI	g113026
BLAST score	611
E value	1.0e-63
Match length	139
% identity	84
NCBI Description	ISOCITRATE LYASE (ISOCITRASE) (ISOCITRATASE) (ICL) >gi_68211_pir__WZRPI isocitrate lyase (EC 4.1.3.1) - rape >gi_255220_bbs_112862 isocitrate lyase, threo-D S-isocitrate glyoxylate-lyase, IL (EC 4.1.3.1) [Brassica napus, seedlings, Peptide, 576 aa] >gi_167144 (L08482) isocitrate lyase [Brassica napus] >gi_447142_prf__1913424A isocitrate lyase [Brassica napus]

Seq. No.	157056
Seq. ID	LIB3176-064-P1-K1-H1
Method	BLASTX
NCBI GI	g166867
BLAST score	180
E value	6.0e-57
Match length	146
% identity	78
NCBI Description	(J05216) ribosomal protein S11 (probable start codon at bp 67) [Arabidopsis thaliana]

Seq. No.	157057
Seq. ID	LIB3176-064-P1-K1-H3
Method	BLASTX
NCBI GI	g3176668
BLAST score	353
E value	6.0e-34
Match length	80
% identity	88
NCBI Description	(AC004393) Similar to ribosomal protein L17 gb_X62724 from Hordeum vulgare. ESTs gb_Z34728, gb_F19974, gb_T75677 and gb_Z33937 come from this gene. [Arabidopsis thaliana]

Seq. No.	157058
Seq. ID	LIB3176-064-P1-K1-H4
Method	BLASTX

NCBI GI	g3805849
BLAST score	699
E value	6.0e-74
Match length	155
% identity	89
NCBI Description	(AL031986) cytoplasmatic aconitate hydratase (citrate hydro-lyase)(aconitase)(EC 4.2.1.3) [Arabidopsis thaliana]

Seq. No.	157059
Seq. ID	LIB3176-064-P1-K1-H5
Method	BLASTN
NCBI GI	g4519192
BLAST score	132
E value	3.0e-68
Match length	216
% identity	91
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MBK21, complete sequence

Seq. No.	157060
Seq. ID	LIB3176-064-P1-K1-H6
Method	BLASTN
NCBI GI	g296084
BLAST score	39
E value	4.0e-13
Match length	59
% identity	92
NCBI Description	A.thaliana mRNA for transmembrane protein A

Seq. No.	157061
Seq. ID	LIB3176-064-P1-K1-H7
Method	BLASTN
NCBI GI	g2894591
BLAST score	218
E value	1.0e-119
Match length	262
% identity	96
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone T6K21 (ESSAII project)

Seq. No.	157062
Seq. ID	LIB3176-065-P1-K1-A1
Method	BLASTN
NCBI GI	g1313927
BLAST score	50
E value	5.0e-19
Match length	202
% identity	82
NCBI Description	B.oleracea mRNA for IFA binding protein (sp10)

Seq. No.	157063
Seq. ID	LIB3176-065-P1-K1-A11
Method	BLASTX
NCBI GI	g2190554
BLAST score	229
E value	5.0e-19
Match length	102

% identity	38
NCBI Description	(AC001229) Similar to Arabidopsis cytochrome P450 CYP90 (gb_X87367). [Arabidopsis thaliana]

Seq. No.	157064
Seq. ID	LIB3176-065-P1-K1-A12
Method	BLASTX
NCBI GI	g1705677
BLAST score	243
E value	1.0e-20
Match length	137
% identity	21
NCBI Description	CELL DIVISION CYCLE PROTEIN 48 HOMOLOG >gi_2118115_pir__S60112 cell division control protein CDC48 homolog - Arabidopsis thaliana >gi_1019904 (U37587) cell division cycle protein [Arabidopsis thaliana]

Seq. No.	157065
Seq. ID	LIB3176-065-P1-K1-A2
Method	BLASTX
NCBI GI	g584882
BLAST score	262
E value	3.0e-54
Match length	122
% identity	88
NCBI Description	CYCLOARTENOL SYNTHASE (2,3-EPOXYSQUALENE--CYCLOARTENOL CYCLASE) >gi_452446 (U02555) cycloartenol synthase; (S)-2,3-epoxysqualene mutase [Arabidopsis thaliana]

Seq. No.	157066
Seq. ID	LIB3176-065-P1-K1-A3
Method	BLASTX
NCBI GI	g132939
BLAST score	47
E value	1.0e-55
Match length	129
% identity	89
NCBI Description	60S RIBOSOMAL PROTEIN L3 >gi_81657_pir__JQ0771 ribosomal protein L3 (ARP1) - Arabidopsis thaliana >gi_166858 (M32654) ribosomal protein [Arabidopsis thaliana]

Seq. No.	157067
Seq. ID	LIB3176-065-P1-K1-A4
Method	BLASTX
NCBI GI	g399013
BLAST score	378
E value	2.0e-36
Match length	85
% identity	88
NCBI Description	ADP,ATP CARRIER PROTEIN 1 PRECURSOR (ADP/ATP TRANSLOCASE 1) (ADENINE NUCLEOTIDE TRANSLOCATOR 1) (ANT 1) >gi_99658_pir__S21313 ADP,ATP carrier protein - Arabidopsis thaliana (fragment) >gi_16175_emb_CAA46518_ (X65549) adenylate translocator [Arabidopsis thaliana] >gi_445607_prf__1909354A adenylate translocator [Arabidopsis thaliana]

Seq. No.	157068
Seq. ID	LIB3176-065-P1-K1-A5
Method	BLASTX
NCBI GI	g4581141
BLAST score	344
E value	2.0e-32
Match length	142
% identity	58
NCBI Description	(AC006919) unknown protein [Arabidopsis thaliana]

Seq. No.	157069
Seq. ID	LIB3176-065-P1-K1-A6
Method	BLASTN
NCBI GI	g4704539
BLAST score	47
E value	3.0e-17
Match length	165
% identity	87
NCBI Description	Alluaudiopsis marnieriana ribosomal protein L16 (rpl16) gene, chloroplast gene encoding chloroplast protein, partial cds

Seq. No.	157070
Seq. ID	LIB3176-065-P1-K1-A7
Method	BLASTX
NCBI GI	g2914703
BLAST score	620
E value	9.0e-65
Match length	120
% identity	97
NCBI Description	(AC003974) unknown protein [Arabidopsis thaliana]

Seq. No.	157071
Seq. ID	LIB3176-065-P1-K1-A9
Method	BLASTX
NCBI GI	g3434971
BLAST score	264
E value	3.0e-54
Match length	119
% identity	88
NCBI Description	(AB008105) ethylene responsive element binding factor 3 [Arabidopsis thaliana]

Seq. No.	157072
Seq. ID	LIB3176-065-P1-K1-B1
Method	BLASTX
NCBI GI	g3927830
BLAST score	192
E value	1.0e-14
Match length	86
% identity	50
NCBI Description	(AC005727) hypothetical protein [Arabidopsis thaliana]

Seq. No.	157073
Seq. ID	LIB3176-065-P1-K1-B10
Method	BLASTX
NCBI GI	g3334141

BLAST score	465
E value	1.0e-46
Match length	115
% identity	77
NCBI Description	CENTROMERE/MICROTUBULE BINDING PROTEIN CBF5 (CENTROMERE-BINDING FACTOR 5) (NUCLEOLAR PROTEIN CBF5) >gi_2737890 (U59149) nucleolar protein CaCbf5p [Candida albicans]

Seq. No.	157074
Seq. ID	LIB3176-065-P1-K1-B2
Method	BLASTX
NCBI GI	g4582430
BLAST score	438
E value	1.0e-43
Match length	85
% identity	92
NCBI Description	(AC007196) nonsense-mediated mRNA decay protein [Arabidopsis thaliana]

Seq. No.	157075
Seq. ID	LIB3176-065-P1-K1-B3
Method	BLASTX
NCBI GI	g3688799
BLAST score	529
E value	3.0e-54
Match length	112
% identity	49
NCBI Description	(AF057137) gamma tonoplast intrinsic protein 2 [Arabidopsis thaliana]

Seq. No.	157076
Seq. ID	LIB3176-065-P1-K1-B4
Method	BLASTN
NCBI GI	g3738275
BLAST score	301
E value	1.0e-169
Match length	349
% identity	97
NCBI Description	Arabidopsis thaliana chromosome II BAC F17A22 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	157077
Seq. ID	LIB3176-065-P1-K1-B6
Method	BLASTN
NCBI GI	g4406752
BLAST score	208
E value	1.0e-113
Match length	259
% identity	94
NCBI Description	Arabidopsis thaliana chromosome II BAC F19B11 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	157078
Seq. ID	LIB3176-065-P1-K1-B7
Method	BLASTN
NCBI GI	g4165340

BLAST score	259
E value	1.0e-144
Match length	420
% identity	99
NCBI Description	Arabidopsis thaliana chromosome I BAC F11M15 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	157079
Seq. ID	LIB3176-065-P1-K1-B8
Method	BLASTX
NCBI GI	g119143
BLAST score	529
E value	1.0e-68
Match length	136
% identity	95
NCBI Description	ELONGATION FACTOR 1-ALPHA (EF-1-ALPHA) >gi_81606_pir__S06724 translation elongation factor eEF-1 alpha chain - Arabidopsis thaliana >gi_295788_emb_CAA34453_ (X16430) elongation factor 1-alpha [Arabidopsis thaliana] >gi_1369927_emb_CAA34454_ (X16431) elongation factor 1-alpha [Arabidopsis thaliana] >gi_1369928_emb_CAA34455_ (X16431) elongation factor 1-alpha [Arabidopsis thaliana] >gi_1532172 (U63815) EF-1alpha-A1 [Arabidopsis thaliana] >gi_1532173 (U63815) EF-1alpha-A2 [Arabidopsis thaliana] >gi_1532174 (U63815) EF-1alpha-A3 [Arabidopsis thaliana]

Seq. No.	157080
Seq. ID	LIB3176-065-P1-K1-C1
Method	BLASTX
NCBI GI	g70642
BLAST score	685
E value	2.0e-72
Match length	141
% identity	22
NCBI Description	ubiquitin precursor - Arabidopsis thaliana >gi_17678_emb_CAA31331_ (X12853) polyubiquitin (AA 1 - 382) [Arabidopsis thaliana] >gi_987519 (U33014) polyubiquitin [Arabidopsis thaliana] >gi_226499_prf__1515347A poly-ubiquitin [Arabidopsis thaliana]

Seq. No.	157081
Seq. ID	LIB3176-065-P1-K1-C10
Method	BLASTN
NCBI GI	g2264311
BLAST score	355
E value	0.0e+00
Match length	388
% identity	97
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MLN1, complete sequence [Arabidopsis thaliana]

Seq. No.	157082
Seq. ID	LIB3176-065-P1-K1-C11
Method	BLASTX
NCBI GI	g2160168
BLAST score	498
E value	2.0e-50



Match length	105
% identity	88
NCBI Description	(AC000132) Strong similarity to R. communis phosphoglycerate mutase (gb_X70652). ESTs gb_T41853,gb_T76648 come from this gene. [Arabidopsis thaliana]

Seq. No.	157083
Seq. ID	LIB3176-065-P1-K1-C12
Method	BLASTN
NCBI GI	g3702735
BLAST score	301
E value	1.0e-169
Match length	434
% identity	99
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MQL5, complete sequence [Arabidopsis thaliana]

Seq. No.	157084
Seq. ID	LIB3176-065-P1-K1-C2
Method	BLASTX
NCBI GI	g2500430
BLAST score	655
E value	7.0e-69
Match length	127
% identity	100
NCBI Description	40S RIBOSOMAL PROTEIN S16

Seq. No.	157085
Seq. ID	LIB3176-065-P1-K1-C3
Method	BLASTX
NCBI GI	g1346194
BLAST score	686
E value	2.0e-72
Match length	140
% identity	96
NCBI Description	GLUTATHIONE REDUCTASE, CYTOSOLIC (GR) (GRASE) (OBP29) >gi_1022797 (U37697) glutathione reductase [Arabidopsis thaliana]

Seq. No.	157086
Seq. ID	LIB3176-065-P1-K1-C4
Method	BLASTX
NCBI GI	g4454036
BLAST score	716
E value	5.0e-76
Match length	134
% identity	97
NCBI Description	(AL035394) putative major latex protein [Arabidopsis thaliana]

Seq. No.	157087
Seq. ID	LIB3176-065-P1-K1-C6
Method	BLASTX
NCBI GI	g3319350
BLAST score	102
E value	2.0e-51

Match length	105
% identity	99
NCBI Description	(AF077407) No definition line found [Arabidopsis thaliana]

Seq. No.	157088
Seq. ID	LIB3176-065-P1-K1-C8
Method	BLASTN
NCBI GI	g3319339
BLAST score	57
E value	3.0e-23
Match length	69
% identity	96
NCBI Description	Arabidopsis thaliana BAC F9D12

Seq. No.	157089
Seq. ID	LIB3176-065-P1-K1-D10
Method	BLASTX
NCBI GI	g115767
BLAST score	684
E value	3.0e-72
Match length	133
% identity	98
NCBI Description	CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR (CAB-165/180) (LHCP) >gi_81603_pir__A29280 chlorophyll a/b-binding protein ab165 - Arabidopsis thaliana >gi_16368_emb_CAA27540_ (X03907) chlorophyll a/b binding protein (LHCP AB 65) [Arabidopsis thaliana] >gi_16372_emb_CAA27541_ (X03908) chlorophyll a/b binding protein (LHCP AB 180) [Arabidopsis thaliana]

Seq. No.	157090
Seq. ID	LIB3176-065-P1-K1-D11
Method	BLASTX
NCBI GI	g3242077
BLAST score	652
E value	2.0e-68
Match length	146
% identity	84
NCBI Description	(AJ003119) protein phosphatase 2C [Arabidopsis thaliana]

Seq. No.	157091
Seq. ID	LIB3176-065-P1-K1-D12
Method	BLASTN
NCBI GI	g1063683
BLAST score	263
E value	1.0e-146
Match length	311
% identity	96
NCBI Description	Arabidopsis thaliana glycine-rich protein (AtGRP2b) mRNA, complete cds

Seq. No.	157092
Seq. ID	LIB3176-065-P1-K1-D2
Method	BLASTX
NCBI GI	g113026
BLAST score	682
E value	5.0e-72

Match length	136
% identity	95
NCBI Description	ISOCITRATE LYASE (ISOCITRASE) (ISOCITRATASE) (ICL) >gi_68211_pir__WZRPI isocitrate lyase (EC 4.1.3.1) - rape >gi_255220_bbs_112862 isocitrate lyase, threo-D S-isocitrate glyoxylate-lyase, IL {EC 4.1.3.1} [Brassica napus, seedlings, Peptide, 576 aa] >gi_167144 (L08482) isocitrate lyase [Brassica napus] >gi_447142_prf__1913424A isocitrate lyase [Brassica napus]

Seq. No.	157093
Seq. ID	LIB3176-065-P1-K1-D3
Method	BLASTX
NCBI GI	g1652678
BLAST score	363
E value	1.0e-34
Match length	126
% identity	54
NCBI Description	(D90907) amidase [Synechocystis sp.]

Seq. No.	157094
Seq. ID	LIB3176-065-P1-K1-D4
Method	BLASTX
NCBI GI	g2506276
BLAST score	406
E value	1.0e-39
Match length	91
% identity	93
NCBI Description	RUBISCO SUBUNIT BINDING-PROTEIN ALPHA SUBUNIT PRECURSOR (60 KD CHAPERONIN ALPHA SUBUNIT) (CPN-60 ALPHA) >gi_2129561_pir__S71235 chaperonin-60 alpha chain - Arabidopsis thaliana >gi_1223910 (U49357) chaperonin-60 alpha subunit [Arabidopsis thaliana] >gi_4510416_gb_AAD21502.1_ (AC006929) putative rubisco binding protein alpha subunit [Arabidopsis thaliana]

Seq. No.	157095
Seq. ID	LIB3176-065-P1-K1-D5
Method	BLASTX
NCBI GI	g4056500
BLAST score	285
E value	2.0e-25
Match length	58
% identity	100
NCBI Description	(AC005896) putative acetyltransferase [Arabidopsis thaliana]

Seq. No.	157096
Seq. ID	LIB3176-065-P1-K1-D6
Method	BLASTX
NCBI GI	g1172873
BLAST score	640
E value	4.0e-67
Match length	144
% identity	82
NCBI Description	CYSTEINE PROTEINASE RD21A PRECURSOR >gi_541857_pir__JN0719 drought-inducible cysteine proteinase (EC 3.4.22.-) RD21A

	precursor - Arabidopsis thaliana >gi_435619_dbj_BAA02374_ (D13043) thiol protease [Arabidopsis thaliana]
Seq. No.	157097
Seq. ID	LIB3176-065-P1-K1-D7
Method	BLASTN
NCBI GI	g2564048
BLAST score	196
E value	1.0e-106
Match length	278
% identity	96
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MKD15, complete sequence [Arabidopsis thaliana]
Seq. No.	157098
Seq. ID	LIB3176-065-P1-K1-D9
Method	BLASTX
NCBI GI	g2499498
BLAST score	394
E value	2.0e-38
Match length	124
% identity	68
NCBI Description	PHOSPHOGLYCERATE KINASE, CYTOSOLIC >gi_1161602_emb_CAA88840_ (Z48976) phosphoglycerate kinase (PGK) [Nicotiana tabacum]
Seq. No.	157099
Seq. ID	LIB3176-065-P1-K1-E1
Method	BLASTN
NCBI GI	g2351061
BLAST score	241
E value	1.0e-133
Match length	426
% identity	99
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MAF19, complete sequence [Arabidopsis thaliana]
Seq. No.	157100
Seq. ID	LIB3176-065-P1-K1-E10
Method	BLASTX
NCBI GI	g399091
BLAST score	407
E value	9.0e-40
Match length	117
% identity	73
NCBI Description	PYROPHOSPHATE-ENERGIZED VACUOLAR MEMBRANE PROTON PUMP (PYROPHOSPHATE-ENERGIZED INORGANIC PYROPHOSPHATASE) (H+-PPASE) >gi_282878_pir__A38230 inorganic pyrophosphatase (EC 3.6.1.1), H+-translocating pyrophosphate-energized - Arabidopsis thaliana >gi_166634 (M81892) vacuolar H+-phosphatase [Arabidopsis thaliana]
Seq. No.	157101
Seq. ID	LIB3176-065-P1-K1-E11
Method	BLASTX
NCBI GI	g99696
BLAST score	416

E value	9.0e-41
Match length	102
% identity	80
NCBI Description	glutamate--ammonia ligase (EC 6.3.1.2) precursor, chloroplast (clone lambdaAtgsl1) - Arabidopsis thaliana >gi_240070_bbs_69728 (S69727) light-regulated glutamine synthetase isoenzyme [Arabidopsis thaliana, Peptide, 430 aa] [Arabidopsis thaliana] >gi_228453_prf__1804333A Gln synthetase [Arabidopsis thaliana]

Seq. No.	157102
Seq. ID	LIB3176-065-P1-K1-E12
Method	BLASTX
NCBI GI	g1169280
BLAST score	519
E value	7.0e-53
Match length	151
% identity	61
NCBI Description	DEHYDRIN COR47 (COLD-INDUCED COR47 PROTEIN) >gi_2627135_dbj_BAA23547_ (AB004872) COR47 [Arabidopsis thaliana]

Seq. No.	157103
Seq. ID	LIB3176-065-P1-K1-E2
Method	BLASTX
NCBI GI	g2982301
BLAST score	189
E value	3.0e-14
Match length	89
% identity	51
NCBI Description	(AF051235) YGL010w-like protein [Picea mariana]

Seq. No.	157104
Seq. ID	LIB3176-065-P1-K1-E3
Method	BLASTX
NCBI GI	g1363489
BLAST score	554
E value	5.0e-57
Match length	115
% identity	91
NCBI Description	thioglucosidase (EC 3.2.3.1) 3D precursor - Arabidopsis thaliana >gi_984052_emb_CAA61592_ (X89413) thioglucoside glucohydrolase [Arabidopsis thaliana]

Seq. No.	157105
Seq. ID	LIB3176-065-P1-K1-E4
Method	BLASTX
NCBI GI	g2677828
BLAST score	418
E value	5.0e-41
Match length	116
% identity	67
NCBI Description	(U93166) cysteine protease [Prunus armeniaca]

Seq. No.	157106
Seq. ID	LIB3176-065-P1-K1-E5
Method	BLASTN

NCBI GI	g16255
BLAST score	147
E value	6.0e-77
Match length	331
% identity	56
NCBI Description	A.thaliana A2 and A3 genes encoding elongation factor 1-alpha

Seq. No.	157107
Seq. ID	LIB3176-065-P1-K1-E6
Method	BLASTX
NCBI GI	g2706450
BLAST score	256
E value	4.0e-22
Match length	69
% identity	72
NCBI Description	(AJ225172) magnesium dependent soluble inorganic pyrophosphatase [Solanum tuberosum]

Seq. No.	157108
Seq. ID	LIB3176-065-P1-K1-E7
Method	BLASTX
NCBI GI	g1076715
BLAST score	234
E value	2.0e-19
Match length	88
% identity	51
NCBI Description	abscisic acid-induced protein HVA22 - barley >gi_404589 (L19119) A22 [Hordeum vulgare]

Seq. No.	157109
Seq. ID	LIB3176-065-P1-K1-E8
Method	BLASTX
NCBI GI	g2832625
BLAST score	175
E value	1.0e-12
Match length	97
% identity	35
NCBI Description	(AL021711) putative protein [Arabidopsis thaliana]

Seq. No.	157110
Seq. ID	LIB3176-065-P1-K1-E9
Method	BLASTX
NCBI GI	g2738248
BLAST score	714
E value	8.0e-76
Match length	140
% identity	98
NCBI Description	(U97200) cobalamin-independent methionine synthase [Arabidopsis thaliana]

Seq. No.	157111
Seq. ID	LIB3176-065-P1-K1-F1
Method	BLASTX
NCBI GI	g3513727
BLAST score	96
E value	2.0e-03

Match length	133
% identity	56
NCBI Description	(AF080118) contains similarity to TPR domains (Pfam: TPR.hmm: score: 11.15) and kinesin motor domains (Pfam: kinesin2.hmm, score: 17.49, 20.52 and 10.94) [Arabidopsis thaliana] >gi_4539358_emb_CAB40052.1_ (AL049525) putative protein [Arabidopsis thaliana]

Seq. No.	157112
Seq. ID	LIB3176-065-P1-K1-F10
Method	BLASTX
NCBI GI	g2865623
BLAST score	456
E value	2.0e-45
Match length	99
% identity	90
NCBI Description	(AF045286) GDP-4-keto-6-deoxy-D-mannose-3,5-epimerase-4-reductase [Arabidopsis thaliana]

Seq. No.	157113
Seq. ID	LIB3176-065-P1-K1-F12
Method	BLASTN
NCBI GI	g2182287
BLAST score	333
E value	0.0e+00
Match length	417
% identity	95
NCBI Description	Genomic sequence for Arabidopsis thaliana BAC T7N9, complete sequence [Arabidopsis thaliana]

Seq. No.	157114
Seq. ID	LIB3176-065-P1-K1-F3
Method	BLASTX
NCBI GI	g1170373
BLAST score	642
E value	3.0e-67
Match length	130
% identity	98
NCBI Description	HEAT SHOCK COGNATE 70 KD PROTEIN 1 >gi_1072473_pir__S46302 heat shock cognate protein 70-1 - Arabidopsis thaliana >gi_397482_emb_CAA52684_ (X74604) heat shock protein 70 cognate [Arabidopsis thaliana]

Seq. No.	157115
Seq. ID	LIB3176-065-P1-K1-F4
Method	BLASTX
NCBI GI	g2062159
BLAST score	491
E value	1.0e-49
Match length	147
% identity	36
NCBI Description	(AC001645) jasmonate inducible protein isolog [Arabidopsis thaliana]

Seq. No.	157116
Seq. ID	LIB3176-065-P1-K1-F5

Method	BLASTX
NCBI GI	g4678935
BLAST score	235
E value	2.0e-19
Match length	64
% identity	67
NCBI Description	(AL049711) putative protein [Arabidopsis thaliana]

Seq. No.	157117
Seq. ID	LIB3176-065-P1-K1-F6
Method	BLASTX
NCBI GI	g4581108
BLAST score	334
E value	3.0e-31
Match length	144
% identity	49
NCBI Description	(AC005825) putative chloroplast outer membrane protein 86,also very similar to GTP-inding protein from pea (GB:L36857) [Arabidopsis thaliana]

Seq. No.	157118
Seq. ID	LIB3176-065-P1-K1-F8
Method	BLASTX
NCBI GI	g1363489
BLAST score	756
E value	1.0e-80
Match length	142
% identity	96
NCBI Description	thioglucosidase (EC 3.2.3.1) 3D precursor - Arabidopsis thaliana >gi_984052_emb_CAA61592_ (X89413) thioglucoside glucohydrolase [Arabidopsis thaliana]

Seq. No.	157119
Seq. ID	LIB3176-065-P1-K1-G1
Method	BLASTX
NCBI GI	g2341034
BLAST score	359
E value	2.0e-34
Match length	102
% identity	77
NCBI Description	(AC000104) F19P19.13 [Arabidopsis thaliana]

Seq. No.	157120
Seq. ID	LIB3176-065-P1-K1-G10
Method	BLASTN
NCBI GI	g3702731
BLAST score	334
E value	0.0e+00
Match length	377
% identity	97
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MFC19, complete sequence [Arabidopsis thaliana]

Seq. No.	157121
Seq. ID	LIB3176-065-P1-K1-G11
Method	BLASTX
NCBI GI	g3915826

BLAST score	574
E value	2.0e-59
Match length	138
% identity	79
NCBI Description	60S RIBOSOMAL PROTEIN L5

Seq. No.	157122
Seq. ID	LIB3176-065-P1-K1-G12
Method	BLASTN
NCBI GI	g4159707
BLAST score	207
E value	1.0e-112
Match length	422
% identity	97
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MJK13, complete sequence

Seq. No.	157123
Seq. ID	LIB3176-065-P1-K1-G2
Method	BLASTX
NCBI GI	g113026
BLAST score	535
E value	8.0e-55
Match length	124
% identity	85
NCBI Description	ISOCITRATE LYASE (ISOCITRASE) (ISOCITRATASE) (ICL) >gi_68211_pir__WZRPI isocitrate lyase (EC 4.1.3.1) - rape >gi_255220_bbs_112862 isocitrate lyase, threo-D S-isocitrate glyoxylate-lyase, IL {EC 4.1.3.1} [Brassica napus, seedlings, Peptide, 576 aa] >gi_167144 (L08482) isocitrate lyase [Brassica napus] >gi_447142_prf__1913424A isocitrate lyase [Brassica napus]

Seq. No.	157124
Seq. ID	LIB3176-065-P1-K1-G3
Method	BLASTX
NCBI GI	g4455253
BLAST score	586
E value	9.0e-61
Match length	144
% identity	78
NCBI Description	(AL035523) superoxide dismutase (EC 1.15.1.1) (Fe)(fragment) [Arabidopsis thaliana]

Seq. No.	157125
Seq. ID	LIB3176-065-P1-K1-G4
Method	BLASTN
NCBI GI	g3337347
BLAST score	290
E value	1.0e-162
Match length	382
% identity	100
NCBI Description	Arabidopsis thaliana chromosome II BAC F13P17 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	157126
Seq. ID	LIB3176-065-P1-K1-G5

Method	BLASTX
NCBI GI	g2062161
BLAST score	693
E value	3.0e-73
Match length	132
% identity	50
NCBI Description	(AC001645) jasmonate inducible protein isolog [Arabidopsis thaliana]

Seq. No.	157127
Seq. ID	LIB3176-065-P1-K1-G6
Method	BLASTX
NCBI GI	g115484
BLAST score	564
E value	4.0e-58
Match length	110
% identity	59
NCBI Description	CALMODULIN 1 >gi_71684_pir__MCPZDC calmodulin - carrot >gi_478632_pir__S22971 calmodulin - trumpet lily >gi_541839_pir__S40301 calmodulin - Red bryony >gi_2129970_pir__S70768 calmodulin CAM81 - garden petunia >gi_18326_emb_CAA42423_ (X59751) calmodulin [Daucus carota] >gi_19447_emb_CAA78301_ (Z12839) calmodulin [Lilium longiflorum] >gi_169207 (M80836) calmodulin [Petunia hybrida] >gi_308900 (L18912) calmodulin [Lilium longiflorum] >gi_505154_emb_CAA43143_ (X60738) Calmodulin [Malus domestica] >gi_535444 (U13882) calmodulin [Pisum sativum] >gi_445602_prf__1909349A calmodulin [Daucus carota]

Seq. No.	157128
Seq. ID	LIB3176-065-P1-K1-G7
Method	BLASTN
NCBI GI	g2262155
BLAST score	63
E value	7.0e-27
Match length	212
% identity	87
NCBI Description	DNA sequence of Arabidopsis thaliana BAC F5J6 from chromosome IV, complete sequence [Arabidopsis thaliana]

Seq. No.	157129
Seq. ID	LIB3176-065-P1-K1-G8
Method	BLASTX
NCBI GI	g113026
BLAST score	580
E value	4.0e-60
Match length	127
% identity	87
NCBI Description	ISOCITRATE LYASE (ISOCITRASE) (ISOCITRATASE) (ICL) >gi_68211_pir__WZRPI isocitrate lyase (EC 4.1.3.1) - rape >gi_255220_bbs_112862 isocitrate lyase, threo-D S-isocitrate glyoxylate-lyase, IL (EC 4.1.3.1) [Brassica napus, seedlings, Peptide, 576 aa] >gi_167144 (L08482) isocitrate lyase [Brassica napus] >gi_447142_prf__1913424A isocitrate lyase [Brassica napus]

Seq. No.	157130
Seq. ID	LIB3176-065-P1-K1-H1
Method	BLASTN
NCBI GI	g1657620
BLAST score	371
E value	0.0e+00
Match length	399
% identity	98
NCBI Description	Arabidopsis thaliana putative acyl-coA dehydrogenase G6p (AtG6) mRNA, complete cds

Seq. No.	157131
Seq. ID	LIB3176-065-P1-K1-H11
Method	BLASTX
NCBI GI	g115767
BLAST score	510
E value	5.0e-52
Match length	102
% identity	95
NCBI Description	CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR (CAB-165/180) (LHCP) >gi_81603_pir__A29280 chlorophyll a/b-binding protein ab165 - Arabidopsis thaliana >gi_16368_emb_CAA27540_ (X03907) chlorophyll a/b binding protein (LHCP AB 65) [Arabidopsis thaliana] >gi_16372_emb_CAA27541_ (X03908) chlorophyll a/b binding protein (LHCP AB 180) [Arabidopsis thaliana]

Seq. No.	157132
Seq. ID	LIB3176-065-P1-K1-H4
Method	BLASTX
NCBI GI	g2970034
BLAST score	697
E value	9.0e-74
Match length	127
% identity	98
NCBI Description	(D88536) delta 9 desaturase [Arabidopsis thaliana]

Seq. No.	157133
Seq. ID	LIB3176-065-P1-K1-H6
Method	BLASTX
NCBI GI	g2586083
BLAST score	66
E value	4.8e+00
Match length	95
% identity	7
NCBI Description	(U72725) receptor kinase-like protein [Oryza longistaminata]

Seq. No.	157134
Seq. ID	LIB3176-065-P1-K1-H7
Method	BLASTX
NCBI GI	g4432855
BLAST score	467
E value	8.0e-47
Match length	96
% identity	100
NCBI Description	(AC006300) unknown protein [Arabidopsis thaliana]

Seq. No.	157135
Seq. ID	LIB3176-066-P1-K1-A1
Method	BLASTX
NCBI GI	g4581156
BLAST score	677
E value	2.0e-71
Match length	148
% identity	93
NCBI Description	(AC006919) putative pyruvate kinase [Arabidopsis thaliana]

Seq. No.	157136
Seq. ID	LIB3176-066-P1-K1-A2
Method	BLASTX
NCBI GI	g113026
BLAST score	598
E value	4.0e-62
Match length	128
% identity	89
NCBI Description	ISOCITRATE LYASE (ISOCITRASE) (ISOCITRATASE) (ICL) >gi_68211_pir__WZRPI isocitrate lyase (EC 4.1.3.1) - rape >gi_255220_bbs_112862 isocitrate lyase, threo-D S-isocitrate glyoxylate-lyase, IL {EC 4.1.3.1} [Brassica napus, seedlings, Peptide, 576 aa] >gi_167144 (L08482) isocitrate lyase [Brassica napus] >gi_447142_prf__1913424A isocitrate lyase [Brassica napus]

Seq. No.	157137
Seq. ID	LIB3176-066-P1-K1-A3
Method	BLASTX
NCBI GI	g1084350
BLAST score	617
E value	2.0e-64
Match length	124
% identity	91
NCBI Description	glutamate--ammonia ligase (EC 6.3.1.2) - rape >gi_599656_emb_CAA58118.1_ (X82997) glutamate--ammonia ligase [Brassica napus]

Seq. No.	157138
Seq. ID	LIB3176-066-P1-K1-A4
Method	BLASTN
NCBI GI	g2829274
BLAST score	75
E value	5.0e-34
Match length	215
% identity	84
NCBI Description	Arabidopsis thaliana nucleoside diphosphate kinase 3 (ndpk3) mRNA, complete cds

Seq. No.	157139
Seq. ID	LIB3176-066-P1-K1-A6
Method	BLASTX
NCBI GI	g4502315
BLAST score	173
E value	2.0e-12
Match length	116

% identity	33
NCBI Description	ATPase, H+ transporting, lysosomal (vacuolar proton pump) 42kD >gi_401329_sp_P21283_VATC_HUMAN VACUOLAR ATP SYNTHASE SUBUNIT C (V-ATPASE C SUBUNIT) >gi_542836_pir__JN0907 H+-transporting ATPase (EC 3.6.1.35) chain C, vacuolar - human >gi_37643_emb_CAA48903_ (X69151) vacuolar proton-ATPase [Homo sapiens]

Seq. No.	157140
Seq. ID	LIB3176-066-P1-K1-B1
Method	BLASTX
NCBI GI	g4103635
BLAST score	145
E value	5.0e-09
Match length	80
% identity	41
NCBI Description	(AF026538) ABA-responsive protein [Hordeum vulgare]

Seq. No.	157141
Seq. ID	LIB3176-066-P1-K1-B2
Method	BLASTN
NCBI GI	g4263694
BLAST score	203
E value	1.0e-110
Match length	227
% identity	97
NCBI Description	Arabidopsis thaliana chromosome II BAC F22D22 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	157142
Seq. ID	LIB3176-066-P1-K1-B6
Method	BLASTN
NCBI GI	g1532162
BLAST score	203
E value	1.0e-110
Match length	301
% identity	46
NCBI Description	Arabidopsis thaliana AT.I.24-1, AT.I.24-2, AT.I.24-3, AT.I.24-4, AT.I.24-5, AT.I.24-6, AT.I.24-9 and AT.I.24-14 genes, partial cds, AT.I.24-7, ascorbate peroxidase (ATHAPX1), EF-1alpha-A1, -A2 and -A3 (EF-1alpha) and AT.I

Seq. No.	157143
Seq. ID	LIB3176-066-P1-K1-B9
Method	BLASTN
NCBI GI	g16472
BLAST score	163
E value	1.0e-86
Match length	238
% identity	92
NCBI Description	A.thaliana rRNA repeat unit, most frequent IGR type

Seq. No.	157144
Seq. ID	LIB3176-066-P1-K1-C1
Method	BLASTX
NCBI GI	g1480347
BLAST score	365

E value	8.0e-35
Match length	122
% identity	59
NCBI Description	(X99419) ferrodoxin NADP oxidoreductase [Pisum sativum]

Seq. No.	157145
Seq. ID	LIB3176-066-P1-K1-C3
Method	BLASTX
NCBI GI	g4582468
BLAST score	584
E value	1.0e-60
Match length	128
% identity	94
NCBI Description	(AC007071) putative 40S ribosomal protein; contains C-terminal domain [Arabidopsis thaliana]

Seq. No.	157146
Seq. ID	LIB3176-066-P1-K1-C4
Method	BLASTN
NCBI GI	g3319339
BLAST score	57
E value	3.0e-23
Match length	69
% identity	96
NCBI Description	Arabidopsis thaliana BAC F9D12

Seq. No.	157147
Seq. ID	LIB3176-066-P1-K1-C5
Method	BLASTX
NCBI GI	g2829897
BLAST score	243
E value	1.0e-20
Match length	90
% identity	62
NCBI Description	(AC002311) Unknown protein [Arabidopsis thaliana]

Seq. No.	157148
Seq. ID	LIB3176-066-P1-K1-C6
Method	BLASTX
NCBI GI	g1169278
BLAST score	293
E value	2.0e-26
Match length	75
% identity	81
NCBI Description	DEHYDRIN ERD14 >gi_556474_dbj_BAA04569_ (D17715) ERD14 protein [Arabidopsis thaliana]

Seq. No.	157149
Seq. ID	LIB3176-066-P1-K1-C8
Method	BLASTN
NCBI GI	g2459406
BLAST score	65
E value	3.0e-28
Match length	189
% identity	84
NCBI Description	Arabidopsis thaliana chromosome II BAC F4P9 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	157150
Seq. ID	LIB3176-066-P1-K1-D1
Method	BLASTX
NCBI GI	g1168749
BLAST score	290
E value	4.0e-26
Match length	112
% identity	33
NCBI Description	CALMODULIN-6 >gi_1076298_pir__S35187 calmodulin 6 - Arabidopsis thaliana >gi_16227_emb_CAA78059_ (Z12024) calmodulin [Arabidopsis thaliana]

Seq. No.	157151
Seq. ID	LIB3176-066-P1-K1-D3
Method	BLASTN
NCBI GI	g3426033
BLAST score	110
E value	6.0e-55
Match length	225
% identity	94
NCBI Description	Arabidopsis thaliana chromosome II BAC F12C20 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	157152
Seq. ID	LIB3176-066-P1-K1-D4
Method	BLASTX
NCBI GI	g2995990
BLAST score	525
E value	1.0e-53
Match length	121
% identity	84
NCBI Description	(AF053746) dormancy-associated protein [Arabidopsis thaliana] >gi_2995992 (AF053747) dormancy-associated protein [Arabidopsis thaliana]

Seq. No.	157153
Seq. ID	LIB3176-066-P1-K1-D5
Method	BLASTN
NCBI GI	g1483217
BLAST score	315
E value	1.0e-177
Match length	418
% identity	98
NCBI Description	A.thaliana gene induced upon wounding stress

Seq. No.	157154
Seq. ID	LIB3176-066-P1-K1-D6
Method	BLASTN
NCBI GI	g4056476
BLAST score	107
E value	4.0e-53
Match length	286
% identity	86
NCBI Description	Arabidopsis thaliana chromosome II BAC F3G5 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	157155
Seq. ID	LIB3176-066-P1-K1-D8
Method	BLASTN
NCBI GI	g4056476
BLAST score	78
E value	1.0e-35
Match length	186
% identity	85
NCBI Description	Arabidopsis thaliana chromosome II BAC F3G5 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	157156
Seq. ID	LIB3176-066-P1-K1-E1
Method	BLASTX
NCBI GI	g2129583
BLAST score	578
E value	8.0e-60
Match length	132
% identity	88
NCBI Description	ferritin - Arabidopsis thaliana >gi_1246401_emb_CAA63932_ (X94248) ferritin [Arabidopsis thaliana]

Seq. No.	157157
Seq. ID	LIB3176-066-P1-K1-E10
Method	BLASTX
NCBI GI	g4759160
BLAST score	332
E value	6.0e-31
Match length	115
% identity	53
NCBI Description	small nuclear ribonucleoprotein D3 polypeptide (18kD) >gi_1173456_sp_P43331_SMD3_HUMAN SMALL NUCLEAR RIBONUCLEOPROTEIN SM D3 (SNRNP CORE PROTEIN D3) (SM-D3) >gi_600750 (U15009) Sm D3 [Homo sapiens]

Seq. No.	157158
Seq. ID	LIB3176-066-P1-K1-E3
Method	BLASTX
NCBI GI	g1363489
BLAST score	637
E value	1.0e-66
Match length	133
% identity	89
NCBI Description	thioglucosidase (EC 3.2.3.1) 3D precursor - Arabidopsis thaliana >gi_984052_emb_CAA61592_ (X89413) thioglucoside glucohydrolase [Arabidopsis thaliana]

Seq. No.	157159
Seq. ID	LIB3176-066-P1-K1-E4
Method	BLASTX
NCBI GI	g3402487
BLAST score	179
E value	3.0e-13
Match length	70
% identity	56
NCBI Description	(AB015138) Vacuolar proton pyrophosphatase [Arabidopsis thaliana]

Seq. No.	157160
Seq. ID	LIB3176-066-P1-K1-E5
Method	BLASTN
NCBI GI	g1531761
BLAST score	46
E value	1.0e-16
Match length	94
% identity	87
NCBI Description	A.thaliana gene encoding S-adenosylmethionine decarboxylase

Seq. No.	157161
Seq. ID	LIB3176-066-P1-K1-E6
Method	BLASTN
NCBI GI	g4757397
BLAST score	43
E value	3.0e-15
Match length	99
% identity	86
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MBG14, complete sequence

Seq. No.	157162
Seq. ID	LIB3176-066-P1-K1-E7
Method	BLASTX
NCBI GI	g120667
BLAST score	466
E value	9.0e-47
Match length	111
% identity	83
NCBI Description	GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE, CYTOSOLIC >gi_81622_pir__JQ1287 glyceraldehyde-3-phosphate dehydrogenase (EC 1.2.1.12), cytosolic - Arabidopsis thaliana >gi_166706 (M64116) cystolic glyceraldehyde-3-phosphate dehydrogenase [Arabidopsis thaliana] >gi_166710 (M64119) glyceraldehyde-3-phosphate dehydrogenase [Arabidopsis thaliana]

Seq. No.	157163
Seq. ID	LIB3176-066-P1-K1-F1
Method	BLASTN
NCBI GI	g2182286
BLAST score	104
E value	2.0e-51
Match length	258
% identity	98
NCBI Description	Sequence of BAC F20P5 from Arabidopsis thaliana chromosome 1, complete sequence [Arabidopsis thaliana]

Seq. No.	157164
Seq. ID	LIB3176-066-P1-K1-F2
Method	BLASTX
NCBI GI	g3617741
BLAST score	597
E value	4.0e-62
Match length	133
% identity	90

NCBI Description	(AC005687) L3 cytoplasmic ribosomal protein [Arabidopsis thaliana]
Seq. No.	157165
Seq. ID	LIB3176-066-P1-K1-F3
Method	BLASTX
NCBI GI	g113026
BLAST score	183
E value	9.0e-14
Match length	93
% identity	42
NCBI Description	ISOCITRATE LYASE (ISOCITRASE) (ISOCITRATASE) (ICL) >gi_68211_pir__WZRPI isocitrate lyase (EC 4.1.3.1) - rape >gi_255220_bbs_112862 isocitrate lyase, threo-D S-isocitrate glyoxylate-lyase, IL (EC 4.1.3.1) [Brassica napus, seedlings, Peptide, 576 aa] >gi_167144 (L08482) isocitrate lyase [Brassica napus] >gi_447142_prf__1913424A isocitrate lyase [Brassica napus]
Seq. No.	157166
Seq. ID	LIB3176-066-P1-K1-F4
Method	BLASTX
NCBI GI	g3021270
BLAST score	214
E value	4.0e-17
Match length	121
% identity	40
NCBI Description	(AL022347) serine/threonine kinase -like protein [Arabidopsis thaliana]
Seq. No.	157167
Seq. ID	LIB3176-066-P1-K1-F6
Method	BLASTN
NCBI GI	g4539448
BLAST score	135
E value	8.0e-70
Match length	362
% identity	95
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone T5C23 (ESSA project)
Seq. No.	157168
Seq. ID	LIB3176-066-P1-K1-F7
Method	BLASTX
NCBI GI	g3402722
BLAST score	568
E value	1.0e-58
Match length	137
% identity	84
NCBI Description	(AC004261) CPDK-related protein [Arabidopsis thaliana]
Seq. No.	157169
Seq. ID	LIB3176-066-P1-K1-F8
Method	BLASTX
NCBI GI	g625977
BLAST score	547
E value	3.0e-56

Match length	112
% identity	94
NCBI Description	p40 protein homolog - Arabidopsis thaliana >gi_402904 (U01955) laminin receptor-like protein [Arabidopsis thaliana]

Seq. No.	157170
Seq. ID	LIB3176-066-P1-K1-G1
Method	BLASTN
NCBI GI	g4056476
BLAST score	56
E value	1.0e-22
Match length	96
% identity	90
NCBI Description	Arabidopsis thaliana chromosome II BAC F3G5 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	157171
Seq. ID	LIB3176-066-P1-K1-G10
Method	BLASTN
NCBI GI	g4589434
BLAST score	101
E value	1.0e-49
Match length	263
% identity	92
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MNJ7, complete sequence

Seq. No.	157172
Seq. ID	LIB3176-066-P1-K1-G2
Method	BLASTX
NCBI GI	g1705677
BLAST score	48
E value	2.0e-11
Match length	68
% identity	27
NCBI Description	CELL DIVISION CYCLE PROTEIN 48 HOMOLOG >gi_2118115_pir__S60112 cell division control protein CDC48 homolog - Arabidopsis thaliana >gi_1019904 (U37587) cell division cycle protein [Arabidopsis thaliana]

Seq. No.	157173
Seq. ID	LIB3176-066-P1-K1-G3
Method	BLASTX
NCBI GI	g4056502
BLAST score	639
E value	5.0e-67
Match length	136
% identity	93
NCBI Description	(AC005896) 40S ribosomal protein S5 [Arabidopsis thaliana]

Seq. No.	157174
Seq. ID	LIB3176-066-P1-K1-G4
Method	BLASTX
NCBI GI	g4314378
BLAST score	402
E value	3.0e-39

Match length	131
% identity	62
NCBI Description	(AC006232) putative lipase [Arabidopsis thaliana]

Seq. No.	157175
Seq. ID	LIB3176-066-P1-K1-G6
Method	BLASTN
NCBI GI	g3450888
BLAST score	110
E value	7.0e-55
Match length	222
% identity	96
NCBI Description	Arabidopsis thaliana 19S proteosome subunit 9 mRNA, complete cds

Seq. No.	157176
Seq. ID	LIB3176-066-P1-K1-H1
Method	BLASTX
NCBI GI	g4185509
BLAST score	564
E value	3.0e-58
Match length	113
% identity	96
NCBI Description	(AF102821) actin depolymerizing factor 3 [Arabidopsis thaliana]

Seq. No.	157177
Seq. ID	LIB3176-066-P1-K1-H2
Method	BLASTX
NCBI GI	g2738248
BLAST score	374
E value	6.0e-48
Match length	131
% identity	83
NCBI Description	(U97200) cobalamin-independent methionine synthase [Arabidopsis thaliana]

Seq. No.	157178
Seq. ID	LIB3176-066-P1-K1-H5
Method	BLASTX
NCBI GI	g4337027
BLAST score	417
E value	4.0e-41
Match length	112
% identity	78
NCBI Description	(AF123254) MFP2 [Arabidopsis thaliana]

Seq. No.	157179
Seq. ID	LIB3176-066-P1-K1-H9
Method	BLASTN
NCBI GI	g2765243
BLAST score	130
E value	6.0e-67
Match length	174
% identity	94
NCBI Description	Arabidopsis thaliana mRNA for invertase inhibitor homolog

Seq. No.	157180
Seq. ID	LIB3176-067-P1-K1-A10
Method	BLASTX
NCBI GI	g3297824
BLAST score	268
E value	2.0e-23
Match length	55
% identity	100
NCBI Description	(AL031032) bZIP transcription factor-like protein [Arabidopsis thaliana]

Seq. No.	157181
Seq. ID	LIB3176-067-P1-K1-A11
Method	BLASTN
NCBI GI	g4521999
BLAST score	128
E value	2.0e-65
Match length	203
% identity	90
NCBI Description	Arabidopsis thaliana chromosome II BAC F2G1 genomic sequence, complete sequence

Seq. No.	157182
Seq. ID	LIB3176-067-P1-K1-A2
Method	BLASTX
NCBI GI	g1545805
BLAST score	171
E value	4.0e-12
Match length	120
% identity	44
NCBI Description	(D64052) cytochrome P450 like_TBP [Nicotiana tabacum]

Seq. No.	157183
Seq. ID	LIB3176-067-P1-K1-A3
Method	BLASTX
NCBI GI	g2492860
BLAST score	640
E value	4.0e-67
Match length	133
% identity	95
NCBI Description	GLUTAMATE-1-SEMIALDEHYDE 2,1-AMINOMUTASE 2 PRECURSOR (GSA 2) (GLUTAMATE-1-SEMIALDEHYDE AMINOTRANSFERASE 2) (GSA-AT 2) >gi_498914 (U10278) glutamate-1-semialdehyde aminotransferase [Arabidopsis thaliana]

Seq. No.	157184
Seq. ID	LIB3176-067-P1-K1-A4
Method	BLASTN
NCBI GI	g2477521
BLAST score	428
E value	0.0e+00
Match length	456
% identity	98
NCBI Description	Arabidopsis thaliana chromosome I BAC F22K20 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No. 157185

Seq. ID	LIB3176-067-P1-K1-A7
Method	BLASTX
NCBI GI	g1402918
BLAST score	474
E value	9.0e-48
Match length	96
% identity	92
NCBI Description	(X98320) peroxidase [Arabidopsis thaliana] >gi_1429215_emb_CAA67310_ (X98774) peroxidase ATP6a [Arabidopsis thaliana]

Seq. No.	157186
Seq. ID	LIB3176-067-P1-K1-A8
Method	BLASTX
NCBI GI	g3122232
BLAST score	196
E value	4.0e-15
Match length	100
% identity	51
NCBI Description	MITOCHONDRIAL HEAT SHOCK 22 KD PROTEIN PRECURSOR >gi_1669866 (U72958) AtHSP23.6-mito [Arabidopsis thaliana] >gi_4454008_emb_CAA23061_ (AL035396) Arabidopsis mitochondrion-localized small heat shock protein (AtHSP23.6-mito) [Arabidopsis thaliana]

Seq. No.	157187
Seq. ID	LIB3176-067-P1-K1-A9
Method	BLASTX
NCBI GI	g2895510
BLAST score	49
E value	8.0e-17
Match length	70
% identity	67
NCBI Description	(AF033204) putative pectin methylesterase [Arabidopsis thaliana]

Seq. No.	157188
Seq. ID	LIB3176-067-P1-K1-B11
Method	BLASTN
NCBI GI	g2443750
BLAST score	40
E value	3.0e-13
Match length	58
% identity	91
NCBI Description	Arabidopsis thaliana fumarase (FUM1) gene, complete cds

Seq. No.	157189
Seq. ID	LIB3176-067-P1-K1-B12
Method	BLASTN
NCBI GI	g3746057
BLAST score	241
E value	1.0e-133
Match length	336
% identity	94
NCBI Description	Arabidopsis thaliana chromosome II BAC T16B12 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	157190
Seq. ID	LIB3176-067-P1-K1-B2
Method	BLASTX
NCBI GI	g3785989
BLAST score	539
E value	3.0e-55
Match length	114
% identity	89
NCBI Description	(AC005560) unknown protein [Arabidopsis thaliana]

Seq. No.	157191
Seq. ID	LIB3176-067-P1-K1-B4
Method	BLASTX
NCBI GI	g1498629
BLAST score	742
E value	5.0e-79
Match length	146
% identity	99
NCBI Description	(U66223) p40 protein homolog [Arabidopsis thaliana]

Seq. No.	157192
Seq. ID	LIB3176-067-P1-K1-B5
Method	BLASTX
NCBI GI	g3096935
BLAST score	42
E value	4.0e-14
Match length	146
% identity	35
NCBI Description	(AL023094) putative protein [Arabidopsis thaliana]

Seq. No.	157193
Seq. ID	LIB3176-067-P1-K1-B6
Method	BLASTN
NCBI GI	g3046848
BLAST score	207
E value	1.0e-113
Match length	267
% identity	96
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K18C1, complete sequence [Arabidopsis thaliana]

Seq. No.	157194
Seq. ID	LIB3176-067-P1-K1-B7
Method	BLASTX
NCBI GI	g3121825
BLAST score	310
E value	3.0e-28
Match length	61
% identity	95
NCBI Description	2-CYS PEROXIREDOXIN BAS1 PRECURSOR (THIOL-SPECIFIC ANTIOXIDANT PROTEIN) >gi_1498247_emb_CAA63910_ (X94219) bas1 protein [Spinacia oleracea]

Seq. No.	157195
Seq. ID	LIB3176-067-P1-K1-B8
Method	BLASTX
NCBI GI	g4115377

BLAST score	367
E value	4.0e-35
Match length	133
% identity	50
NCBI Description	(AC005967) unknown protein [Arabidopsis thaliana]

Seq. No.	157196
Seq. ID	LIB3176-067-P1-K1-B9
Method	BLASTX
NCBI GI	g3273743
BLAST score	595
E value	9.0e-62
Match length	118
% identity	97
NCBI Description	(AF057357) lipid transfer protein 2 precursor [Arabidopsis thaliana] >gi_3786019 (AC005499) unknown protein [Arabidopsis thaliana]

Seq. No.	157197
Seq. ID	LIB3176-067-P1-K1-C1
Method	BLASTX
NCBI GI	g2191182
BLAST score	194
E value	9.0e-15
Match length	140
% identity	11
NCBI Description	(AF007271) similar to N. tabacum membrane-associated salt-inducible protein (PID:g473874) [Arabidopsis thaliana]

Seq. No.	157198
Seq. ID	LIB3176-067-P1-K1-C10
Method	BLASTX
NCBI GI	g4704613
BLAST score	352
E value	1.0e-33
Match length	94
% identity	76
NCBI Description	(AF109695) monodehydroascorbate reductase [Brassica juncea]

Seq. No.	157199
Seq. ID	LIB3176-067-P1-K1-C12
Method	BLASTX
NCBI GI	g4406816
BLAST score	68
E value	2.0e-38
Match length	91
% identity	93
NCBI Description	(AC006201) 60S ribosomal protein L2 [Arabidopsis thaliana]

Seq. No.	157200
Seq. ID	LIB3176-067-P1-K1-C3
Method	BLASTX
NCBI GI	g4538939
BLAST score	514
E value	2.0e-52
Match length	126
% identity	80

NCBI Description	(AL049483) Col-0 casein kinase I-like protein [Arabidopsis thaliana]

Seq. No.	157201
Seq. ID	LIB3176-067-P1-K1-C5
Method	BLASTX
NCBI GI	g4406816
BLAST score	725
E value	4.0e-77
Match length	143
% identity	97
NCBI Description	(AC006201) 60S ribosomal protein L2 [Arabidopsis thaliana]

Seq. No.	157202
Seq. ID	LIB3176-067-P1-K1-C6
Method	BLASTX
NCBI GI	g3318617
BLAST score	550
E value	1.0e-56
Match length	123
% identity	85
NCBI Description	(AB016066) mitochondrial phosphate transporter [Arabidopsis thaliana]

Seq. No.	157203
Seq. ID	LIB3176-067-P1-K1-C8
Method	BLASTN
NCBI GI	g4314374
BLAST score	389
E value	0.0e+00
Match length	440
% identity	97
NCBI Description	Arabidopsis thaliana chromosome II BAC F10A12 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	157204
Seq. ID	LIB3176-067-P1-K1-C9
Method	BLASTX
NCBI GI	g4586050
BLAST score	258
E value	2.0e-22
Match length	51
% identity	96
NCBI Description	(AC007020) unknown protein [Arabidopsis thaliana] >gi_4588009_gb_AAD25950.1_AF085279_23 (AF085279) hypothetical protein [Arabidopsis thaliana]

Seq. No.	157205
Seq. ID	LIB3176-067-P1-K1-D1
Method	BLASTX
NCBI GI	g2342687
BLAST score	219
E value	9.0e-18
Match length	82
% identity	54
NCBI Description	(AC000106) Similar to Beta integral membrane protein (gb_U43629). EST gb_W43122 comes from this gene.

[Arabidopsis thaliana]

Seq. No.	157206
Seq. ID	LIB3176-067-P1-K1-D10
Method	BLASTX
NCBI GI	g549056
BLAST score	283
E value	3.0e-25
Match length	82
% identity	70
NCBI Description	T-COMPLEX PROTEIN 1, BETA SUBUNIT (TCP-1-BETA) (CCT-BETA) >gi_631651_pir__S43059 CCT (chaperonin containing TCP-1) beta chain - mouse >gi_468546_emb_CAA83428_ (Z31553) CCT (chaperonin containing TCP-1) beta subunit [Mus musculus]

Seq. No.	157207
Seq. ID	LIB3176-067-P1-K1-D11
Method	BLASTX
NCBI GI	g2499542
BLAST score	638
E value	8.0e-67
Match length	139
% identity	85
NCBI Description	IRON(III)-ZINC(II) PURPLE ACID PHOSPHATASE PRECURSOR (PAP) >gi_1218042 (U48448) secreted purple acid phosphatase precursor [Arabidopsis thaliana]

Seq. No.	157208
Seq. ID	LIB3176-067-P1-K1-D12
Method	BLASTN
NCBI GI	g2914688
BLAST score	113
E value	9.0e-57
Match length	189
% identity	71
NCBI Description	Arabidopsis thaliana chromosome II BAC F24L7 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	157209
Seq. ID	LIB3176-067-P1-K1-D2
Method	BLASTX
NCBI GI	g1652105
BLAST score	191
E value	2.0e-14
Match length	76
% identity	50
NCBI Description	(D90902) hypothetical protein [Synechocystis sp.]

Seq. No.	157210
Seq. ID	LIB3176-067-P1-K1-D4
Method	BLASTX
NCBI GI	g2440029
BLAST score	182
E value	3.0e-13
Match length	71
% identity	54
NCBI Description	(Y14851) DAL1 protein [Arabidopsis thaliana]

>gi_2440031_emb_CAA75115_ (Y14850) DAL1 protein [Arabidopsis thaliana]

Seq. No.	157211
Seq. ID	LIB3176-067-P1-K1-D5
Method	BLASTN
NCBI GI	g3510336
BLAST score	417
E value	0.0e+00
Match length	449
% identity	98
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K18J17, complete sequence [Arabidopsis thaliana]

Seq. No.	157212
Seq. ID	LIB3176-067-P1-K1-D6
Method	BLASTX
NCBI GI	g499301
BLAST score	192
E value	2.0e-14
Match length	35
% identity	100
NCBI Description	(X77116) ABI1 [Arabidopsis thaliana] >gi_549981 (U12856) abscisic acid insensitive protein [Arabidopsis thaliana] >gi_4538937_emb_CAB39673.1_ (AL049483) protein phosphatase ABI1 [Arabidopsis thaliana]

Seq. No.	157213
Seq. ID	LIB3176-067-P1-K1-D7
Method	BLASTN
NCBI GI	g3928074
BLAST score	129
E value	3.0e-66
Match length	376
% identity	92
NCBI Description	Arabidopsis thaliana chromosome II BAC T7F6 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	157214
Seq. ID	LIB3176-067-P1-K1-D8
Method	BLASTX
NCBI GI	g2245136
BLAST score	375
E value	3.0e-36
Match length	98
% identity	68
NCBI Description	(Z97344) trehalose-6-phosphate synthase homolog [Arabidopsis thaliana]

Seq. No.	157215
Seq. ID	LIB3176-067-P1-K1-D9
Method	BLASTN
NCBI GI	g3985957
BLAST score	175
E value	8.0e-94
Match length	232
% identity	94

NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MYN8, complete sequence [Arabidopsis thaliana]
Seq. No.	157216
Seq. ID	LIB3176-067-P1-K1-E1
Method	BLASTX
NCBI GI	g1363489
BLAST score	696
E value	1.0e-73
Match length	144
% identity	90
NCBI Description	thioglucosidase (EC 3.2.3.1) 3D precursor - Arabidopsis thaliana >gi_984052_emb_CAA61592_ (X89413) thioglucoside glucohydrolase [Arabidopsis thaliana]
Seq. No.	157217
Seq. ID	LIB3176-067-P1-K1-E10
Method	BLASTX
NCBI GI	g399013
BLAST score	131
E value	2.0e-62
Match length	151
% identity	72
NCBI Description	ADP,ATP CARRIER PROTEIN 1 PRECURSOR (ADP/ATP TRANSLOCASE 1) (ADENINE NUCLEOTIDE TRANSLOCATOR 1) (ANT 1) >gi_99658_pir__S21313 ADP,ATP carrier protein - Arabidopsis thaliana (fragment) >gi_16175_emb_CAA46518_ (X65549) adenylate translocator [Arabidopsis thaliana] >gi_445607_prf__1909354A adenylate translocator [Arabidopsis thaliana]
Seq. No.	157218
Seq. ID	LIB3176-067-P1-K1-E11
Method	BLASTX
NCBI GI	g115767
BLAST score	516
E value	4.0e-54
Match length	120
% identity	93
NCBI Description	CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR (CAB-165/180) (LHCP) >gi_81603_pir__A29280 chlorophyll a/b-binding protein ab165 - Arabidopsis thaliana >gi_16368_emb_CAA27540_ (X03907) chlorophyll a/b binding protein (LHCP AB 65) [Arabidopsis thaliana] >gi_16372_emb_CAA27541_ (X03908) chlorophyll a/b binding protein (LHCP AB 180) [Arabidopsis thaliana]
Seq. No.	157219
Seq. ID	LIB3176-067-P1-K1-E12
Method	BLASTX
NCBI GI	g1769907
BLAST score	802
E value	4.0e-86
Match length	151
% identity	98
NCBI Description	(X92975) xyloglucan endo-transglycosylase [Arabidopsis thaliana]

Seq. No.	157220
Seq. ID	LIB3176-067-P1-K1-E2
Method	BLASTX
NCBI GI	g1702872
BLAST score	672
E value	7.0e-71
Match length	142
% identity	94
NCBI Description	(Y09667) ferredoxin-dependent glutamate synthase [Arabidopsis thaliana]

Seq. No.	157221
Seq. ID	LIB3176-067-P1-K1-E3
Method	BLASTX
NCBI GI	g115587
BLAST score	94
E value	5.0e-71
Match length	148
% identity	86
NCBI Description	PHOSPHOENOLPYRUVATE CARBOXYLASE 1 (PEPCASE) (CP21) >gi_418801_pir__S31159 phosphoenolpyruvate carboxylase (EC 4.1.1.31) CP21 - sorghum >gi_21630_emb_CAA39197_ (X55664) phosphoenolpyruvate carboxylase [Sorghum bicolor] >gi_22615_emb_CAA46267_ (X65137) phosphoenolpyruvate carboxylase [Sorghum bicolor]

Seq. No.	157222
Seq. ID	LIB3176-067-P1-K1-E4
Method	BLASTX
NCBI GI	g1710840
BLAST score	673
E value	5.0e-71
Match length	135
% identity	93
NCBI Description	ADENOSYLHOMOCYSTEINASE (S-ADENOSYL-L-HOMOCYSTEINE HYDROLASE) (ADOHCYASE) (CYTOKININ BINDING PROTEIN CBP57) >gi_441217_dbj_BAA03709_ (D16138) S-adenosyl-L-homocystein hydrolase [Nicotiana sylvestris] >gi_1857024_dbj_BAA08142_ (D45204) S-adenosyl-L-homocysteine hydrolase [Nicotiana tabacum] >gi_2588781_dbj_BAA23164_ (D49804) S-adenosyl-L-homocysteine hydrolase [Nicotiana tabacum]

Seq. No.	157223
Seq. ID	LIB3176-067-P1-K1-E5
Method	BLASTX
NCBI GI	g2497539
BLAST score	648
E value	5.0e-68
Match length	144
% identity	85
NCBI Description	PYRUVATE KINASE, CHLOROPLAST ISOZYME A PRECURSOR >gi_169703 (M64736) ATP:pyruvate phosphotransferase [Ricinus communis]

Seq. No.	157224
Seq. ID	LIB3176-067-P1-K1-E6
Method	BLASTX

NCBI GI	g4415907
BLAST score	550
E value	2.0e-56
Match length	108
% identity	99
NCBI Description	(AC006282) 60S ribosomal protein L24 [Arabidopsis thaliana] >gi_4581159_gb_AAD24643.1_AC006919_21 (AC006919) putative 60S ribosomal protein L24 [Arabidopsis thaliana]

Seq. No.	157225
Seq. ID	LIB3176-067-P1-K1-F1
Method	BLASTX
NCBI GI	g3355617
BLAST score	371
E value	2.0e-35
Match length	86
% identity	77
NCBI Description	(AJ000229) unnamed protein product [Hordeum vulgare]

Seq. No.	157226
Seq. ID	LIB3176-067-P1-K1-F11
Method	BLASTN
NCBI GI	g2264315
BLAST score	280
E value	1.0e-156
Match length	292
% identity	99
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MRN17, complete sequence [Arabidopsis thaliana]

Seq. No.	157227
Seq. ID	LIB3176-067-P1-K1-F12
Method	BLASTX
NCBI GI	g3335355
BLAST score	75
E value	1.0e-10
Match length	47
% identity	28
NCBI Description	(AC004512) Match to polyubiquitin DNA gb_L05401 from A. thaliana. Contains insertion of mitochondrial NADH dehydrogenase gb_X82618 and gb_X98301. May be a pseudogene with an expressed insert. EST gb_AA586248 comes from this region. [Arabi

Seq. No.	157228
Seq. ID	LIB3176-067-P1-K1-F4
Method	BLASTX
NCBI GI	g462650
BLAST score	800
E value	8.0e-86
Match length	155
% identity	98
NCBI Description	DNA (CYTOSINE-5)-METHYLTRANSFERASE (DNA METHYLTRANSFERASE) (DNA METASE) >gi_1363480_pir__S59604 DNA (cytosine-5-)-methyltransferase (EC 2.1.1.37) - Arabidopsis thaliana >gi_304107 (L10692) cytosine-5 methyltransferase [Arabidopsis thaliana]

Seq. No.	157229
Seq. ID	LIB3176-067-P1-K1-F5
Method	BLASTX
NCBI GI	g3881976
BLAST score	372
E value	2.0e-49
Match length	130
% identity	74
NCBI Description	(AJ012409) hypothetical protein [Homo sapiens]

Seq. No.	157230
Seq. ID	LIB3176-067-P1-K1-F7
Method	BLASTX
NCBI GI	g99696
BLAST score	525
E value	1.0e-53
Match length	131
% identity	81
NCBI Description	glutamate--ammonia ligase (EC 6.3.1.2) precursor, chloroplast (clone lambdaAtgs11) - Arabidopsis thaliana >gi_240070_bbs_69728 (S69727) light-regulated glutamine synthetase isoenzyme [Arabidopsis thaliana, Peptide, 430 aa] [Arabidopsis thaliana] >gi_228453_prf__1804333A Gln synthetase [Arabidopsis thaliana]

Seq. No.	157231
Seq. ID	LIB3176-067-P1-K1-F8
Method	BLASTX
NCBI GI	g4371282
BLAST score	247
E value	6.0e-21
Match length	68
% identity	76
NCBI Description	(AC006260) putative 60S ribosomal protein L12 [Arabidopsis thaliana]

Seq. No.	157232
Seq. ID	LIB3176-067-P1-K1-F9
Method	BLASTX
NCBI GI	g4263712
BLAST score	287
E value	3.0e-33
Match length	87
% identity	87
NCBI Description	(AC006223) putative ribosomal protein S12 [Arabidopsis thaliana]

Seq. No.	157233
Seq. ID	LIB3176-067-P1-K1-G1
Method	BLASTX
NCBI GI	g2160175
BLAST score	626
E value	2.0e-65
Match length	123
% identity	96
NCBI Description	(AC000132) Strong similarity to Dianthus cysteine

proteinase (gb_U17135). [Arabidopsis thaliana]

Seq. No.	157234
Seq. ID	LIB3176-067-P1-K1-G10
Method	BLASTX
NCBI GI	g2146797
BLAST score	61
E value	2.0e-31
Match length	107
% identity	41
NCBI Description	protein disulfide-isomerase (EC 5.3.4.1) - Castor bean >gi_1134968 (U41385) protein disulphide isomerase PDI [Ricinus communis] >gi_1587210_prf__2206331A protein disulfide isomerase [Ricinus communis]

Seq. No.	157235
Seq. ID	LIB3176-067-P1-K1-G11
Method	BLASTX
NCBI GI	g4586256
BLAST score	532
E value	1.0e-54
Match length	111
% identity	95
NCBI Description	(AL049640) probable photosystem I chain XI precursor [Arabidopsis thaliana]

Seq. No.	157236
Seq. ID	LIB3176-067-P1-K1-G2
Method	BLASTN
NCBI GI	g3128142
BLAST score	237
E value	1.0e-130
Match length	360
% identity	92
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MQN23, complete sequence [Arabidopsis thaliana]

Seq. No.	157237
Seq. ID	LIB3176-067-P1-K1-G3
Method	BLASTN
NCBI GI	g2815519
BLAST score	150
E value	1.0e-78
Match length	415
% identity	95
NCBI Description	Arabidopsis thaliana BAC T5J8 from chromosome IV, top arm, complete sequence [Arabidopsis thaliana]

Seq. No.	157238
Seq. ID	LIB3176-067-P1-K1-G5
Method	BLASTX
NCBI GI	g3334140
BLAST score	116
E value	8.0e-06
Match length	104
% identity	53
NCBI Description	CENTROMERE/MICROTUBULE BINDING PROTEIN CBF5

(CENTROMERE-BINDING FACTOR 5) (NUCLEOLAR PROTEIN CBF5)
>gi_2737888 (U59148) nucleolar protein AnCbf5p [Emericella nidulans]

Seq. No.	157239
Seq. ID	LIB3176-067-P1-K1-G6
Method	BLASTN
NCBI GI	g3785992
BLAST score	70
E value	3.0e-31
Match length	250
% identity	64
NCBI Description	Arabidopsis thaliana chromosome II BAC T6A23 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	157240
Seq. ID	LIB3176-067-P1-K1-G7
Method	BLASTN
NCBI GI	g4159709
BLAST score	81
E value	2.0e-37
Match length	197
% identity	86
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MLN21, complete sequence

Seq. No.	157241
Seq. ID	LIB3176-067-P1-K1-H1
Method	BLASTN
NCBI GI	g4580745
BLAST score	188
E value	1.0e-101
Match length	418
% identity	98
NCBI Description	Arabidopsis thaliana chromosome 1 BAC F1003 sequence, complete sequence

Seq. No.	157242
Seq. ID	LIB3176-067-P1-K1-H11
Method	BLASTN
NCBI GI	g4468103
BLAST score	314
E value	1.0e-176
Match length	422
% identity	97
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone M3E9 (ESSA project)

Seq. No.	157243
Seq. ID	LIB3176-067-P1-K1-H12
Method	BLASTX
NCBI GI	g1255951
BLAST score	477
E value	5.0e-48
Match length	107
% identity	80
NCBI Description	(X96932) PS60 [Nicotiana tabacum]

Seq. No.	157244
Seq. ID	LIB3176-067-P1-K1-H2
Method	BLASTX
NCBI GI	g3421096
BLAST score	504
E value	3.0e-51
Match length	118
% identity	88
NCBI Description	(AF043528) 20S proteasome subunit PAG1 [Arabidopsis thaliana] >gi_3885332 (AC005623) proteasome component [Arabidopsis thaliana]

Seq. No.	157245
Seq. ID	LIB3176-067-P1-K1-H3
Method	BLASTN
NCBI GI	g3810584
BLAST score	222
E value	1.0e-121
Match length	347
% identity	95
NCBI Description	Arabidopsis thaliana chromosome II BAC T6B13 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	157246
Seq. ID	LIB3176-067-P1-K1-H4
Method	BLASTX
NCBI GI	g2130028
BLAST score	352
E value	2.0e-33
Match length	86
% identity	73
NCBI Description	B12D protein - barley >gi_471319_emb_CAA54065.1_ (X76604) HvB12D [Hordeum vulgare] >gi_3445292_emb_CAA70936_ (Y09805) B12Dg1 [Hordeum vulgare]

Seq. No.	157247
Seq. ID	LIB3176-067-P1-K1-H5
Method	BLASTX
NCBI GI	g2832625
BLAST score	557
E value	1.0e-57
Match length	110
% identity	98
NCBI Description	(AL021711) putative protein [Arabidopsis thaliana]

Seq. No.	157248
Seq. ID	LIB3176-067-P1-K1-H6
Method	BLASTX
NCBI GI	g1906826
BLAST score	339
E value	2.0e-32
Match length	64
% identity	100
NCBI Description	(Y11827) heat shock protein [Arabidopsis thaliana]

Seq. No.	157249

Seq. ID	LIB3176-067-P1-K1-H8
Method	BLASTX
NCBI GI	g3319349
BLAST score	52
E value	1.0e-64
Match length	137
% identity	91
NCBI Description	(AF077407) No definition line found [Arabidopsis thaliana]

Seq. No.	157250
Seq. ID	LIB3176-067-P1-K1-H9
Method	BLASTN
NCBI GI	g3766106
BLAST score	125
E value	5.0e-64
Match length	263
% identity	96
NCBI Description	Arabidopsis thaliana chromosome 1 BAC F9K20 sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	157251
Seq. ID	LIB3176-068-P1-K1-A10
Method	BLASTX
NCBI GI	g3702352
BLAST score	495
E value	5.0e-50
Match length	97
% identity	100
NCBI Description	(AC005397) putative mitochondrial carrier protein [Arabidopsis thaliana]

Seq. No.	157252
Seq. ID	LIB3176-068-P1-K1-A2
Method	BLASTN
NCBI GI	g2062153
BLAST score	95
E value	2.0e-46
Match length	130
% identity	35
NCBI Description	Arabidopsis thaliana chromosome III BAC T02O04 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	157253
Seq. ID	LIB3176-068-P1-K1-A3
Method	BLASTX
NCBI GI	g4262239
BLAST score	273
E value	5.0e-24
Match length	142
% identity	41
NCBI Description	(AC006200) putative membrane transporter [Arabidopsis thaliana]

Seq. No.	157254
Seq. ID	LIB3176-068-P1-K1-A5
Method	BLASTN
NCBI GI	g4519191

BLAST score	148
E value	8.0e-78
Match length	209
% identity	95
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K9P8, complete sequence

Seq. No.	157255
Seq. ID	LIB3176-068-P1-K1-A8
Method	BLASTN
NCBI GI	g4585890
BLAST score	119
E value	3.0e-60
Match length	257
% identity	91
NCBI Description	Arabidopsis thaliana chromosome II BAC T3G21 genomic sequence, complete sequence

Seq. No.	157256
Seq. ID	LIB3176-068-P1-K1-A9
Method	BLASTN
NCBI GI	g2736154
BLAST score	40
E value	5.0e-13
Match length	152
% identity	83
NCBI Description	Arabidopsis thaliana sulfolipid biosynthesis protein (SQD1) mRNA, complete cds

Seq. No.	157257
Seq. ID	LIB3176-068-P1-K1-B10
Method	BLASTN
NCBI GI	g2656028
BLAST score	49
E value	9.0e-19
Match length	135
% identity	83
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MNF13

Seq. No.	157258
Seq. ID	LIB3176-068-P1-K1-B12
Method	BLASTX
NCBI GI	g3915826
BLAST score	616
E value	3.0e-64
Match length	144
% identity	81
NCBI Description	60S RIBOSOMAL PROTEIN L5

Seq. No.	157259
Seq. ID	LIB3176-068-P1-K1-B2
Method	BLASTX
NCBI GI	g4096693
BLAST score	191
E value	5.0e-21
Match length	105

% identity	57
NCBI Description	(U37235) cinnamate 4-hydroxylase [Arabidopsis thaliana]

Seq. No.	157260
Seq. ID	LIB3176-068-P1-K1-B6
Method	BLASTX
NCBI GI	g1946331
BLAST score	275
E value	2.0e-24
Match length	79
% identity	72
NCBI Description	(U69155) prohibitin [Arabidopsis thaliana] >gi_4097692 (U66593) prohibitin 3 [Arabidopsis thaliana]

Seq. No.	157261
Seq. ID	LIB3176-068-P1-K1-B7
Method	BLASTN
NCBI GI	g16327
BLAST score	290
E value	1.0e-162
Match length	317
% identity	98
NCBI Description	A.thaliana homeobox gene Athb-1 mRNA

Seq. No.	157262
Seq. ID	LIB3176-068-P1-K1-B8
Method	BLASTX
NCBI GI	g2695931
BLAST score	300
E value	3.0e-27
Match length	77
% identity	73
NCBI Description	(AJ222779) hypothetical protein [Hordeum vulgare]

Seq. No.	157263
Seq. ID	LIB3176-068-P1-K1-B9
Method	BLASTX
NCBI GI	g3421123
BLAST score	433
E value	7.0e-43
Match length	111
% identity	80
NCBI Description	(AF043538) 20S proteasome beta subunit PBG1 [Arabidopsis thaliana]

Seq. No.	157264
Seq. ID	LIB3176-068-P1-K1-C1
Method	BLASTX
NCBI GI	g2341028
BLAST score	658
E value	4.0e-69
Match length	129
% identity	98
NCBI Description	(AC000104) Strong similarity to 60S ribosomal protein L17 (gb_X01694). EST gb_AA042332 comes from this gene. [Arabidopsis thaliana]

Seq. No.	157265
Seq. ID	LIB3176-068-P1-K1-C10
Method	BLASTX
NCBI GI	g2854070
BLAST score	361
E value	1.0e-34
Match length	89
% identity	83
NCBI Description	(AF044914) putative histone deacetylase [Arabidopsis thaliana]

Seq. No.	157266
Seq. ID	LIB3176-068-P1-K1-C11
Method	BLASTX
NCBI GI	g1742951
BLAST score	93
E value	3.0e-03
Match length	82
% identity	63
NCBI Description	(Y09817) Ca2+-ATPase [Arabidopsis thaliana]

Seq. No.	157267
Seq. ID	LIB3176-068-P1-K1-C12
Method	BLASTN
NCBI GI	g2351066
BLAST score	40
E value	3.0e-13
Match length	48
% identity	96
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MOP9, complete sequence [Arabidopsis thaliana]

Seq. No.	157268
Seq. ID	LIB3176-068-P1-K1-C2
Method	BLASTX
NCBI GI	g3023848
BLAST score	682
E value	5.0e-72
Match length	142
% identity	51
NCBI Description	GUANINE NUCLEOTIDE-BINDING PROTEIN BETA SUBUNIT-LIKE PROTEIN (WD-40 REPEAT AUXIN-DEPENDENT PROTEIN ARCA) >gi_2289095 (U77381) WD-40 repeat protein [Arabidopsis thaliana]

Seq. No.	157269
Seq. ID	LIB3176-068-P1-K1-C3
Method	BLASTX
NCBI GI	g4741952
BLAST score	675
E value	4.0e-71
Match length	132
% identity	73
NCBI Description	(AF134126) Lhcb3 protein [Arabidopsis thaliana]

Seq. No.	157270
Seq. ID	LIB3176-068-P1-K1-C5

Method	BLASTX
NCBI GI	g126766
BLAST score	759
E value	5.0e-81
Match length	149
% identity	96
NCBI Description	MALATE SYNTHASE, GLYOXYSOMAL >gi_68216_pir__SYRPMA malate synthase (EC 4.1.3.2), glyoxysomal - rape >gi_167150 (J04468) malate synthase (EC 4.1.3.2) [Brassica napus]

Seq. No.	157271
Seq. ID	LIB3176-068-P1-K1-C6
Method	BLASTX
NCBI GI	g113024
BLAST score	487
E value	3.0e-49
Match length	97
% identity	94
NCBI Description	ISOCITRATE LYASE (ISOCITRASE) (ISOCITRATASE) (ICL) >gi_553043 (M83534) isocitrate lyase [Arabidopsis thaliana]

Seq. No.	157272
Seq. ID	LIB3176-068-P1-K1-C7
Method	BLASTN
NCBI GI	g2708736
BLAST score	46
E value	4.0e-17
Match length	66
% identity	92
NCBI Description	Arabidopsis thaliana BAC T13L16 from chromosome II, near 33 cM, complete sequence [Arabidopsis thaliana]

Seq. No.	157273
Seq. ID	LIB3176-068-P1-K1-C8
Method	BLASTN
NCBI GI	g2244829
BLAST score	133
E value	1.0e-68
Match length	171
% identity	94
NCBI Description	Arabidopsis thaliana DNA chromosome 4, ESSA I contig fragment No

Seq. No.	157274
Seq. ID	LIB3176-068-P1-K1-D1
Method	BLASTN
NCBI GI	g1931636
BLAST score	182
E value	8.0e-98
Match length	410
% identity	95
NCBI Description	Arabidopsis thaliana BAC T19D16 genomic sequence

Seq. No.	157275
Seq. ID	LIB3176-068-P1-K1-D11
Method	BLASTN
NCBI GI	g1657620

BLAST score 234
E value 1.0e-129
Match length 269
% identity 97
NCBI Description Arabidopsis thaliana putative acyl-coA dehydrogenase G6p (AtG6) mRNA, complete cds

Seq. No. 157276
Seq. ID LIB3176-068-P1-K1-D12
Method BLASTX
NCBI GI g3212877
BLAST score 642
E value 3.0e-67
Match length 150
% identity 87
NCBI Description (AC004005) Lea-like protein [Arabidopsis thaliana]

Seq. No. 157277
Seq. ID LIB3176-068-P1-K1-D2
Method BLASTX
NCBI GI g4127456
BLAST score 480
E value 2.0e-48
Match length 122
% identity 54
NCBI Description (AJ010818) Cpn21 protein [Arabidopsis thaliana]

Seq. No. 157278
Seq. ID LIB3176-068-P1-K1-D4
Method BLASTN
NCBI GI g4220633
BLAST score 126
E value 1.0e-64
Match length 227
% identity 90
NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K7J8, complete sequence [Arabidopsis thaliana]

Seq. No. 157279
Seq. ID LIB3176-068-P1-K1-D5
Method BLASTX
NCBI GI g135442
BLAST score 623
E value 4.0e-65
Match length 115
% identity 99
NCBI Description TUBULIN BETA-1 CHAIN >gi_71590_pir__UBMUBM tubulin beta-1 chain - Arabidopsis thaliana >gi_166922 (M20405) beta-1 tubulin [Arabidopsis thaliana]

Seq. No. 157280
Seq. ID LIB3176-068-P1-K1-E1
Method BLASTX
NCBI GI g3096931
BLAST score 558
E value 2.0e-57
Match length 113

% identity	96
NCBI Description	(AL023094) putative ribosomal protein S16 [Arabidopsis thaliana]

Seq. No.	157281
Seq. ID	LIB3176-068-P1-K1-E10
Method	BLASTX
NCBI GI	g3785981
BLAST score	504
E value	4.0e-51
Match length	125
% identity	73
NCBI Description	(AC005560) putative major latex protein [Arabidopsis thaliana]

Seq. No.	157282
Seq. ID	LIB3176-068-P1-K1-E12
Method	BLASTX
NCBI GI	g1621268
BLAST score	547
E value	4.0e-56
Match length	127
% identity	78
NCBI Description	(Z81012) unknown [Ricinus communis]

Seq. No.	157283
Seq. ID	LIB3176-068-P1-K1-E2
Method	BLASTN
NCBI GI	g3600062
BLAST score	141
E value	2.0e-73
Match length	434
% identity	15
NCBI Description	Arabidopsis thaliana BAC T25C13

Seq. No.	157284
Seq. ID	LIB3176-068-P1-K1-E3
Method	BLASTX
NCBI GI	g1732570
BLAST score	60
E value	1.0e-64
Match length	139
% identity	87
NCBI Description	(U72153) beta-glucosidase [Arabidopsis thaliana]

Seq. No.	157285
Seq. ID	LIB3176-068-P1-K1-E5
Method	BLASTX
NCBI GI	g4455365
BLAST score	79
E value	3.0e-32
Match length	78
% identity	78
NCBI Description	(AL035524) putative protein [Arabidopsis thaliana]

Seq. No.	157286
Seq. ID	LIB3176-068-P1-K1-E6

Method	BLASTX
NCBI GI	g2062157
BLAST score	92
E value	6.0e-23
Match length	79
% identity	33
NCBI Description	(AC001645) jasmonate inducible protein isolog [Arabidopsis thaliana]

Seq. No.	157287
Seq. ID	LIB3176-068-P1-K1-E8
Method	BLASTX
NCBI GI	g399091
BLAST score	112
E value	4.0e-37
Match length	93
% identity	96
NCBI Description	PYROPHOSPHATE-ENERGIZED VACUOLAR MEMBRANE PROTON PUMP (PYROPHOSPHATE-ENERGIZED INORGANIC PYROPHOSPHATASE) (H+-PPASE) >gi_282878_pir__A38230 inorganic pyrophosphatase (EC 3.6.1.1), H+-translocating pyrophosphate-energized - Arabidopsis thaliana >gi_166634 (M81892) vacuolar H+-phosphatase [Arabidopsis thaliana]

Seq. No.	157288
Seq. ID	LIB3176-068-P1-K1-F1
Method	BLASTN
NCBI GI	g2673901
BLAST score	270
E value	1.0e-150
Match length	301
% identity	98
NCBI Description	Arabidopsis thaliana chromosome II BAC T24P15 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	157289
Seq. ID	LIB3176-068-P1-K1-F10
Method	BLASTX
NCBI GI	g3023848
BLAST score	431
E value	1.0e-42
Match length	94
% identity	49
NCBI Description	GUANINE NUCLEOTIDE-BINDING PROTEIN BETA SUBUNIT-LIKE PROTEIN (WD-40 REPEAT AUXIN-DEPENDENT PROTEIN ARCA) >gi_2289095 (U77381) WD-40 repeat protein [Arabidopsis thaliana]

Seq. No.	157290
Seq. ID	LIB3176-068-P1-K1-F11
Method	BLASTX
NCBI GI	g3157937
BLAST score	713
E value	1.0e-75
Match length	143
% identity	97
NCBI Description	(AC002131) Identical to aspartic proteinase cDNA gb_U51036

from A. thaliana. ESTs gb_N96313, gb_T21893, gb_R30158, gb_T21482, gb_T43650, gb_R64749, gb_R65157, gb_T88269, gb_T44552, gb_T22542, gb_T76533, gb_T44350, gb_Z34591, gb_AA728734, gb

Seq. No.	157291
Seq. ID	LIB3176-068-P1-K1-F12
Method	BLASTN
NCBI GI	g4678258
BLAST score	157
E value	7.0e-83
Match length	472
% identity	99
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F6I7 (ESSA project)

Seq. No.	157292
Seq. ID	LIB3176-068-P1-K1-F2
Method	BLASTX
NCBI GI	g1175011
BLAST score	519
E value	5.0e-53
Match length	99
% identity	98
NCBI Description	PLASMA MEMBRANE INTRINSIC PROTEIN 1B (TRANSMEMBRANE PROTEIN A) (TMP-A) >gi_296085_emb_CAA48356_ (X68293) transmembrane protein [Arabidopsis thaliana] >gi_3386599 (AC004665) plasma membrane intrinsic protein 1B [Arabidopsis thaliana]

Seq. No.	157293
Seq. ID	LIB3176-068-P1-K1-F4
Method	BLASTX
NCBI GI	g1619300
BLAST score	384
E value	4.0e-37
Match length	87
% identity	83
NCBI Description	(X95269) LRR protein [Lycopersicon esculentum]

Seq. No.	157294
Seq. ID	LIB3176-068-P1-K1-F5
Method	BLASTN
NCBI GI	g2121272
BLAST score	115
E value	4.0e-58
Match length	197
% identity	90
NCBI Description	Arabidopsis thaliana dihydroorotase (pyr4) mRNA, complete cds

Seq. No.	157295
Seq. ID	LIB3176-068-P1-K1-F6
Method	BLASTN
NCBI GI	g2924653
BLAST score	53
E value	8.0e-22
Match length	60

% identity	97
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MDA7, complete sequence [Arabidopsis thaliana]
Seq. No.	157296
Seq. ID	LIB3176-068-P1-K1-F8
Method	BLASTN
NCBI GI	g2341023
BLAST score	34
E value	2.0e-10
Match length	46
% identity	93
NCBI Description	Sequence of BAC F19P19 from Arabidopsis thaliana chromosome 1, complete sequence [Arabidopsis thaliana]
Seq. No.	157297
Seq. ID	LIB3176-068-P1-K1-G10
Method	BLASTX
NCBI GI	g3334404
BLAST score	738
E value	1.0e-78
Match length	146
% identity	97
NCBI Description	VACUOLAR ATP SYNTHASE CATALYTIC SUBUNIT A (V-ATPASE 69 KD SUBUNIT) >gi_2266990 (U65638) vacuolar type ATPase subunit A [Arabidopsis thaliana] >gi_3834305 (AC005679) Identical to gb_U65638 Arabidopsis thaliana vacuolar type ATPase subunit A mRNA. ESTs gb_N96435, gb_N96106, gb_N96189, gb_N96091, gb_AA042286, gb_F14324, gb_W43643, gb_N96027, gb_N96299, gb_R29943, gb_T43460, gb_T43544, gb_T22472
Seq. No.	157298
Seq. ID	LIB3176-068-P1-K1-G11
Method	BLASTX
NCBI GI	g113024
BLAST score	757
E value	9.0e-81
Match length	156
% identity	90
NCBI Description	ISOCITRATE LYASE (ISOCITRASE) (ISOCITRATASE) (ICL) >gi_553043 (M83534) isocitrate lyase [Arabidopsis thaliana]
Seq. No.	157299
Seq. ID	LIB3176-068-P1-K1-G12
Method	BLASTN
NCBI GI	g2191157
BLAST score	326
E value	0.0e+00
Match length	385
% identity	100
NCBI Description	Arabidopsis thaliana BAC IG002P16
Seq. No.	157300
Seq. ID	LIB3176-068-P1-K1-G2
Method	BLASTX
NCBI GI	g124224
BLAST score	267

E value	9.0e-25
Match length	82
% identity	74
NCBI Description	INITIATION FACTOR 5A-1 (EIF-5A) (EIF-4D) >gi_100345_pir__S21060 translation initiation factor eIF-5A - common tobacco >gi_19887_emb_CAA45105_ (X63543) eukaryotic initiatin factor 5A (3) [Nicotiana tabacum]

Seq. No.	157301
Seq. ID	LIB3176-068-P1-K1-G3
Method	BLASTX
NCBI GI	g2244750
BLAST score	574
E value	3.0e-59
Match length	124
% identity	85
NCBI Description	(Z97335) adenosylhomocysteinase [Arabidopsis thaliana] >gi_3088579 (AF059581) S-adenosyl-L-homocysteine hydrolase [Arabidopsis thaliana]

Seq. No.	157302
Seq. ID	LIB3176-068-P1-K1-G6
Method	BLASTX
NCBI GI	g4512675
BLAST score	173
E value	6.0e-13
Match length	53
% identity	74
NCBI Description	(AC006931) putative citrate synthase [Arabidopsis thaliana]

Seq. No.	157303
Seq. ID	LIB3176-068-P1-K1-G9
Method	BLASTN
NCBI GI	g4589440
BLAST score	282
E value	1.0e-157
Match length	465
% identity	99
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MSD21, complete sequence

Seq. No.	157304
Seq. ID	LIB3176-068-P1-K1-H10
Method	BLASTX
NCBI GI	g3334244
BLAST score	581
E value	3.0e-60
Match length	129
% identity	85
NCBI Description	LACTOYLGLUTATHIONE LYASE (METHYLGLYOXALASE) (ALDOKETOMUTASE) (GLYOXALASE I) (GLX I) (KETONE-ALDEHYDE MUTASE) (S-D-LACTOYLGLUTATHIONE METHYLGLYOXAL LYASE) >gi_2113825_emb_CAA73691_ (Y13239) Glyoxalase I [Brassica juncea]

Seq. No.	157305
Seq. ID	LIB3176-068-P1-K1-H11

Method	BLASTN
NCBI GI	g2244901
BLAST score	192
E value	1.0e-104
Match length	449
% identity	76
NCBI Description	Arabidopsis thaliana DNA chromosome 4, ESSA I contig fragment No

Seq. No.	157306
Seq. ID	LIB3176-068-P1-K1-H2
Method	BLASTX
NCBI GI	g1169128
BLAST score	383
E value	5.0e-37
Match length	114
% identity	68
NCBI Description	SERINE/THREONINE-PROTEIN KINASE CTR1 >gi_166680 (L08789) protein kinase [Arabidopsis thaliana] >gi_166682 (L08790) protein kinase [Arabidopsis thaliana]

Seq. No.	157307
Seq. ID	LIB3176-068-P1-K1-H3
Method	BLASTX
NCBI GI	g99772
BLAST score	343
E value	1.0e-32
Match length	99
% identity	76
NCBI Description	ubiquitin 81-aa extension protein 2 - Arabidopsis thaliana >gi_166936 (J05540) ubiquitin extension protein (UBQ6) [Arabidopsis thaliana] >gi_3522953 (AC004411) ubiquitin extension protein (UBQ6) [Arabidopsis thaliana]

Seq. No.	157308
Seq. ID	LIB3176-068-P1-K1-H5
Method	BLASTX
NCBI GI	g2062157
BLAST score	490
E value	1.0e-49
Match length	102
% identity	34
NCBI Description	(AC001645) jasmonate inducible protein isolog [Arabidopsis thaliana]

Seq. No.	157309
Seq. ID	LIB3176-068-P1-K1-H6
Method	BLASTX
NCBI GI	g231587
BLAST score	502
E value	7.0e-51
Match length	150
% identity	69
NCBI Description	ATP SYNTHASE BETA CHAIN, MITOCHONDRIAL PRECURSOR >gi_283001_pir__S25304 H+-transporting ATP synthase (EC 3.6.1.34) beta chain precursor, mitochondrial - rice >gi_218147_dbj_BAA01372_ (D10491) mitochondrial F1-ATPase

[Oryza sativa]

Seq. No.	157310
Seq. ID	LIB3176-069-P1-K1-A1
Method	BLASTX
NCBI GI	g4455258
BLAST score	317
E value	3.0e-29
Match length	106
% identity	53
NCBI Description	(AL035523) acid phosphatase-like protein [Arabidopsis thaliana]

Seq. No.	157311
Seq. ID	LIB3176-069-P1-K1-A11
Method	BLASTX
NCBI GI	g3169182
BLAST score	331
E value	8.0e-31
Match length	75
% identity	83
NCBI Description	(AC004401) unknown protein [Arabidopsis thaliana]

Seq. No.	157312
Seq. ID	LIB3176-069-P1-K1-A12
Method	BLASTX
NCBI GI	g4193388
BLAST score	536
E value	7.0e-55
Match length	143
% identity	73
NCBI Description	(AF091455) translationally controlled tumor protein [Hevea brasiliensis]

Seq. No.	157313
Seq. ID	LIB3176-069-P1-K1-A2
Method	BLASTN
NCBI GI	g2832689
BLAST score	335
E value	0.0e+00
Match length	448
% identity	40
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone T9A21 (ESSAII project)

Seq. No.	157314
Seq. ID	LIB3176-069-P1-K1-A3
Method	BLASTX
NCBI GI	g1546698
BLAST score	346
E value	6.0e-33
Match length	83
% identity	82
NCBI Description	(X98808) peroxidase ATP3a [Arabidopsis thaliana]

Seq. No.	157315
Seq. ID	LIB3176-069-P1-K1-A5

Method	BLASTX
NCBI GI	g1350680
BLAST score	89
E value	1.0e-74
Match length	149
% identity	97
NCBI Description	60S RIBOSOMAL PROTEIN L1

Seq. No.	157316
Seq. ID	LIB3176-069-P1-K1-A8
Method	BLASTX
NCBI GI	g170354
BLAST score	364
E value	9.0e-35
Match length	83
% identity	19
NCBI Description	(M74156) pentameric polyubiquitin [Nicotiana sylvestris]

Seq. No.	157317
Seq. ID	LIB3176-069-P1-K1-B1
Method	BLASTX
NCBI GI	g113026
BLAST score	744
E value	3.0e-79
Match length	148
% identity	94
NCBI Description	ISOCITRATE LYASE (ISOCITRASE) (ISOCITRATASE) (ICL) >gi_68211_pir__WZRPI isocitrate lyase (EC 4.1.3.1) - rape >gi_255220_bbs_112862 isocitrate lyase, threo-D S-isocitrate glyoxylate-lyase, IL {EC 4.1.3.1} [Brassica napus, seedlings, Peptide, 576 aa] >gi_167144 (L08482) isocitrate lyase [Brassica napus] >gi_447142_prf__1913424A isocitrate lyase [Brassica napus]

Seq. No.	157318
Seq. ID	LIB3176-069-P1-K1-B10
Method	BLASTN
NCBI GI	g4468801
BLAST score	359
E value	0.0e+00
Match length	416
% identity	98
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F6G17 (ESSA project)

Seq. No.	157319
Seq. ID	LIB3176-069-P1-K1-B11
Method	BLASTX
NCBI GI	g2262167
BLAST score	661
E value	2.0e-69
Match length	126
% identity	100
NCBI Description	(AC002329) cytosolic ribosomal protein S4 [Arabidopsis thaliana]

Seq. No.	157320

Seq. ID	LIB3176-069-P1-K1-B2
Method	BLASTN
NCBI GI	g2288979
BLAST score	36
E value	7.0e-11
Match length	88
% identity	85
NCBI Description	Arabidopsis thaliana chromosome II BAC T01O24 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	157321
Seq. ID	LIB3176-069-P1-K1-B9
Method	BLASTX
NCBI GI	g3738257
BLAST score	297
E value	5.0e-27
Match length	85
% identity	73
NCBI Description	(AB018410) cytosolic phosphoglycerate kinase 1 [Populus nigra]

Seq. No.	157322
Seq. ID	LIB3176-069-P1-K1-C1
Method	BLASTN
NCBI GI	g4585890
BLAST score	148
E value	2.0e-77
Match length	412
% identity	96
NCBI Description	Arabidopsis thaliana chromosome II BAC T3G21 genomic sequence, complete sequence

Seq. No.	157323
Seq. ID	LIB3176-069-P1-K1-C10
Method	BLASTX
NCBI GI	g4335723
BLAST score	569
E value	1.0e-58
Match length	149
% identity	74
NCBI Description	(AC006248) putative thioredoxin M [Arabidopsis thaliana]

Seq. No.	157324
Seq. ID	LIB3176-069-P1-K1-C11
Method	BLASTN
NCBI GI	g2980757
BLAST score	434
E value	0.0e+00
Match length	450
% identity	99
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F6I18 (ESSAII project)

Seq. No.	157325
Seq. ID	LIB3176-069-P1-K1-C7
Method	BLASTN
NCBI GI	g3492855

BLAST score	241
E value	1.0e-133
Match length	301
% identity	90
NCBI Description	Genomic sequence for Arabidopsis thaliana BAC F20N2, complete sequence [Arabidopsis thaliana]

Seq. No.	157326
Seq. ID	LIB3176-069-P1-K1-C9
Method	BLASTX
NCBI GI	g2894563
BLAST score	465
E value	1.0e-46
Match length	92
% identity	96
NCBI Description	(AL021890) putative protein [Arabidopsis thaliana]

Seq. No.	157327
Seq. ID	LIB3176-069-P1-K1-D10
Method	BLASTX
NCBI GI	g3885943
BLAST score	673
E value	6.0e-71
Match length	135
% identity	98
NCBI Description	(AF095455) PII protein [Arabidopsis thaliana] >gi_4558559_gb_AAD22652.1_AC007138_16 (AC007138) P II nitrogen sensing protein GLB I [Arabidopsis thaliana]

Seq. No.	157328
Seq. ID	LIB3176-069-P1-K1-D11
Method	BLASTX
NCBI GI	g2529721
BLAST score	233
E value	2.0e-19
Match length	110
% identity	41
NCBI Description	(AF001891) unknown [Homo sapiens]

Seq. No.	157329
Seq. ID	LIB3176-069-P1-K1-D12
Method	BLASTN
NCBI GI	g4589410
BLAST score	101
E value	2.0e-49
Match length	424
% identity	99
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: F2O15, complete sequence

Seq. No.	157330
Seq. ID	LIB3176-069-P1-K1-D2
Method	BLASTX
NCBI GI	g2851455
BLAST score	417
E value	6.0e-41
Match length	85

% identity	99
NCBI Description	DYNAMIN-LIKE PROTEIN >gi_2267213 (L36939) dynamin-like GTP binding protein [Arabidopsis thaliana]
Seq. No.	157331
Seq. ID	LIB3176-069-P1-K1-D3
Method	BLASTX
NCBI GI	g477819
BLAST score	43
E value	2.0e-50
Match length	148
% identity	69
NCBI Description	mitochondrial processing peptidase (EC 3.4.99.41) beta chain precursor - potato >gi_410634_bbs_136741 cytochrome c reductase-processing peptidase subunit II, MPP subunit II, P53 [potatoes, var. Marfona, tuber, Peptide Mitochondrial, 530 aa]
Seq. No.	157332
Seq. ID	LIB3176-069-P1-K1-D4
Method	BLASTX
NCBI GI	g4679028
BLAST score	249
E value	2.0e-21
Match length	86
% identity	52
NCBI Description	(AF077207) HSPC021 [Homo sapiens]
Seq. No.	157333
Seq. ID	LIB3176-069-P1-K1-D5
Method	BLASTN
NCBI GI	g4115352
BLAST score	262
E value	1.0e-145
Match length	289
% identity	63
NCBI Description	Arabidopsis thaliana chromosome II BAC T15J14 genomic sequence, complete sequence [Arabidopsis thaliana]
Seq. No.	157334
Seq. ID	LIB3176-069-P1-K1-D7
Method	BLASTN
NCBI GI	g2281081
BLAST score	308
E value	1.0e-173
Match length	433
% identity	97
NCBI Description	Arabidopsis thaliana chromosome II BAC F18O19 genomic sequence, complete sequence [Arabidopsis thaliana]
Seq. No.	157335
Seq. ID	LIB3176-069-P1-K1-D9
Method	BLASTX
NCBI GI	g2507455
BLAST score	557
E value	2.0e-57
Match length	125

% identity	84
NCBI Description	FORMATE--TETRAHYDROFOLATE LIGASE (FORMYLTETRAHYDROFOLATE SYNTHETASE) (FHS) (FTHFS) >gi_322401_pir__A43350 formate--tetrahydrofolate ligase (EC 6.3.4.3) - spinach >gi_170145 (M83940) 10-formyltetrahydrofolate synthetase [Spinacia oleracea]
Seq. No.	157336
Seq. ID	LIB3176-069-P1-K1-E1
Method	BLASTX
NCBI GI	g2338712
BLAST score	257
E value	4.0e-22
Match length	69
% identity	72
NCBI Description	(AF013959) metallothionein-like protein [Arabidopsis thaliana]
Seq. No.	157337
Seq. ID	LIB3176-069-P1-K1-E10
Method	BLASTN
NCBI GI	g2827698
BLAST score	49
E value	2.0e-18
Match length	140
% identity	77
NCBI Description	Arabidopsis thaliana DNA chromosome 5, BAC clone F6H11 (ESSAII project)
Seq. No.	157338
Seq. ID	LIB3176-069-P1-K1-E11
Method	BLASTX
NCBI GI	g4678342
BLAST score	627
E value	1.0e-65
Match length	131
% identity	93
NCBI Description	(AL049659) lipase-like protein [Arabidopsis thaliana]
Seq. No.	157339
Seq. ID	LIB3176-069-P1-K1-E12
Method	BLASTX
NCBI GI	g1899188
BLAST score	248
E value	4.0e-21
Match length	74
% identity	33
NCBI Description	(U90212) DNA binding protein ACBF [Nicotiana tabacum]
Seq. No.	157340
Seq. ID	LIB3176-069-P1-K1-E2
Method	BLASTX
NCBI GI	g3859606
BLAST score	270
E value	3.0e-24
Match length	68
% identity	78

NCBI Description	(AF104919) contains similarity to cysteine proteases (Pfam: PF00112, E=1.3e-79, N=1) [Arabidopsis thaliana]

Seq. No.	157341
Seq. ID	LIB3176-069-P1-K1-E3
Method	BLASTX
NCBI GI	g3123264
BLAST score	567
E value	2.0e-58
Match length	126
% identity	90
NCBI Description	60S RIBOSOMAL PROTEIN L27 >gi_2244857_emb_CAB10279_ (Z97337) hypothetical protein [Arabidopsis thaliana]

Seq. No.	157342
Seq. ID	LIB3176-069-P1-K1-E4
Method	BLASTX
NCBI GI	g115783
BLAST score	697
E value	9.0e-74
Match length	137
% identity	97
NCBI Description	CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR (CAB-140) (LHCP) >gi_16376_emb_CAA27543_ (X03909) chlorophyll a/b binding protein (LHCP AB 140) [Arabidopsis thaliana]

Seq. No.	157343
Seq. ID	LIB3176-069-P1-K1-E5
Method	BLASTX
NCBI GI	g3885328
BLAST score	715
E value	7.0e-76
Match length	151
% identity	91
NCBI Description	(AC005623) putative serine/threonine protein kinase [Arabidopsis thaliana]

Seq. No.	157344
Seq. ID	LIB3176-069-P1-K1-E6
Method	BLASTN
NCBI GI	g2351070
BLAST score	196
E value	1.0e-106
Match length	362
% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MTH12, complete sequence [Arabidopsis thaliana]

Seq. No.	157345
Seq. ID	LIB3176-069-P1-K1-E7
Method	BLASTX
NCBI GI	g115767
BLAST score	560
E value	9.0e-58
Match length	112
% identity	96

NCBI Description	CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR (CAB-165/180) (LHCP) >gi_81603_pir__A29280 chlorophyll a/b-binding protein abl65 - Arabidopsis thaliana >gi_16368_emb_CAA27540_ (X03907) chlorophyll a/b binding protein (LHCP AB 65) [Arabidopsis thaliana] >gi_16372_emb_CAA27541_ (X03908) chlorophyll a/b binding protein (LHCP AB 180) [Arabidopsis thaliana]
Seq. No.	157346
Seq. ID	LIB3176-069-P1-K1-E8
Method	BLASTX
NCBI GI	g3688799
BLAST score	648
E value	5.0e-68
Match length	132
% identity	97
NCBI Description	(AF057137) gamma tonoplast intrinsic protein 2 [Arabidopsis thaliana]
Seq. No.	157347
Seq. ID	LIB3176-069-P1-K1-E9
Method	BLASTX
NCBI GI	g2129769
BLAST score	659
E value	3.0e-69
Match length	127
% identity	98
NCBI Description	xyloglucan endo-transglycosylase precursor - Arabidopsis thaliana >gi_944810_dbj_BAA09783_ (D63508) endo-xyloglucan transferase [Arabidopsis thaliana]
Seq. No.	157348
Seq. ID	LIB3176-069-P1-K1-F1
Method	BLASTX
NCBI GI	g2244759
BLAST score	602
E value	1.0e-62
Match length	139
% identity	81
NCBI Description	(Z97335) selenium-binding protein [Arabidopsis thaliana]
Seq. No.	157349
Seq. ID	LIB3176-069-P1-K1-F10
Method	BLASTX
NCBI GI	g4263712
BLAST score	188
E value	4.0e-14
Match length	107
% identity	46
NCBI Description	(AC006223) putative ribosomal protein S12 [Arabidopsis thaliana]
Seq. No.	157350
Seq. ID	LIB3176-069-P1-K1-F11
Method	BLASTN
NCBI GI	g4589434
BLAST score	286

E value	1.0e-160
Match length	446
% identity	55
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MNJ7, complete sequence

Seq. No.	157351
Seq. ID	LIB3176-069-P1-K1-F12
Method	BLASTX
NCBI GI	g4539388
BLAST score	219
E value	1.0e-17
Match length	62
% identity	71
NCBI Description	(AL035526) putative protein [Arabidopsis thaliana]

Seq. No.	157352
Seq. ID	LIB3176-069-P1-K1-F2
Method	BLASTN
NCBI GI	g3241927
BLAST score	184
E value	5.0e-99
Match length	458
% identity	99
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MTE17, complete sequence [Arabidopsis thaliana]

Seq. No.	157353
Seq. ID	LIB3176-069-P1-K1-F3
Method	BLASTX
NCBI GI	g3242785
BLAST score	466
E value	1.0e-46
Match length	90
% identity	100
NCBI Description	(AF055355) respiratory burst oxidase protein C [Arabidopsis thaliana]

Seq. No.	157354
Seq. ID	LIB3176-069-P1-K1-F4
Method	BLASTN
NCBI GI	g4220468
BLAST score	356
E value	0.0e+00
Match length	424
% identity	97
NCBI Description	Arabidopsis thaliana chromosome II BAC T8O11 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	157355
Seq. ID	LIB3176-069-P1-K1-F5
Method	BLASTX
NCBI GI	g3540198
BLAST score	550
E value	2.0e-56
Match length	121
% identity	88

NCBI Description (AC004260) Unknown protein [Arabidopsis thaliana]

Seq. No. 157356
Seq. ID LIB3176-069-P1-K1-F7
Method BLASTX
NCBI GI g4006883
BLAST score 225
E value 1.0e-18
Match length 99
% identity 49
NCBI Description (Z99707) cysteine proteinase [Arabidopsis thaliana]

Seq. No. 157357
Seq. ID LIB3176-069-P1-K1-F8
Method BLASTX
NCBI GI g99807
BLAST score 203
E value 4.0e-16
Match length 71
% identity 59
NCBI Description gene Bp10 protein - rape >gi_17782_emb_CAA47176_ (X66607) Bplo [Brassica napus]

Seq. No. 157358
Seq. ID LIB3176-069-P1-K1-F9
Method BLASTX
NCBI GI g3738261
BLAST score 190
E value 2.0e-14
Match length 109
% identity 48
NCBI Description (AB018412) chloroplast phosphoglycerate kinase [Populus nigra]

Seq. No. 157359
Seq. ID LIB3176-069-P1-K1-G1
Method BLASTX
NCBI GI g2129577
BLAST score 438
E value 2.0e-43
Match length 121
% identity 74
NCBI Description DnaJ homolog protein - Arabidopsis thaliana >gi_727357 (U22340) DnaJ homolog [Arabidopsis thaliana]

Seq. No. 157360
Seq. ID LIB3176-069-P1-K1-G10
Method BLASTX
NCBI GI g3738257
BLAST score 317
E value 2.0e-29
Match length 95
% identity 69
NCBI Description (AB018410) cytosolic phosphoglycerate kinase 1 [Populus nigra]

Seq. No. 157361

Seq. ID	LIB3176-069-P1-K1-G11
Method	BLASTX
NCBI GI	g585536
BLAST score	796
E value	2.0e-85
Match length	151
% identity	99
NCBI Description	MYROSINASE PRECURSOR (SINIGRINASE) (THIOGLUCOSIDASE) >gi_1362006_pir__S56653 thioglucosidase (EC 3.2.3.1) - Arabidopsis thaliana >gi_304115 (L11454) thioglucosidase [Arabidopsis thaliana] >gi_871990_emb_CAA55786_ (X79194) thioglucosidase [Arabidopsis thaliana]

Seq. No.	157362
Seq. ID	LIB3176-069-P1-K1-G2
Method	BLASTX
NCBI GI	g1361987
BLAST score	602
E value	1.0e-62
Match length	123
% identity	99
NCBI Description	GF14 protein chi chain - Arabidopsis thaliana

Seq. No.	157363
Seq. ID	LIB3176-069-P1-K1-G3
Method	BLASTX
NCBI GI	g1086263
BLAST score	331
E value	8.0e-31
Match length	147
% identity	48
NCBI Description	TMV resistance protein N - tobacco (Nicotiana glutinosa) >gi_558887 (U15605) N [Nicotiana glutinosa]

Seq. No.	157364
Seq. ID	LIB3176-069-P1-K1-G4
Method	BLASTX
NCBI GI	g584882
BLAST score	618
E value	2.0e-64
Match length	131
% identity	89
NCBI Description	CYCLOARTENOL SYNTHASE (2,3-EPOXYSQUALENE--CYCLOARTENOL CYCLASE) >gi_452446 (U02555) cycloartenol synthase; (S)-2,3-epoxysqualene mutase [Arabidopsis thaliana]

Seq. No.	157365
Seq. ID	LIB3176-069-P1-K1-G5
Method	BLASTX
NCBI GI	g4432856
BLAST score	137
E value	1.0e-08
Match length	66
% identity	47
NCBI Description	(AC006300) putative 2A6 protein [Arabidopsis thaliana]

Seq. No. 157366

Seq. ID	LIB3176-069-P1-K1-G7
Method	BLASTX
NCBI GI	g3273743
BLAST score	545
E value	7.0e-56
Match length	115
% identity	91
NCBI Description	(AF057357) lipid transfer protein 2 precursor [Arabidopsis thaliana] >gi_3786019 (AC005499) unknown protein [Arabidopsis thaliana]

Seq. No.	157367
Seq. ID	LIB3176-069-P1-K1-G9
Method	BLASTX
NCBI GI	g4587514
BLAST score	666
E value	4.0e-70
Match length	127
% identity	98
NCBI Description	(AC007060) Similar to WO8E3.3 gi_3880615 putative GTP-binding protein from C. elegans cosmid gb_Z92773. EST gb_AA597331 comes from this gene. [Arabidopsis thaliana]

Seq. No.	157368
Seq. ID	LIB3176-069-P1-K1-H1
Method	BLASTN
NCBI GI	g2618599
BLAST score	66
E value	1.0e-28
Match length	185
% identity	84
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MBD2, complete sequence [Arabidopsis thaliana]

Seq. No.	157369
Seq. ID	LIB3176-069-P1-K1-H10
Method	BLASTX
NCBI GI	g1710780
BLAST score	491
E value	1.0e-49
Match length	128
% identity	74
NCBI Description	40S RIBOSOMAL PROTEIN S9 (S7) >gi_1321917_emb_CAA65433_ (X96613) cytoplasmic ribosomal protein S7 [Podospora anserina]

Seq. No.	157370
Seq. ID	LIB3176-069-P1-K1-H11
Method	BLASTX
NCBI GI	g2492519
BLAST score	483
E value	1.0e-48
Match length	108
% identity	85
NCBI Description	26S PROTEASE REGULATORY SUBUNIT 7 (26S PROTEASOME SUBUNIT 7) >gi_1395191_dbj_BAA13021_ (D86121) 26S proteasome ATPase subunit [Spinacia oleracea]

Seq. No.	157371
Seq. ID	LIB3176-069-P1-K1-H12
Method	BLASTX
NCBI GI	g135191
BLAST score	371
E value	1.0e-35
Match length	109
% identity	59
NCBI Description	TRYPTOPHANYL-TRNA SYNTHETASE (TRYPTOPHAN--TRNA LIGASE) (TRPRS) (IFP53) >gi_107990_pir__A41706 tryptophan--tRNA ligase homolog - human >gi_30821_emb_CAA42545_ (X59892) 471 aa polypeptide (gamma2) [Homo sapiens] >gi_184657 (M77804) transfer RNA-Trp synthetase [Homo sapiens]

Seq. No.	157372
Seq. ID	LIB3176-069-P1-K1-H3
Method	BLASTX
NCBI GI	g2499327
BLAST score	431
E value	2.0e-42
Match length	130
% identity	68
NCBI Description	NADH-UBIQUINONE OXIDOREDUCTASE 20 KD SUBUNIT PRECURSOR (COMPLEX I-20KD) (CI-20KD) >gi_1084345_pir__S52286 NADH dehydrogenase (EC 1.6.99.3) - Arabidopsis thaliana >gi_643090_emb_CAA58887.1_ (X84078) NADH dehydrogenase [Arabidopsis thaliana]

Seq. No.	157373
Seq. ID	LIB3176-069-P1-K1-H4
Method	BLASTN
NCBI GI	g4678705
BLAST score	198
E value	1.0e-107
Match length	457
% identity	98
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F10N7 (ESSA project)

Seq. No.	157374
Seq. ID	LIB3176-069-P1-K1-H6
Method	BLASTX
NCBI GI	g3142294
BLAST score	673
E value	6.0e-71
Match length	144
% identity	94
NCBI Description	(AC002411) Strong similarity to initiation factor eIF-2, gb_U37354 from S. pombe. ESTs gb_T41979, gb_N37284 and gb_N37529 come from this gene. [Arabidopsis thaliana]

Seq. No.	157375
Seq. ID	LIB3176-069-P1-K1-H7
Method	BLASTX
NCBI GI	g1363488
BLAST score	509

E value	1.0e-51
Match length	99
% identity	100
NCBI Description	IAA8 protein - Arabidopsis thaliana >gi_972919 (U18410) IAA8 [Arabidopsis thaliana] >gi_4314364_gb_AAD15575_ (AC006340) auxin-induced IAA8 protein [Arabidopsis thaliana]

Seq. No.	157376
Seq. ID	LIB3176-069-P1-K1-H8
Method	BLASTX
NCBI GI	g4539326
BLAST score	165
E value	2.0e-11
Match length	49
% identity	36
NCBI Description	(AL035679) putative zinc finger protein [Arabidopsis thaliana]

Seq. No.	157377
Seq. ID	LIB3176-069-P1-K1-H9
Method	BLASTX
NCBI GI	g399013
BLAST score	558
E value	2.0e-57
Match length	111
% identity	99
NCBI Description	ADP,ATP CARRIER PROTEIN 1 PRECURSOR (ADP/ATP TRANSLOCASE 1) (ADENINE NUCLEOTIDE TRANSLOCATOR 1) (ANT 1) >gi_99658_pir__S21313 ADP,ATP carrier protein - Arabidopsis thaliana (fragment) >gi_16175_emb_CAA46518_ (X65549) adenylate translocator [Arabidopsis thaliana] >gi_445607_prf__1909354A adenylate translocator [Arabidopsis thaliana]

Seq. No.	157378
Seq. ID	LIB3176-070-P1-K1-A1
Method	BLASTN
NCBI GI	g4587641
BLAST score	222
E value	1.0e-121
Match length	418
% identity	91
NCBI Description	Arabidopsis thaliana chromosome I BAC F20D21 genomic sequence, complete sequence

Seq. No.	157379
Seq. ID	LIB3176-070-P1-K1-A10
Method	BLASTX
NCBI GI	g1362078
BLAST score	108
E value	2.0e-38
Match length	119
% identity	66
NCBI Description	endo-1,4-beta-D-glucanase, xyloglucan-specific (clone NXG1) - common nasturtium >gi_311835_emb_CAA48324_ (X68254) cellulase [Tropaeolum majus]

Seq. No.	157380
Seq. ID	LIB3176-070-P1-K1-A12
Method	BLASTX
NCBI GI	g1707364
BLAST score	363
E value	1.0e-34
Match length	128
% identity	64
NCBI Description	(X94626) AATP2 [Arabidopsis thaliana]

Seq. No.	157381
Seq. ID	LIB3176-070-P1-K1-A2
Method	BLASTN
NCBI GI	g3420042
BLAST score	139
E value	4.0e-72
Match length	422
% identity	98
NCBI Description	Arabidopsis thaliana chromosome II BAC T13E15 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	157382
Seq. ID	LIB3176-070-P1-K1-A4
Method	BLASTN
NCBI GI	g4159704
BLAST score	471
E value	0.0e+00
Match length	483
% identity	66
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MCB17, complete sequence

Seq. No.	157383
Seq. ID	LIB3176-070-P1-K1-A5
Method	BLASTX
NCBI GI	g1345655
BLAST score	358
E value	3.0e-34
Match length	66
% identity	100
NCBI Description	CINNAMYL-ALCOHOL DEHYDROGENASE 2 (CAD) >gi_757535_emb_CAA83508_ (Z31715) cinnamyl alcohol dehydrogenase [Arabidopsis thaliana]

Seq. No.	157384
Seq. ID	LIB3176-070-P1-K1-A7
Method	BLASTX
NCBI GI	g2160168
BLAST score	261
E value	7.0e-29
Match length	83
% identity	80
NCBI Description	(AC000132) Strong similarity to R. communis phosphoglycerate mutase (gb_X70652). ESTs gb_T41853,gb_T76648 come from this gene. [Arabidopsis thaliana]

Seq. No.	157385
Seq. ID	LIB3176-070-P1-K1-A8
Method	BLASTN
NCBI GI	g3128137
BLAST score	314
E value	1.0e-176
Match length	379
% identity	97
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K9I9, complete sequence [Arabidopsis thaliana]

Seq. No.	157386
Seq. ID	LIB3176-070-P1-K1-A9
Method	BLASTN
NCBI GI	g4063737
BLAST score	216
E value	1.0e-118
Match length	310
% identity	96
NCBI Description	Arabidopsis thaliana chromosome II BAC F24D13 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	157387
Seq. ID	LIB3176-070-P1-K1-B10
Method	BLASTX
NCBI GI	g119143
BLAST score	491
E value	1.0e-49
Match length	102
% identity	92
NCBI Description	ELONGATION FACTOR 1-ALPHA (EF-1-ALPHA) >gi_81606_pir__S06724 translation elongation factor eEF-1 alpha chain - Arabidopsis thaliana >gi_295788_emb_CAA34453_ (X16430) elongation factor 1-alpha [Arabidopsis thaliana] >gi_1369927_emb_CAA34454_ (X16431) elongation factor 1-alpha [Arabidopsis thaliana] >gi_1369928_emb_CAA34455_ (X16431) elongation factor 1-alpha [Arabidopsis thaliana] >gi_1532172 (U63815) EF-1alpha-A1 [Arabidopsis thaliana] >gi_1532173 (U63815) EF-1alpha-A2 [Arabidopsis thaliana] >gi_1532174 (U63815) EF-1alpha-A3 [Arabidopsis thaliana]

Seq. No.	157388
Seq. ID	LIB3176-070-P1-K1-B11
Method	BLASTX
NCBI GI	g4185136
BLAST score	711
E value	2.0e-75
Match length	151
% identity	91
NCBI Description	(AC005724) putative trehalose-6-phosphate synthase [Arabidopsis thaliana]

Seq. No.	157389
Seq. ID	LIB3176-070-P1-K1-B2
Method	BLASTX
NCBI GI	g1943751

BLAST score	647
E value	5.0e-68
Match length	131
% identity	96
NCBI Description	(U93845) Arabidopsis thaliana ER-type calcium pump protein, complete sequence >gi_2078292 (U96455) ER-type Ca2+-pumping ATPase; ECA1p [Arabidopsis thaliana]

Seq. No.	157390
Seq. ID	LIB3176-070-P1-K1-B3
Method	BLASTX
NCBI GI	g1750376
BLAST score	482
E value	2.0e-48
Match length	114
% identity	84
NCBI Description	(U80808) ubiquitin activating enzyme [Arabidopsis thaliana] >gi_3150409 (AC004165) ubiquitin activating enzyme (UBA1) [Arabidopsis thaliana]

Seq. No.	157391
Seq. ID	LIB3176-070-P1-K1-B4
Method	BLASTN
NCBI GI	g11957
BLAST score	188
E value	1.0e-101
Match length	321
% identity	46
NCBI Description	Rice complete chloroplast genome

Seq. No.	157392
Seq. ID	LIB3176-070-P1-K1-B5
Method	BLASTX
NCBI GI	g2558962
BLAST score	412
E value	2.0e-40
Match length	92
% identity	92
NCBI Description	(AF025667) histone H2B1 [Gossypium hirsutum]

Seq. No.	157393
Seq. ID	LIB3176-070-P1-K1-B9
Method	BLASTX
NCBI GI	g115767
BLAST score	45
E value	2.0e-61
Match length	126
% identity	86
NCBI Description	CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR (CAB-165/180) (LHCP) >gi_81603_pir__A29280 chlorophyll a/b-binding protein ab165 - Arabidopsis thaliana >gi_16368_emb_CAA27540_ (X03907) chlorophyll a/b binding protein (LHCP AB 65) [Arabidopsis thaliana] >gi_16372_emb_CAA27541_ (X03908) chlorophyll a/b binding protein (LHCP AB 180) [Arabidopsis thaliana]

Seq. No.	157394

Seq. ID	LIB3176-070-P1-K1-C1
Method	BLASTX
NCBI GI	g4191778
BLAST score	489
E value	8.0e-51
Match length	134
% identity	80
NCBI Description	(AC005917) putative nucleosome assembly protein I [Arabidopsis thaliana]

Seq. No.	157395
Seq. ID	LIB3176-070-P1-K1-C10
Method	BLASTX
NCBI GI	g1928991
BLAST score	700
E value	4.0e-74
Match length	143
% identity	95
NCBI Description	(U92815) heat shock protein 70 precursor [Citrullus lanatus]

Seq. No.	157396
Seq. ID	LIB3176-070-P1-K1-C12
Method	BLASTX
NCBI GI	g1710509
BLAST score	473
E value	2.0e-47
Match length	88
% identity	100
NCBI Description	60S RIBOSOMAL PROTEIN L18A

Seq. No.	157397
Seq. ID	LIB3176-070-P1-K1-C5
Method	BLASTX
NCBI GI	g3860315
BLAST score	99
E value	1.0e-32
Match length	94
% identity	74
NCBI Description	(AJ012684) 40S ribosomal protein S19 [Cicer arietinum]

Seq. No.	157398
Seq. ID	LIB3176-070-P1-K1-C8
Method	BLASTX
NCBI GI	g421826
BLAST score	648
E value	5.0e-68
Match length	148
% identity	82
NCBI Description	chlorophyll a/b-binding protein CP29 - Arabidopsis thaliana >gi_298036_emb_CAA50712_ (X71878) CP29 [Arabidopsis thaliana]

Seq. No.	157399
Seq. ID	LIB3176-070-P1-K1-C9
Method	BLASTN
NCBI GI	g4589436

BLAST score	220
E value	1.0e-120
Match length	276
% identity	95
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MPA22, complete sequence

Seq. No.	157400
Seq. ID	LIB3176-070-P1-K1-D1
Method	BLASTN
NCBI GI	g1209241
BLAST score	374
E value	0.0e+00
Match length	410
% identity	97
NCBI Description	Arabidopsis thaliana metallothionein mRNA sequence

Seq. No.	157401
Seq. ID	LIB3176-070-P1-K1-D11
Method	BLASTX
NCBI GI	g2252857
BLAST score	237
E value	8.0e-20
Match length	58
% identity	86
NCBI Description	(AF013294) similar to acidic ribosomal protein p1 [Arabidopsis thaliana]

Seq. No.	157402
Seq. ID	LIB3176-070-P1-K1-D12
Method	BLASTX
NCBI GI	g120667
BLAST score	217
E value	1.0e-20
Match length	78
% identity	77
NCBI Description	GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE, CYTOSOLIC >gi_81622_pir__JQ1287 glyceraldehyde-3-phosphate dehydrogenase (EC 1.2.1.12), cytosolic - Arabidopsis thaliana >gi_166706 (M64116) cystolic glyceraldehyde-3-phosphate dehydrogenase [Arabidopsis thaliana] >gi_166710 (M64119) glyceraldehyde-3-phosphate dehydrogenase [Arabidopsis thaliana]

Seq. No.	157403
Seq. ID	LIB3176-070-P1-K1-D2
Method	BLASTX
NCBI GI	g1350680
BLAST score	673
E value	7.0e-71
Match length	144
% identity	92
NCBI Description	60S RIBOSOMAL PROTEIN L1

Seq. No.	157404
Seq. ID	LIB3176-070-P1-K1-D3
Method	BLASTX

NCBI GI	g4490732
BLAST score	57
E value	3.0e-61
Match length	129
% identity	96
NCBI Description	(AL035709) phosphoenolpyruvate carboxykinase (ATP)-like protein [Arabidopsis thaliana]

Seq. No.	157405
Seq. ID	LIB3176-070-P1-K1-D4
Method	BLASTX
NCBI GI	g2062161
BLAST score	476
E value	8.0e-48
Match length	137
% identity	34
NCBI Description	(AC001645) jasmonate inducible protein isolog [Arabidopsis thaliana]

Seq. No.	157406
Seq. ID	LIB3176-070-P1-K1-D6
Method	BLASTX
NCBI GI	g4581146
BLAST score	333
E value	3.0e-31
Match length	121
% identity	60
NCBI Description	(AC006919) putative fructose-bisphosphate aldolase, cytoplasmic [Arabidopsis thaliana]

Seq. No.	157407
Seq. ID	LIB3176-070-P1-K1-D7
Method	BLASTX
NCBI GI	g2499706
BLAST score	561
E value	8.0e-58
Match length	110
% identity	95
NCBI Description	PHOSPHOLIPASE D PRECURSOR (PLD) (CHOLINE PHOSPHATASE) (PHOSPHATIDYLCHOLINE-HYDROLYZING PHOSPHOLIPASE D) >gi_1297302 (U36381) phospholipase D [Arabidopsis thaliana]

Seq. No.	157408
Seq. ID	LIB3176-070-P1-K1-D8
Method	BLASTX
NCBI GI	g4158219
BLAST score	83
E value	4.6e-02
Match length	91
% identity	58
NCBI Description	(Y18623) amylogenin [Oryza sativa]

Seq. No.	157409
Seq. ID	LIB3176-070-P1-K1-D9
Method	BLASTX
NCBI GI	g1172977
BLAST score	88

E value	5.0e-46
Match length	129
% identity	82
NCBI Description	60S RIBOSOMAL PROTEIN L18 >gi_606970 (U15741) cytoplasmic ribosomal protein L18 [Arabidopsis thaliana]

Seq. No.	157410
Seq. ID	LIB3176-070-P1-K1-E10
Method	BLASTX
NCBI GI	g2252840
BLAST score	443
E value	7.0e-44
Match length	108
% identity	80
NCBI Description	(AF013293) contains regions of similarity to Haemophilus influenzae permease (SP:P38767) [Arabidopsis thaliana]

Seq. No.	157411
Seq. ID	LIB3176-070-P1-K1-E12
Method	BLASTN
NCBI GI	g2264312
BLAST score	222
E value	1.0e-122
Match length	258
% identity	97
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MOK16, complete sequence [Arabidopsis thaliana]

Seq. No.	157412
Seq. ID	LIB3176-070-P1-K1-E2
Method	BLASTN
NCBI GI	g4454004
BLAST score	162
E value	4.0e-86
Match length	233
% identity	93
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F24A6 (ESSAII project)

Seq. No.	157413
Seq. ID	LIB3176-070-P1-K1-E3
Method	BLASTX
NCBI GI	g4582787
BLAST score	300
E value	2.0e-27
Match length	105
% identity	59
NCBI Description	(AJ012281) adenosine kinase [Zea mays]

Seq. No.	157414
Seq. ID	LIB3176-070-P1-K1-E4
Method	BLASTX
NCBI GI	g1710581
BLAST score	293
E value	2.0e-60
Match length	146
% identity	89

NCBI Description	60S RIBOSOMAL PROTEIN L9 >gi_2129720_pir__S71255 ribosomal protein L9 - Arabidopsis thaliana >gi_1107489_emb_CAA63024_ (X91958) 60S ribosomal protein L9 [Arabidopsis thaliana]
Seq. No.	157415
Seq. ID	LIB3176-070-P1-K1-E5
Method	BLASTX
NCBI GI	g4512653
BLAST score	709
E value	3.0e-75
Match length	144
% identity	99
NCBI Description	(AC007048) unknown protein [Arabidopsis thaliana]
Seq. No.	157416
Seq. ID	LIB3176-070-P1-K1-F1
Method	BLASTX
NCBI GI	g3979818
BLAST score	158
E value	1.0e-10
Match length	116
% identity	39
NCBI Description	(Z49967) cDNA EST EMBL:T00743 comes from this gene; cDNA EST EMBL:D69356 comes from this gene; cDNA EST EMBL:D65790 comes from this gene; cDNA EST EMBL:D70463 comes from this gene; cDNA EST EMBL:D66620 comes from this gene; cDN
Seq. No.	157417
Seq. ID	LIB3176-070-P1-K1-F10
Method	BLASTX
NCBI GI	g2119846
BLAST score	495
E value	4.0e-50
Match length	105
% identity	66
NCBI Description	chlorophyll a/b-binding protein type I precursor Lhb1B2 - Arabidopsis thaliana >gi_16364_emb_CAA45790_ (X64460) photosystem II type I chlorophyll a /b binding protein [Arabidopsis thaliana] >gi_3128230 (AC004077) photosystem II type I chlorophyll a/b binding protein [Arabidopsis thaliana] >gi_3337371 (AC004481) photosystem II type I chlorophyll a/b binding protein [Arabidopsis thaliana]
Seq. No.	157418
Seq. ID	LIB3176-070-P1-K1-F12
Method	BLASTX
NCBI GI	g4115918
BLAST score	254
E value	9.0e-22
Match length	74
% identity	65
NCBI Description	(AF118222) similar to nascent polypeptide associated complex alpha chain [Arabidopsis thaliana]
Seq. No.	157419
Seq. ID	LIB3176-070-P1-K1-F3
Method	BLASTX

NCBI GI	g4582468
BLAST score	506
E value	2.0e-51
Match length	110
% identity	94
NCBI Description	(AC007071) putative 40S ribosomal protein; contains C-terminal domain [Arabidopsis thaliana]

Seq. No.	157420
Seq. ID	LIB3176-070-P1-K1-F4
Method	BLASTN
NCBI GI	g3047074
BLAST score	467
E value	0.0e+00
Match length	482
% identity	99
NCBI Description	Arabidopsis thaliana BAC F21E10

Seq. No.	157421
Seq. ID	LIB3176-070-P1-K1-F5
Method	BLASTX
NCBI GI	g1621539
BLAST score	463
E value	2.0e-46
Match length	120
% identity	54
NCBI Description	(U28415) annexin-like protein [Arabidopsis thaliana]

Seq. No.	157422
Seq. ID	LIB3176-070-P1-K1-F8
Method	BLASTX
NCBI GI	g2129634
BLAST score	97
E value	1.0e-55
Match length	125
% identity	92
NCBI Description	lectin-like protein - Arabidopsis thaliana >gi_995619_emb_CAA62665_ (X91259) lectin like protein [Arabidopsis thaliana]

Seq. No.	157423
Seq. ID	LIB3176-070-P1-K1-F9
Method	BLASTX
NCBI GI	g2244993
BLAST score	464
E value	2.0e-46
Match length	93
% identity	97
NCBI Description	(Z97341) similarity to AMP-activated protein kinase beta [Arabidopsis thaliana]

Seq. No.	157424
Seq. ID	LIB3176-070-P1-K1-G12
Method	BLASTX
NCBI GI	g2443751
BLAST score	465
E value	2.0e-46

Match length	92
% identity	97
NCBI Description	(AF020303) fumarase [Arabidopsis thaliana] >gi_2529676 (AC002535) putative fumarase [Arabidopsis thaliana]

Seq. No.	157425
Seq. ID	LIB3176-070-P1-K1-G2
Method	BLASTX
NCBI GI	g4581856
BLAST score	104
E value	1.0e-52
Match length	139
% identity	82
NCBI Description	(AF116825) 1-deoxy-D-xylulose-5-phosphate reductoisomerase [Mentha x piperita]

Seq. No.	157426
Seq. ID	LIB3176-070-P1-K1-G3
Method	BLASTX
NCBI GI	g1071912
BLAST score	75
E value	6.0e-42
Match length	108
% identity	83
NCBI Description	cysteine synthase (EC 4.2.99.8) cpACS1 - Arabidopsis thaliana >gi_572517_emb_CAA57344_ (X81698) cysteine synthase [Arabidopsis thaliana]

Seq. No.	157427
Seq. ID	LIB3176-070-P1-K1-G4
Method	BLASTN
NCBI GI	g2252823
BLAST score	166
E value	3.0e-88
Match length	248
% identity	94
NCBI Description	Arabidopsis thaliana BAC IG005I10

Seq. No.	157428
Seq. ID	LIB3176-070-P1-K1-G5
Method	BLASTX
NCBI GI	g2809242
BLAST score	722
E value	1.0e-76
Match length	148
% identity	98
NCBI Description	(AC002560) F21B7.11 [Arabidopsis thaliana]

Seq. No.	157429
Seq. ID	LIB3176-070-P1-K1-G7
Method	BLASTN
NCBI GI	g2191126
BLAST score	211
E value	1.0e-115
Match length	454
% identity	99
NCBI Description	Arabidopsis thaliana BAC IG002N01

Seq. No.	157430
Seq. ID	LIB3176-070-P1-K1-G8
Method	BLASTN
NCBI GI	g2924651
BLAST score	285
E value	1.0e-159
Match length	376
% identity	97
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K2A18, complete sequence [Arabidopsis thaliana]

Seq. No.	157431
Seq. ID	LIB3176-070-P1-K1-G9
Method	BLASTN
NCBI GI	g4263694
BLAST score	58
E value	7.0e-24
Match length	142
% identity	85
NCBI Description	Arabidopsis thaliana chromosome II BAC F22D22 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	157432
Seq. ID	LIB3176-070-P1-K1-H1
Method	BLASTX
NCBI GI	g3036808
BLAST score	334
E value	1.0e-49
Match length	124
% identity	85
NCBI Description	(AL022373) DnaJ-like protein [Arabidopsis thaliana]

Seq. No.	157433
Seq. ID	LIB3176-070-P1-K1-H10
Method	BLASTX
NCBI GI	g4262174
BLAST score	555
E value	3.0e-57
Match length	100
% identity	98
NCBI Description	(AC005508) 9058 [Arabidopsis thaliana]

Seq. No.	157434
Seq. ID	LIB3176-070-P1-K1-H2
Method	BLASTX
NCBI GI	g2160756
BLAST score	335
E value	2.0e-31
Match length	89
% identity	72
NCBI Description	(U96879) CLV1 receptor kinase [Arabidopsis thaliana]

Seq. No.	157435
Seq. ID	LIB3176-070-P1-K1-H3
Method	BLASTX
NCBI GI	g2829891

BLAST score	463
E value	3.0e-46
Match length	93
% identity	97
NCBI Description	(AC002311) Unknown protein [Arabidopsis thaliana]

Seq. No.	157436
Seq. ID	LIB3176-070-P1-K1-H5
Method	BLASTX
NCBI GI	g1335862
BLAST score	717
E value	4.0e-76
Match length	151
% identity	95
NCBI Description	(U42608) clathrin heavy chain [Glycine max]

Seq. No.	157437
Seq. ID	LIB3176-070-P1-K1-H6
Method	BLASTX
NCBI GI	g4006902
BLAST score	155
E value	2.0e-10
Match length	73
% identity	45
NCBI Description	(Z99708) putative protein [Arabidopsis thaliana]

Seq. No.	157438
Seq. ID	LIB3176-070-P1-K1-H7
Method	BLASTX
NCBI GI	g132090
BLAST score	699
E value	5.0e-74
Match length	138
% identity	96
NCBI Description	RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN 1B PRECURSOR (RUBISCO SMALL SUBUNIT 1B) >gi_68062_pir__RKMUB1 ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain B1 precursor - Arabidopsis thaliana >gi_16193_emb_CAA32700_ (X14564) ribulose bisphosphate carboxylase [Arabidopsis thaliana]

Seq. No.	157439
Seq. ID	LIB3176-070-P1-K1-H8
Method	BLASTX
NCBI GI	g3980384
BLAST score	312
E value	2.0e-28
Match length	69
% identity	83
NCBI Description	(AC004561) hypothetical protein [Arabidopsis thaliana]

Seq. No.	157440
Seq. ID	LIB3176-071-P1-K1-A10
Method	BLASTX
NCBI GI	g2231312
BLAST score	592
E value	2.0e-61

Match length	120
% identity	95
NCBI Description	(U75603) AtRab18 [Arabidopsis thaliana]

Seq. No.	157441
Seq. ID	LIB3176-071-P1-K1-A11
Method	BLASTX
NCBI GI	g231536
BLAST score	81
E value	3.0e-18
Match length	91
% identity	66
NCBI Description	CYTOSOL AMINOPEPTIDASE (LEUCINE AMINOPEPTIDASE) (LAP) (LEUCYL AMINOPEPTIDASE) (PROLINE AMINOPEPTIDASE) (PROLYL AMINOPEPTIDASE) >gi_99683_pir__S22399 leucyl aminopeptidase (EC 3.4.11.1) - Arabidopsis thaliana >gi_16394_emb_CAA45040_ (X63444) leucine aminopeptidase [Arabidopsis thaliana] >gi_4115380 (AC005967) putative leucine aminopeptidase [Arabidopsis thaliana]

Seq. No.	157442
Seq. ID	LIB3176-071-P1-K1-A12
Method	BLASTX
NCBI GI	g3413714
BLAST score	235
E value	1.0e-19
Match length	121
% identity	45
NCBI Description	(AC004747) putative myrosinase-binding protein [Arabidopsis thaliana]

Seq. No.	157443
Seq. ID	LIB3176-071-P1-K1-A2
Method	BLASTN
NCBI GI	g2702261
BLAST score	335
E value	0.0e+00
Match length	386
% identity	99
NCBI Description	Arabidopsis thaliana chromosome II BAC T21L14 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	157444
Seq. ID	LIB3176-071-P1-K1-A3
Method	BLASTN
NCBI GI	g3256065
BLAST score	322
E value	0.0e+00
Match length	362
% identity	97
NCBI Description	Arabidopsis thaliana mRNA for chloroplast NAD-dependent malate dehydrogenase

Seq. No.	157445
Seq. ID	LIB3176-071-P1-K1-A6
Method	BLASTX
NCBI GI	g2464899

BLAST score	358
E value	6.0e-34
Match length	142
% identity	54
NCBI Description	(Z99708) geranylgeranyl pyrophosphate synthase [Arabidopsis thaliana]

Seq. No.	157446
Seq. ID	LIB3176-071-P1-K1-A7
Method	BLASTX
NCBI GI	g2828296
BLAST score	616
E value	2.0e-64
Match length	122
% identity	97
NCBI Description	(AL021687) RNase L inhibitor [Arabidopsis thaliana]

Seq. No.	157447
Seq. ID	LIB3176-071-P1-K1-A8
Method	BLASTN
NCBI GI	g2494106
BLAST score	149
E value	4.0e-78
Match length	421
% identity	97
NCBI Description	Arabidopsis thaliana chromosome 1 YAC YUP8H12R sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	157448
Seq. ID	LIB3176-071-P1-K1-B1
Method	BLASTX
NCBI GI	g1684857
BLAST score	525
E value	1.0e-53
Match length	110
% identity	38
NCBI Description	(U77940) polyubiquitin [Phaseolus vulgaris]

Seq. No.	157449
Seq. ID	LIB3176-071-P1-K1-B10
Method	BLASTN
NCBI GI	g4115370
BLAST score	58
E value	6.0e-24
Match length	198
% identity	83
NCBI Description	Arabidopsis thaliana chromosome II BAC F27D4 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	157450
Seq. ID	LIB3176-071-P1-K1-B11
Method	BLASTX
NCBI GI	g2980774
BLAST score	77
E value	3.0e-18
Match length	103
% identity	60

NCBI Description	(AL022198) leucyl aminopeptidase - like protein [Arabidopsis thaliana]
Seq. No.	157451
Seq. ID	LIB3176-071-P1-K1-B12
Method	BLASTX
NCBI GI	g4585882
BLAST score	419
E value	3.0e-41
Match length	103
% identity	85
NCBI Description	(AC005850) PSI type III chlorophyll a/b-binding protein [Arabidopsis thaliana]
Seq. No.	157452
Seq. ID	LIB3176-071-P1-K1-B2
Method	BLASTX
NCBI GI	g101245
BLAST score	163
E value	4.0e-11
Match length	87
% identity	36
NCBI Description	cell division control protein CDC15 - yeast (Saccharomyces cerevisiae) >gi_349757 (L22015) Cdc15p: Putative kinase [Saccharomyces cerevisiae]
Seq. No.	157453
Seq. ID	LIB3176-071-P1-K1-B3
Method	BLASTX
NCBI GI	g4220446
BLAST score	533
E value	1.0e-54
Match length	136
% identity	79
NCBI Description	(AC006216) Strong similarity to gi_2062155 T02O04.2 mitochondrial processing peptidase alpha subunit precusor isolog from Arabidopsis thaliana BAC gb_AC001645. ESTs gb_Z18504 and gb_AA395715 come from this gene. [Arabidopsis thaliana]
Seq. No.	157454
Seq. ID	LIB3176-071-P1-K1-B5
Method	BLASTX
NCBI GI	g3860277
BLAST score	522
E value	3.0e-53
Match length	131
% identity	81
NCBI Description	(AC005824) putative ribosomal protein L10 [Arabidopsis thaliana] >gi_4314394_gb_AAD15604_ (AC006232) putative ribosomal protein L10A [Arabidopsis thaliana]
Seq. No.	157455
Seq. ID	LIB3176-071-P1-K1-B6
Method	BLASTX
NCBI GI	g3236242
BLAST score	482

E value	1.0e-48
Match length	112
% identity	88
NCBI Description	(AC004684) putative ribosomal protein L36 [Arabidopsis thaliana]

Seq. No.	157456
Seq. ID	LIB3176-071-P1-K1-B8
Method	BLASTX
NCBI GI	g231536
BLAST score	141
E value	2.0e-33
Match length	111
% identity	76
NCBI Description	CYTOSOL AMINOPEPTIDASE (LEUCINE AMINOPEPTIDASE) (LAP) (LEUCYL AMINOPEPTIDASE) (PROLINE AMINOPEPTIDASE) (PROLYL AMINOPEPTIDASE) >gi_99683_pir__S22399 leucyl aminopeptidase (EC 3.4.11.1) - Arabidopsis thaliana >gi_16394_emb_CAA45040_ (X63444) leucine aminopeptidase [Arabidopsis thaliana] >gi_4115380 (AC005967) putative leucine aminopeptidase [Arabidopsis thaliana]

Seq. No.	157457
Seq. ID	LIB3176-071-P1-K1-B9
Method	BLASTX
NCBI GI	g231536
BLAST score	144
E value	3.0e-09
Match length	66
% identity	52
NCBI Description	CYTOSOL AMINOPEPTIDASE (LEUCINE AMINOPEPTIDASE) (LAP) (LEUCYL AMINOPEPTIDASE) (PROLINE AMINOPEPTIDASE) (PROLYL AMINOPEPTIDASE) >gi_99683_pir__S22399 leucyl aminopeptidase (EC 3.4.11.1) - Arabidopsis thaliana >gi_16394_emb_CAA45040_ (X63444) leucine aminopeptidase [Arabidopsis thaliana] >gi_4115380 (AC005967) putative leucine aminopeptidase [Arabidopsis thaliana]

Seq. No.	157458
Seq. ID	LIB3176-071-P1-K1-C1
Method	BLASTX
NCBI GI	g2244750
BLAST score	484
E value	7.0e-49
Match length	109
% identity	83
NCBI Description	(Z97335) adenosylhomocysteinase [Arabidopsis thaliana] >gi_3088579 (AF059581) S-adenosyl-L-homocysteine hydrolase [Arabidopsis thaliana]

Seq. No.	157459
Seq. ID	LIB3176-071-P1-K1-C11
Method	BLASTN
NCBI GI	g16393
BLAST score	35
E value	2.0e-10
Match length	164

% identity	52
NCBI Description	A.thaliana mRNA for leucine aminopeptidase

Seq. No.	157460
Seq. ID	LIB3176-071-P1-K1-C2
Method	BLASTX
NCBI GI	g4539316
BLAST score	508
E value	1.0e-51
Match length	111
% identity	95
NCBI Description	(AL035679) putative fructose-bisphosphate aldolase [Arabidopsis thaliana]

Seq. No.	157461
Seq. ID	LIB3176-071-P1-K1-C6
Method	BLASTX
NCBI GI	g2708750
BLAST score	553
E value	7.0e-57
Match length	136
% identity	83
NCBI Description	(AC003952) putative physical impedence protein [Arabidopsis thaliana]

Seq. No.	157462
Seq. ID	LIB3176-071-P1-K1-C7
Method	BLASTX
NCBI GI	g4587615
BLAST score	263
E value	3.0e-23
Match length	76
% identity	71
NCBI Description	(AC006951) putative acyl-CoA synthetase [Arabidopsis thaliana] >gi_4689469_gb_AAD27905.1_AC007213_3 (AC007213) putative acyl-CoA synthetase [Arabidopsis thaliana]

Seq. No.	157463
Seq. ID	LIB3176-071-P1-K1-C9
Method	BLASTX
NCBI GI	g231536
BLAST score	82
E value	8.0e-15
Match length	81
% identity	53
NCBI Description	CYTOSOL AMINOPEPTIDASE (LEUCINE AMINOPEPTIDASE) (LAP) (LEUCYL AMINOPEPTIDASE) (PROLINE AMINOPEPTIDASE) (PROLYL AMINOPEPTIDASE) >gi_99683_pir__S22399 leucyl aminopeptidase (EC 3.4.11.1) - Arabidopsis thaliana >gi_16394_emb_CAA45040_ (X63444) leucine aminopeptidase [Arabidopsis thaliana] >gi_4115380 (AC005967) putative leucine aminopeptidase [Arabidopsis thaliana]

Seq. No.	157464
Seq. ID	LIB3176-071-P1-K1-D1
Method	BLASTN
NCBI GI	g4467094

BLAST score	103
E value	7.0e-51
Match length	218
% identity	97
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F20D10 (ESSA project)

Seq. No.	157465
Seq. ID	LIB3176-071-P1-K1-D11
Method	BLASTX
NCBI GI	g2982303
BLAST score	219
E value	6.0e-18
Match length	58
% identity	69
NCBI Description	(AF051236) hypothetical protein [Picea mariana]

Seq. No.	157466
Seq. ID	LIB3176-071-P1-K1-D2
Method	BLASTN
NCBI GI	g2435510
BLAST score	331
E value	0.0e+00
Match length	359
% identity	98
NCBI Description	Arabidopsis thaliana BAC TM017A05

Seq. No.	157467
Seq. ID	LIB3176-071-P1-K1-D3
Method	BLASTX
NCBI GI	g3319355
BLAST score	470
E value	5.0e-47
Match length	97
% identity	97
NCBI Description	(AF077407) similar to chaperonin containing TCP-1 complex gamma chain [Arabidopsis thaliana]

Seq. No.	157468
Seq. ID	LIB3176-071-P1-K1-D4
Method	BLASTX
NCBI GI	g2262167
BLAST score	696
E value	1.0e-73
Match length	135
% identity	99
NCBI Description	(AC002329) cytosolic ribosomal protein S4 [Arabidopsis thaliana]

Seq. No.	157469
Seq. ID	LIB3176-071-P1-K1-D5
Method	BLASTX
NCBI GI	g2495365
BLAST score	375
E value	5.0e-36
Match length	111
% identity	72

NCBI Description	HEAT SHOCK PROTEIN 81-2 (HSP81-2) >gi_445127_prf__1908431B heat shock protein HSP81-2 [Arabidopsis thaliana]
Seq. No.	157470
Seq. ID	LIB3176-071-P1-K1-D8
Method	BLASTX
NCBI GI	g3281850
BLAST score	615
E value	3.0e-64
Match length	125
% identity	97
NCBI Description	(AL031004) monogalactosyldiacylglycerol synthase - like protein [Arabidopsis thaliana]
Seq. No.	157471
Seq. ID	LIB3176-071-P1-K1-D9
Method	BLASTX
NCBI GI	g3421104
BLAST score	440
E value	9.0e-44
Match length	84
% identity	99
NCBI Description	(AF043531) 20S proteasome beta subunit PBB2 [Arabidopsis thaliana]
Seq. No.	157472
Seq. ID	LIB3176-071-P1-K1-E1
Method	BLASTX
NCBI GI	g3650029
BLAST score	295
E value	5.0e-28
Match length	86
% identity	73
NCBI Description	(AC005396) hypothetical protein [Arabidopsis thaliana]
Seq. No.	157473
Seq. ID	LIB3176-071-P1-K1-E11
Method	BLASTX
NCBI GI	g4544409
BLAST score	568
E value	1.0e-58
Match length	134
% identity	78
NCBI Description	(AC006955) putative transcription factor [Arabidopsis thaliana] >gi_4585920_gb_AAD25580.1_AC007211_2 (AC007211) putative scarecrow homolog [Arabidopsis thaliana]
Seq. No.	157474
Seq. ID	LIB3176-071-P1-K1-E2
Method	BLASTX
NCBI GI	g2245098
BLAST score	480
E value	8.0e-54
Match length	139
% identity	82
NCBI Description	(Z97343) ribosomal protein [Arabidopsis thaliana]

Seq. No.	157475
Seq. ID	LIB3176-071-P1-K1-E4
Method	BLASTN
NCBI GI	g3873174
BLAST score	121
E value	1.0e-61
Match length	274
% identity	95
NCBI Description	Genomic sequence for Arabidopsis thaliana BAC F14N23, complete sequence [Arabidopsis thaliana]

Seq. No.	157476
Seq. ID	LIB3176-071-P1-K1-E6
Method	BLASTX
NCBI GI	g136739
BLAST score	393
E value	4.0e-38
Match length	129
% identity	63
NCBI Description	UTP--GLUCOSE-1-PHOSPHATE URIDYLYLTRANSFERASE (UDP-GLUCOSE PYROPHOSPHORYLASE) (UDPGP) >gi_67061_pir__XNPOU UTP--glucose-1-phosphate uridylyltransferase (EC 2.7.7.9) - potato >gi_218001_dbj_BAA00570_ (D00667) UDP-glucose pyrophosphorylase precursor [Solanum tuberosum]

Seq. No.	157477
Seq. ID	LIB3176-071-P1-K1-E7
Method	BLASTN
NCBI GI	g4220635
BLAST score	136
E value	1.0e-70
Match length	196
% identity	94
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MDB19, complete sequence [Arabidopsis thaliana]

Seq. No.	157478
Seq. ID	LIB3176-071-P1-K1-F1
Method	BLASTX
NCBI GI	g1170878
BLAST score	135
E value	8.0e-61
Match length	129
% identity	91
NCBI Description	MALATE SYNTHASE, GLYOXYSOMAL (MS) >gi_170026 (L01629) malate synthase [Glycine max]

Seq. No.	157479
Seq. ID	LIB3176-071-P1-K1-F11
Method	BLASTN
NCBI GI	g166709
BLAST score	153
E value	1.0e-80
Match length	262
% identity	99
NCBI Description	Arabidopsis thaliana cytosolic glyceraldehyde-3-phosphate dehydrogenase (GapC) gene, exons 1-9, complete cds

Seq. No.	157480
Seq. ID	LIB3176-071-P1-K1-F2
Method	BLASTN
NCBI GI	g3335356
BLAST score	164
E value	5.0e-87
Match length	387
% identity	97
NCBI Description	Arabidopsis thaliana chromosome II BAC F16M14 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	157481
Seq. ID	LIB3176-071-P1-K1-F3
Method	BLASTX
NCBI GI	g4336752
BLAST score	714
E value	1.0e-75
Match length	140
% identity	96
NCBI Description	(AF104451) catalase [Brassica juncea]

Seq. No.	157482
Seq. ID	LIB3176-071-P1-K1-F4
Method	BLASTX
NCBI GI	g2982466
BLAST score	190
E value	8.0e-15
Match length	68
% identity	59
NCBI Description	(AL022223) putative protein [Arabidopsis thaliana]

Seq. No.	157483
Seq. ID	LIB3176-071-P1-K1-F5
Method	BLASTX
NCBI GI	g267073
BLAST score	500
E value	8.0e-51
Match length	93
% identity	99
NCBI Description	TUBULIN BETA-2/BETA-3 CHAIN >gi_320184_pir__JQ1587 tubulin beta chain - Arabidopsis thaliana >gi_166898 (M84700) beta-2 tubulin [Arabidopsis thaliana] >gi_166900 (M84701) beta-3 tubulin [Arabidopsis thaliana]

Seq. No.	157484
Seq. ID	LIB3176-071-P1-K1-F6
Method	BLASTN
NCBI GI	g3869069
BLAST score	266
E value	1.0e-148
Match length	352
% identity	97
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MEB5, complete sequence [Arabidopsis thaliana]

Seq. No.	157485

Seq. ID	LIB3176-071-P1-K1-F7
Method	BLASTX
NCBI GI	g1170503
BLAST score	315
E value	3.0e-29
Match length	60
% identity	100
NCBI Description	EUKARYOTIC INITIATION FACTOR 4A-1 (EIF-4A-1) >gi_322503_pir__JC1452 translation initiation factor eIF-4A1 - Arabidopsis thaliana >gi_16554_emb_CAA46188_ (X65052) eukaryotic translation initiation factor 4A-1 [Arabidopsis thaliana]

Seq. No.	157486
Seq. ID	LIB3176-071-P1-K1-F8
Method	BLASTX
NCBI GI	g4220537
BLAST score	411
E value	2.0e-40
Match length	117
% identity	61
NCBI Description	(AL035356) PsRT17-1 like protein [Arabidopsis thaliana]

Seq. No.	157487
Seq. ID	LIB3176-071-P1-K1-G1
Method	BLASTX
NCBI GI	g1170767
BLAST score	248
E value	4.0e-21
Match length	86
% identity	58
NCBI Description	26S PROTEASE REGULATORY SUBUNIT 8 HOMOLOG (LET1 PROTEIN) >gi_626074_pir__S45176 transcription factor SUG1 homolog - fission yeast (Schizosaccharomyces pombe) >gi_406051 (U02280) Let1 [Schizosaccharomyces pombe] >gi_4106689_emb_CAA22628_ (AL035065) 26s protease regulatory subunit 8 homolog [Schizosaccharomyces pombe]

Seq. No.	157488
Seq. ID	LIB3176-071-P1-K1-G10
Method	BLASTX
NCBI GI	g2924779
BLAST score	410
E value	2.0e-40
Match length	84
% identity	96
NCBI Description	(AC002334) putative 3-ketoacyl-CoA thiolase [Arabidopsis thaliana] >gi_2981616_dbj_BAA25248_ (AB008854) 3-ketoacyl-CoA thiolase [Arabidopsis thaliana] >gi_2981618_dbj_BAA25249_ (AB008855) 3-ketoacyl-CoA thiolase [Arabidopsis thaliana]

Seq. No.	157489
Seq. ID	LIB3176-071-P1-K1-G3
Method	BLASTX
NCBI GI	g4103987
BLAST score	508

E value	2.0e-51
Match length	135
% identity	73
NCBI Description	(AF030516) 5,10-methylenetetrahydrofolate dehydrogenase-5,10-methenyltetrahydrofolate cyclohydrolase [Pisum sativum]

Seq. No.	157490
Seq. ID	LIB3176-071-P1-K1-G4
Method	BLASTX
NCBI GI	g2661422
BLAST score	324
E value	4.0e-30
Match length	88
% identity	77
NCBI Description	(AJ001342) Putative S-phase-specific ribosomal protein [Arabidopsis thaliana] >gi_3096936_emb_CAA18846.1_ (AL023094) Putative S-phase-specific ribosomal protein [Arabidopsis thaliana]

Seq. No.	157491
Seq. ID	LIB3176-071-P1-K1-G5
Method	BLASTX
NCBI GI	g2654122
BLAST score	342
E value	4.0e-37
Match length	106
% identity	74
NCBI Description	(AF034694) ribosomal protein L23a [Arabidopsis thaliana]

Seq. No.	157492
Seq. ID	LIB3176-071-P1-K1-G9
Method	BLASTX
NCBI GI	g3288821
BLAST score	54
E value	4.0e-55
Match length	134
% identity	85
NCBI Description	(AF063901) alanine:glyoxylate aminotransferase; transaminase [Arabidopsis thaliana] >gi_4733989_gb_AAD28669.1_AC007209_5 (AC007209) alanine-glyoxylate aminotransferase [Arabidopsis thaliana]

Seq. No.	157493
Seq. ID	LIB3176-071-P1-K1-H1
Method	BLASTN
NCBI GI	g4056429
BLAST score	139
E value	3.0e-72
Match length	268
% identity	91
NCBI Description	Arabidopsis thaliana chromosome 1 BAC F5O8 sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	157494
Seq. ID	LIB3176-071-P1-K1-H11
Method	BLASTX

NCBI GI	g3023848
BLAST score	704
E value	1.0e-74
Match length	138
% identity	53
NCBI Description	GUANINE NUCLEOTIDE-BINDING PROTEIN BETA SUBUNIT-LIKE PROTEIN (WD-40 REPEAT AUXIN-DEPENDENT PROTEIN ARCA) >gi_2289095 (U77381) WD-40 repeat protein [Arabidopsis thaliana]

Seq. No.	157495
Seq. ID	LIB3176-071-P1-K1-H2
Method	BLASTX
NCBI GI	g4006941
BLAST score	666
E value	4.0e-70
Match length	145
% identity	90
NCBI Description	(AJ131391) voltage-dependent anion-selective channel protein [Arabidopsis thaliana]

Seq. No.	157496
Seq. ID	LIB3176-071-P1-K1-H3
Method	BLASTX
NCBI GI	g4191788
BLAST score	668
E value	2.0e-70
Match length	133
% identity	96
NCBI Description	(AC005917) putative 1-aminocyclopropane-1-carboxylate oxidase [Arabidopsis thaliana]

Seq. No.	157497
Seq. ID	LIB3176-071-P1-K1-H6
Method	BLASTX
NCBI GI	g1071913
BLAST score	263
E value	7.0e-23
Match length	87
% identity	62
NCBI Description	cysteine synthase (EC 4.2.99.8) C precursor, mitochondrial - spinach >gi_1066153_dbj_BAA07177_ (D37963) cysteine synthase [Spinacia oleracea]

Seq. No.	157498
Seq. ID	LIB3176-071-P1-K1-H7
Method	BLASTX
NCBI GI	g4512680
BLAST score	197
E value	4.0e-15
Match length	100
% identity	45
NCBI Description	(AC006931) hypothetical protein [Arabidopsis thaliana]

Seq. No.	157499
Seq. ID	LIB3176-071-P1-K1-H8
Method	BLASTN

NCBI GI	g4757662
BLAST score	434
E value	0.0e+00
Match length	458
% identity	99
NCBI Description	Genomic sequence for Arabidopsis thaliana BAC F10B6 from chromosome I, complete sequence

Seq. No.	157500
Seq. ID	LIB3176-071-P1-K1-H9
Method	BLASTN
NCBI GI	g4589428
BLAST score	306
E value	1.0e-172
Match length	322
% identity	99
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MFH8, complete sequence

Seq. No.	157501
Seq. ID	LIB3176-073-P1-K1-A1
Method	BLASTX
NCBI GI	g99688
BLAST score	650
E value	2.0e-68
Match length	126
% identity	98
NCBI Description	translation elongation factor eEF-1 alpha chain (gene A4) - Arabidopsis thaliana >gi_295789_emb_CAA34456_ (X16432) elongation factor 1-alpha [Arabidopsis thaliana]

Seq. No.	157502
Seq. ID	LIB3176-073-P1-K1-A11
Method	BLASTX
NCBI GI	g4415931
BLAST score	567
E value	2.0e-58
Match length	145
% identity	69
NCBI Description	(AC006418) unknown protein [Arabidopsis thaliana] >gi_4559393_gb_AAD23053.1_AC006526_18 (AC006526) unknown protein [Arabidopsis thaliana]

Seq. No.	157503
Seq. ID	LIB3176-073-P1-K1-A3
Method	BLASTX
NCBI GI	g1076316
BLAST score	494
E value	5.0e-50
Match length	92
% identity	100
NCBI Description	drought-induced protein Di19 - Arabidopsis thaliana >gi_469110_emb_CAA55321_ (X78584) Di19 [Arabidopsis thaliana]

Seq. No.	157504
Seq. ID	LIB3176-073-P1-K1-A4

Method	BLASTX
NCBI GI	g2129772
BLAST score	506
E value	2.0e-51
Match length	114
% identity	82
NCBI Description	xyloglucan endotransglycosylase-related protein XTR-7 - Arabidopsis thaliana >gi_1244760 (U43489) xyloglucan endotransglycosylase-related protein [Arabidopsis thaliana]

Seq. No.	157505
Seq. ID	LIB3176-073-P1-K1-A6
Method	BLASTX
NCBI GI	g2738248
BLAST score	605
E value	5.0e-63
Match length	138
% identity	91
NCBI Description	(U97200) cobalamin-independent methionine synthase [Arabidopsis thaliana]

Seq. No.	157506
Seq. ID	LIB3176-073-P1-K1-A7
Method	BLASTX
NCBI GI	g1419388
BLAST score	391
E value	2.0e-38
Match length	84
% identity	89
NCBI Description	(X98925) stromal ascorbate peroxidase [Arabidopsis thaliana]

Seq. No.	157507
Seq. ID	LIB3176-073-P1-K1-A8
Method	BLASTN
NCBI GI	g2398520
BLAST score	318
E value	1.0e-179
Match length	394
% identity	95
NCBI Description	Arabidopsis thaliana mRNA for Hap2a transcription factor

Seq. No.	157508
Seq. ID	LIB3176-073-P1-K1-A9
Method	BLASTX
NCBI GI	g119975
BLAST score	372
E value	6.0e-36
Match length	85
% identity	91
NCBI Description	FERREDOXIN PRECURSOR >gi_99692_pir__S09979 ferredoxin [2Fe-2S] precursor - Arabidopsis thaliana >gi_16437_emb_CAA35754_ (X51370) ferredoxin precursor [Arabidopsis thaliana] >gi_166698 (M35868) ferrodoxin A [Arabidopsis thaliana]

Seq. No.	157509

Seq. ID	LIB3176-073-P1-K1-B1
Method	BLASTX
NCBI GI	g2688544
BLAST score	184
E value	1.0e-13
Match length	97
% identity	38
NCBI Description	(AE001163) 4-methyl-5(b-hydroxyethyl)-thiazole monophosphate biosynthesis protein (thiJ) [Borrelia burgdorferi]

Seq. No.	157510
Seq. ID	LIB3176-073-P1-K1-B10
Method	BLASTX
NCBI GI	g4335745
BLAST score	473
E value	1.0e-47
Match length	139
% identity	63
NCBI Description	(AC006284) putative hydrolase (contains an esterase/lipase/thioesterase active site serine domain (prosite: PS50187) [Arabidopsis thaliana]

Seq. No.	157511
Seq. ID	LIB3176-073-P1-K1-B11
Method	BLASTN
NCBI GI	g4757405
BLAST score	397
E value	0.0e+00
Match length	433
% identity	98
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MOJ10, complete sequence

Seq. No.	157512
Seq. ID	LIB3176-073-P1-K1-B12
Method	BLASTX
NCBI GI	g113026
BLAST score	539
E value	3.0e-55
Match length	124
% identity	85
NCBI Description	ISOCITRATE LYASE (ISOCITRASE) (ISOCITRATASE) (ICL) >gi_68211_pir__WZRPI isocitrate lyase (EC 4.1.3.1) - rape >gi_255220_bbs_112862 isocitrate lyase, threo-D S-isocitrate glyoxylate-lyase, IL {EC 4.1.3.1} [Brassica napus, seedlings, Peptide, 576 aa] >gi_167144 (L08482) isocitrate lyase [Brassica napus] >gi_447142_prf__1913424A isocitrate lyase [Brassica napus]

Seq. No.	157513
Seq. ID	LIB3176-073-P1-K1-B2
Method	BLASTN
NCBI GI	g484109
BLAST score	122
E value	5.0e-62
Match length	468

% identity	97
NCBI Description	Arabidopsis thaliana chloroplast glyceraldehyde-3-phosphate dehydrogenase B subunit gene, 5'end

Seq. No.	157514
Seq. ID	LIB3176-073-P1-K1-B3
Method	BLASTX
NCBI GI	g3914117
BLAST score	606
E value	4.0e-63
Match length	140
% identity	84
NCBI Description	NUCLEOSIDE DIPHOSPHATE KINASE II PRECURSOR (NDK II) (NDP KINASE II) >gi_3093480 (AF017640) nucleoside diphosphate kinase type 2 [Arabidopsis thaliana]

Seq. No.	157515
Seq. ID	LIB3176-073-P1-K1-B4
Method	BLASTX
NCBI GI	g3158370
BLAST score	108
E value	2.0e-46
Match length	99
% identity	98
NCBI Description	(AF035382) catalase 3 [Arabidopsis thaliana]

Seq. No.	157516
Seq. ID	LIB3176-073-P1-K1-B5
Method	BLASTN
NCBI GI	g4713943
BLAST score	206
E value	1.0e-112
Match length	279
% identity	93
NCBI Description	Arabidopsis thaliana chromosome 1 BAC T8K14 sequence, complete sequence

Seq. No.	157517
Seq. ID	LIB3176-073-P1-K1-B6
Method	BLASTX
NCBI GI	g2924779
BLAST score	573
E value	3.0e-59
Match length	118
% identity	97
NCBI Description	(AC002334) putative 3-ketoacyl-CoA thiolase [Arabidopsis thaliana] >gi_2981616_dbj_BAA25248_ (AB008854) 3-ketoacyl-CoA thiolase [Arabidopsis thaliana] >gi_2981618_dbj_BAA25249_ (AB008855) 3-ketoacyl-CoA thiolase [Arabidopsis thaliana]

Seq. No.	157518
Seq. ID	LIB3176-073-P1-K1-B7
Method	BLASTN
NCBI GI	g2182286
BLAST score	78
E value	5.0e-36

Match length	186
% identity	85
NCBI Description	Sequence of BAC F20P5 from Arabidopsis thaliana chromosome 1, complete sequence [Arabidopsis thaliana]

Seq. No.	157519
Seq. ID	LIB3176-073-P1-K1-B8
Method	BLASTX
NCBI GI	g1169451
BLAST score	159
E value	4.0e-11
Match length	83
% identity	36
NCBI Description	PROBABLE GLUCAN ENDO-1,3-BETA-GLUCOSIDASE A6 PRECURSOR ((1->3)-BETA-GLUCAN ENDOHYDROLASE) ((1->3)-BETA-GLUCANASE) (BETA-1,3-ENDOGLUCANASE) >gi_322510_pir__S31906 beta-1,3-glucanase homolog - Arabidopsis thaliana >gi_22677_emb_CAA49853_ (X70409) A6 [Arabidopsis thaliana] >gi_2244764_emb_CAB10187_ (Z97335) AMP-binding protein [Arabidopsis thaliana]

Seq. No.	157520
Seq. ID	LIB3176-073-P1-K1-B9
Method	BLASTX
NCBI GI	g1174448
BLAST score	576
E value	1.0e-59
Match length	127
% identity	91
NCBI Description	TRANSLOCON-ASSOCIATED PROTEIN, ALPHA SUBUNIT PRECURSOR (TRAP-ALPHA) (SIGNAL SEQUENCE RECEPTOR ALPHA SUBUNIT) (SSR-ALPHA) >gi_547391 (L32016) alpha-subunit; putative [Arabidopsis thaliana]

Seq. No.	157521
Seq. ID	LIB3176-073-P1-K1-C1
Method	BLASTX
NCBI GI	g3337095
BLAST score	525
E value	1.0e-53
Match length	146
% identity	53
NCBI Description	(AB016206) polygalacturonase inhibitor (PGIP) [Citrus iyo]

Seq. No.	157522
Seq. ID	LIB3176-073-P1-K1-C10
Method	BLASTX
NCBI GI	g1363489
BLAST score	632
E value	3.0e-66
Match length	133
% identity	89
NCBI Description	thioglucosidase (EC 3.2.3.1) 3D precursor - Arabidopsis thaliana >gi_984052_emb_CAA61592_ (X89413) thioglucoside glucohydrolase [Arabidopsis thaliana]

Seq. No. 157523

Seq. ID	LIB3176-073-P1-K1-C11
Method	BLASTX
NCBI GI	g399046
BLAST score	570
E value	7.0e-59
Match length	112
% identity	99
NCBI Description	ADENINE PHOSPHORIBOSYLTRANSFERASE 1 (APRT) >gi_99657_pir__S20867 adenine phosphoribosyltransferase (EC 2.4.2.7) - Arabidopsis thaliana >gi_16164_emb_CAA41497_ (X58640) adenine phosphoribosyltransferase [Arabidopsis thaliana] >gi_433050 (L19637) adenine phosphoribosyltransferase [Arabidopsis thaliana] >gi_3935182 (AC004557) F17L21.25 [Arabidopsis thaliana]

Seq. No.	157524
Seq. ID	LIB3176-073-P1-K1-C12
Method	BLASTX
NCBI GI	g548355
BLAST score	659
E value	2.0e-69
Match length	125
% identity	99
NCBI Description	NITRATE REDUCTASE 1 (NR1) >gi_486751_pir__S35228 nitrate reductase (NADH) (EC 1.6.6.1) 1 - Arabidopsis thaliana >gi_22757_emb_CAA79494_ (Z19050) nitrate reductase [Arabidopsis thaliana] >gi_448286_prf__1916406A nitrate reductase [Arabidopsis thaliana]

Seq. No.	157525
Seq. ID	LIB3176-073-P1-K1-C3
Method	BLASTX
NCBI GI	g3023848
BLAST score	664
E value	7.0e-70
Match length	133
% identity	52
NCBI Description	GUANINE NUCLEOTIDE-BINDING PROTEIN BETA SUBUNIT-LIKE PROTEIN (WD-40 REPEAT AUXIN-DEPENDENT PROTEIN ARCA) >gi_2289095 (U77381) WD-40 repeat protein [Arabidopsis thaliana]

Seq. No.	157526
Seq. ID	LIB3176-073-P1-K1-C4
Method	BLASTN
NCBI GI	g4510360
BLAST score	63
E value	8.0e-27
Match length	159
% identity	85
NCBI Description	Arabidopsis thaliana chromosome II BAC F11F19 genomic sequence, complete sequence

Seq. No.	157527
Seq. ID	LIB3176-073-P1-K1-C5
Method	BLASTX
NCBI GI	g2443755

BLAST score	552
E value	9.0e-57
Match length	118
% identity	85
NCBI Description	(AF020433) cyclophilin [Arabidopsis thaliana]

Seq. No.	157528
Seq. ID	LIB3176-073-P1-K1-C7
Method	BLASTN
NCBI GI	g4490291
BLAST score	88
E value	6.0e-42
Match length	144
% identity	90
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F17M5 (ESSA project)

Seq. No.	157529
Seq. ID	LIB3176-073-P1-K1-D1
Method	BLASTX
NCBI GI	g4006883
BLAST score	779
E value	2.0e-83
Match length	150
% identity	98
NCBI Description	(Z99707) cysteine proteinase [Arabidopsis thaliana]

Seq. No.	157530
Seq. ID	LIB3176-073-P1-K1-D10
Method	BLASTX
NCBI GI	g3551954
BLAST score	263
E value	6.0e-23
Match length	112
% identity	47
NCBI Description	(AF082030) senescence-associated protein 5 [Hemerocallis hybrid cultivar]

Seq. No.	157531
Seq. ID	LIB3176-073-P1-K1-D11
Method	BLASTX
NCBI GI	g4218120
BLAST score	444
E value	4.0e-44
Match length	113
% identity	78
NCBI Description	(AL035353) Proline-rich APG-like protein [Arabidopsis thaliana]

Seq. No.	157532
Seq. ID	LIB3176-073-P1-K1-D12
Method	BLASTX
NCBI GI	g2583130
BLAST score	259
E value	2.0e-22
Match length	94
% identity	56

NCBI Description	(AC002387) putative reverse transcriptase [Arabidopsis thaliana]
Seq. No.	157533
Seq. ID	LIB3176-073-P1-K1-D2
Method	BLASTX
NCBI GI	g3096931
BLAST score	535
E value	9.0e-55
Match length	113
% identity	94
NCBI Description	(AL023094) putative ribosomal protein S16 [Arabidopsis thaliana]
Seq. No.	157534
Seq. ID	LIB3176-073-P1-K1-D3
Method	BLASTX
NCBI GI	g1352258
BLAST score	70
E value	5.0e-11
Match length	142
% identity	39
NCBI Description	CARBONYL REDUCTASE (NADPH) (NADPH-DEPENDENT CARBONYL REDUCTASE) >gi_1083618_pir__S52349 carbonyl reductase (NADPH) (EC 1.1.1.184) - rat >gi_666087_emb_CAA59088_ (X84349) carbonyl reductase (NADPH) [Rattus norvegicus] >gi_1217651_emb_CAA65230_ (X95986) carbonyl reductase (NADPH) [Rattus norvegicus]
Seq. No.	157535
Seq. ID	LIB3176-073-P1-K1-D4
Method	BLASTX
NCBI GI	g3377813
BLAST score	232
E value	2.0e-19
Match length	112
% identity	42
NCBI Description	(AF076275) No definition line found [Arabidopsis thaliana]
Seq. No.	157536
Seq. ID	LIB3176-073-P1-K1-D5
Method	BLASTX
NCBI GI	g1710581
BLAST score	423
E value	8.0e-42
Match length	105
% identity	84
NCBI Description	60S RIBOSOMAL PROTEIN L9 >gi_2129720_pir__S71255 ribosomal protein L9 - Arabidopsis thaliana >gi_1107489_emb_CAA63024_ (X91958) 60S ribosomal protein L9 [Arabidopsis thaliana]
Seq. No.	157537
Seq. ID	LIB3176-073-P1-K1-D6
Method	BLASTX
NCBI GI	g1363489
BLAST score	494
E value	4.0e-50

Match length	91
% identity	99
NCBI Description	thioglucosidase (EC 3.2.3.1) 3D precursor - Arabidopsis thaliana >gi_984052_emb_CAA61592_ (X89413) thioglucoside glucohydrolase [Arabidopsis thaliana]

Seq. No.	157538
Seq. ID	LIB3176-073-P1-K1-D8
Method	BLASTX
NCBI GI	g4704613
BLAST score	398
E value	9.0e-39
Match length	102
% identity	79
NCBI Description	(AF109695) monodehydroascorbate reductase [Brassica juncea]

Seq. No.	157539
Seq. ID	LIB3176-073-P1-K1-E1
Method	BLASTN
NCBI GI	g3128134
BLAST score	356
E value	0.0e+00
Match length	419
% identity	95
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K18G13, complete sequence [Arabidopsis thaliana]

Seq. No.	157540
Seq. ID	LIB3176-073-P1-K1-E10
Method	BLASTX
NCBI GI	g119143
BLAST score	157
E value	2.0e-10
Match length	32
% identity	97
NCBI Description	ELONGATION FACTOR 1-ALPHA (EF-1-ALPHA) >gi_81606_pir__S06724 translation elongation factor eEF-1 alpha chain - Arabidopsis thaliana >gi_295788_emb_CAA34453_ (X16430) elongation factor 1-alpha [Arabidopsis thaliana] >gi_1369927_emb_CAA34454_ (X16431) elongation factor 1-alpha [Arabidopsis thaliana] >gi_1369928_emb_CAA34455_ (X16431) elongation factor 1-alpha [Arabidopsis thaliana] >gi_1532172 (U63815) EF-1alpha-A1 [Arabidopsis thaliana] >gi_1532173 (U63815) EF-1alpha-A2 [Arabidopsis thaliana] >gi_1532174 (U63815) EF-1alpha-A3 [Arabidopsis thaliana]

Seq. No.	157541
Seq. ID	LIB3176-073-P1-K1-E12
Method	BLASTN
NCBI GI	g4079614
BLAST score	272
E value	1.0e-151
Match length	441
% identity	99
NCBI Description	Arabidopsis thaliana chromosome I BAC F21M11 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	157542
Seq. ID	LIB3176-073-P1-K1-E2
Method	BLASTN
NCBI GI	g3046853
BLAST score	357
E value	0.0e+00
Match length	444
% identity	99
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MRA19, complete sequence [Arabidopsis thaliana]

Seq. No.	157543
Seq. ID	LIB3176-073-P1-K1-E3
Method	BLASTX
NCBI GI	g1531762
BLAST score	186
E value	7.0e-14
Match length	51
% identity	73
NCBI Description	(Y07765) S-adenosylmethionine decarboxylase [Arabidopsis thaliana]

Seq. No.	157544
Seq. ID	LIB3176-073-P1-K1-E4
Method	BLASTX
NCBI GI	g2738248
BLAST score	368
E value	3.0e-35
Match length	120
% identity	64
NCBI Description	(U97200) cobalamin-independent methionine synthase [Arabidopsis thaliana]

Seq. No.	157545
Seq. ID	LIB3176-073-P1-K1-E5
Method	BLASTN
NCBI GI	g3985954
BLAST score	374
E value	0.0e+00
Match length	418
% identity	97
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MRG21, complete sequence [Arabidopsis thaliana]

Seq. No.	157546
Seq. ID	LIB3176-073-P1-K1-E9
Method	BLASTX
NCBI GI	g2864617
BLAST score	602
E value	1.0e-62
Match length	145
% identity	87
NCBI Description	(AL021811) H+-transporting ATP synthase chain9 - like protein [Arabidopsis thaliana]

Seq. No.	157547
Seq. ID	LIB3176-073-P1-K1-F10

Method	BLASTX
NCBI GI	g1899188
BLAST score	396
E value	2.0e-38
Match length	108
% identity	44
NCBI Description	(U90212) DNA binding protein ACBF [Nicotiana tabacum]

Seq. No.	157548
Seq. ID	LIB3176-073-P1-K1-F12
Method	BLASTN
NCBI GI	g4587641
BLAST score	212
E value	1.0e-115
Match length	373
% identity	99
NCBI Description	Arabidopsis thaliana chromosome I BAC F20D21 genomic sequence, complete sequence

Seq. No.	157549
Seq. ID	LIB3176-073-P1-K1-F2
Method	BLASTN
NCBI GI	g4589439
BLAST score	113
E value	1.0e-56
Match length	383
% identity	98
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MQM1, complete sequence

Seq. No.	157550
Seq. ID	LIB3176-073-P1-K1-F3
Method	BLASTN
NCBI GI	g4760411
BLAST score	190
E value	1.0e-102
Match length	277
% identity	99
NCBI Description	Arabidopsis thaliana chromosome 1 BAC F25C20 sequence, complete sequence

Seq. No.	157551
Seq. ID	LIB3176-073-P1-K1-F4
Method	BLASTN
NCBI GI	g2645198
BLAST score	45
E value	4.0e-16
Match length	162
% identity	83
NCBI Description	Arabidopsis thaliana chromosome I BAC T26J12 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	157552
Seq. ID	LIB3176-073-P1-K1-F5
Method	BLASTX
NCBI GI	g228456
BLAST score	401

E value	2.0e-39
Match length	83
% identity	95
NCBI Description	Gln synthetase [Arabidopsis thaliana]

Seq. No.	157553
Seq. ID	LIB3176-073-P1-K1-F6
Method	BLASTN
NCBI GI	g4469002
BLAST score	342
E value	0.0e+00
Match length	422
% identity	95
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone T29A15 (ESSA project)

Seq. No.	157554
Seq. ID	LIB3176-073-P1-K1-F8
Method	BLASTX
NCBI GI	g3367521
BLAST score	132
E value	1.0e-58
Match length	117
% identity	89
NCBI Description	(AC004392) Similar to gb_U08285 membrane-associated salt-inducible protein from Nicotiana tabacum. ESTs gb_T44131 and gb_T04378 come from this gene. [Arabidopsis thaliana]

Seq. No.	157555
Seq. ID	LIB3176-073-P1-K1-F9
Method	BLASTX
NCBI GI	g2645971
BLAST score	148
E value	2.0e-09
Match length	28
% identity	96
NCBI Description	(AF034255) reversibly glycosylated polypeptide-3. [Arabidopsis thaliana]

Seq. No.	157556
Seq. ID	LIB3176-073-P1-K1-G1
Method	BLASTX
NCBI GI	g4325370
BLAST score	296
E value	9.0e-27
Match length	128
% identity	92
NCBI Description	(AF128396) similar to human phosphotyrosyl phosphatase activator PTPA (GB:X73478) [Arabidopsis thaliana]

Seq. No.	157557
Seq. ID	LIB3176-073-P1-K1-G10
Method	BLASTX
NCBI GI	g4587542
BLAST score	55
E value	6.0e-50

Match length	122
% identity	86
NCBI Description	(AC006577) Belongs to the PF_00657 Lipase/Acylhydrolase with GDSL-motif family. ESTs gb_T45815, gb_T45130 and gb_Z38046 come from this gene. [Arabidopsis thaliana]

Seq. No.	157558
Seq. ID	LIB3176-073-P1-K1-G11
Method	BLASTX
NCBI GI	g4835228
BLAST score	538
E value	4.0e-55
Match length	137
% identity	79
NCBI Description	(AL049862) calmodulin-like protein [Arabidopsis thaliana]

Seq. No.	157559
Seq. ID	LIB3176-073-P1-K1-G12
Method	BLASTX
NCBI GI	g3540181
BLAST score	179
E value	5.0e-13
Match length	134
% identity	33
NCBI Description	(AC004122) Unknown protein [Arabidopsis thaliana]

Seq. No.	157560
Seq. ID	LIB3176-073-P1-K1-G2
Method	BLASTN
NCBI GI	g3212846
BLAST score	188
E value	1.0e-101
Match length	333
% identity	95
NCBI Description	Arabidopsis thaliana chromosome II BAC F6E13 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	157561
Seq. ID	LIB3176-073-P1-K1-G3
Method	BLASTN
NCBI GI	g4335744
BLAST score	114
E value	3.0e-57
Match length	334
% identity	93
NCBI Description	Arabidopsis thaliana chromosome II BAC T4M8 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	157562
Seq. ID	LIB3176-073-P1-K1-G4
Method	BLASTX
NCBI GI	g2924779
BLAST score	581
E value	3.0e-60
Match length	128
% identity	91
NCBI Description	(AC002334) putative 3-ketoacyl-CoA thiolase [Arabidopsis

thaliana] >gi_2981616_dbj_BAA25248_ (AB008854) 3-ketoacyl-CoA thiolase [Arabidopsis thaliana] >gi_2981618_dbj_BAA25249_ (AB008855) 3-ketoacyl-CoA thiolase [Arabidopsis thaliana]

Seq. No.	157563
Seq. ID	LIB3176-073-P1-K1-G5
Method	BLASTX
NCBI GI	g1352345
BLAST score	601
E value	1.0e-62
Match length	125
% identity	92
NCBI Description	ELONGATION FACTOR 1-ALPHA (EF-1-ALPHA) >gi_18765_emb_CAA40182_ (X56856) eEF-1a [Glycine max]

Seq. No.	157564
Seq. ID	LIB3176-073-P1-K1-G6
Method	BLASTX
NCBI GI	g1350680
BLAST score	661
E value	1.0e-69
Match length	130
% identity	97
NCBI Description	60S RIBOSOMAL PROTEIN L1

Seq. No.	157565
Seq. ID	LIB3176-073-P1-K1-G7
Method	BLASTX
NCBI GI	g3292817
BLAST score	235
E value	4.0e-21
Match length	128
% identity	48
NCBI Description	(AL031018) hypothetical protein [Arabidopsis thaliana]

Seq. No.	157566
Seq. ID	LIB3176-073-P1-K1-G8
Method	BLASTX
NCBI GI	g1702986
BLAST score	458
E value	9.0e-46
Match length	96
% identity	97
NCBI Description	14-3-3-LIKE PROTEIN GF14 CHI >gi_1255987 (U09377) GF14chi isoform [Arabidopsis thaliana] >gi_1256534 (L09112) GF14 chi chain [Arabidopsis thaliana]

Seq. No.	157567
Seq. ID	LIB3176-073-P1-K1-G9
Method	BLASTX
NCBI GI	g2317729
BLAST score	662
E value	1.0e-69
Match length	125
% identity	98
NCBI Description	(AF013627) reversibly glycosylated polypeptide-1

[Arabidopsis thaliana]

Seq. No.	157568
Seq. ID	LIB3176-073-P1-K1-H1
Method	BLASTX
NCBI GI	g2230757
BLAST score	484
E value	8.0e-49
Match length	110
% identity	89
NCBI Description	(Y11969) dnaJ-like protein [Arabidopsis thaliana]

Seq. No.	157569
Seq. ID	LIB3176-073-P1-K1-H12
Method	BLASTN
NCBI GI	g2760172
BLAST score	434
E value	0.0e+00
Match length	434
% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MUB3, complete sequence [Arabidopsis thaliana]

Seq. No.	157570
Seq. ID	LIB3176-073-P1-K1-H2
Method	BLASTX
NCBI GI	g4510363
BLAST score	486
E value	5.0e-49
Match length	100
% identity	92
NCBI Description	(AC007017) putative DNA-binding protein [Arabidopsis thaliana]

Seq. No.	157571
Seq. ID	LIB3176-073-P1-K1-H4
Method	BLASTX
NCBI GI	g3292836
BLAST score	216
E value	1.0e-17
Match length	61
% identity	75
NCBI Description	(AL031018) gamma-glutamylcysteine synthetase [Arabidopsis thaliana] >gi_4262277_gb_AAD14544_ (AF068299) gamma-glutamylcysteine synthetase [Arabidopsis thaliana]

Seq. No.	157572
Seq. ID	LIB3176-073-P1-K1-H5
Method	BLASTX
NCBI GI	g4580920
BLAST score	389
E value	9.0e-38
Match length	122
% identity	68
NCBI Description	(AF113545) vacuole-associated annexin VCaB42 [Nicotiana tabacum]

Seq. No.	157573
Seq. ID	LIB3176-073-P1-K1-H6
Method	BLASTN
NCBI GI	g2765243
BLAST score	127
E value	6.0e-65
Match length	223
% identity	89
NCBI Description	Arabidopsis thaliana mRNA for invertase inhibitor homolog

Seq. No.	157574
Seq. ID	LIB3176-073-P1-K1-H7
Method	BLASTX
NCBI GI	g2244750
BLAST score	259
E value	4.0e-23
Match length	63
% identity	81
NCBI Description	(Z97335) adenosylhomocysteinase [Arabidopsis thaliana] >gi_3088579 (AF059581) S-adenosyl-L-homocysteine hydrolase [Arabidopsis thaliana]

Seq. No.	157575
Seq. ID	LIB3176-074-P1-K1-A12
Method	BLASTN
NCBI GI	g3449322
BLAST score	412
E value	0.0e+00
Match length	420
% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MXC17, complete sequence [Arabidopsis thaliana]

Seq. No.	157576
Seq. ID	LIB3176-074-P1-K1-A2
Method	BLASTX
NCBI GI	g2911085
BLAST score	296
E value	9.0e-27
Match length	126
% identity	56
NCBI Description	(AL021960) photosystem II oxygen-evolving complex protein 3-like [Arabidopsis thaliana] >gi_3402748_emb_CAA20194.1_ (AL031187) photosystem II oxygen-evolving complex protein 3 - like [Arabidopsis thaliana]

Seq. No.	157577
Seq. ID	LIB3176-074-P1-K1-A3
Method	BLASTX
NCBI GI	g3924611
BLAST score	849
E value	2.0e-91
Match length	163
% identity	98
NCBI Description	(AF069442) hypothetical protein [Arabidopsis thaliana]

Seq. No.	157578

Seq. ID	LIB3176-074-P1-K1-A4
Method	BLASTX
NCBI GI	g1076303
BLAST score	501
E value	9.0e-51
Match length	116
% identity	86
NCBI Description	RNA-binding protein cp29 precursor - Arabidopsis thaliana >gi_681902_dbj_BAA06518_ (D31710) cp29 [Arabidopsis thaliana]

Seq. No.	157579
Seq. ID	LIB3176-074-P1-K1-A5
Method	BLASTN
NCBI GI	g166705
BLAST score	107
E value	1.0e-53
Match length	115
% identity	98
NCBI Description	Arabidopsis thaliana glyceraldehyde-3-phosphate dehydrogenase C subunit (GapC) gene, complete cds

Seq. No.	157580
Seq. ID	LIB3176-074-P1-K1-A6
Method	BLASTX
NCBI GI	g99735
BLAST score	92
E value	1.0e-37
Match length	105
% identity	77
NCBI Description	L-ascorbate peroxidase (EC 1.11.1.11) precursor - Arabidopsis thaliana (fragment)

Seq. No.	157581
Seq. ID	LIB3176-074-P1-K1-A7
Method	BLASTX
NCBI GI	g2144501
BLAST score	245
E value	9.0e-21
Match length	74
% identity	59
NCBI Description	actinidain (EC 3.4.22.14) precursor - kiwi fruit >gi_166317 (M38422) actinidin [Actinidia deliciosa]

Seq. No.	157582
Seq. ID	LIB3176-074-P1-K1-A8
Method	BLASTX
NCBI GI	g1362005
BLAST score	594
E value	1.0e-61
Match length	156
% identity	78
NCBI Description	secY protein homolog precursor - Arabidopsis thaliana

Seq. No.	157583
Seq. ID	LIB3176-074-P1-K1-A9
Method	BLASTN

NCBI GI	g2477521
BLAST score	180
E value	1.0e-96
Match length	409
% identity	52
NCBI Description	Arabidopsis thaliana chromosome I BAC F22K20 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	157584
Seq. ID	LIB3176-074-P1-K1-B12
Method	BLASTN
NCBI GI	g2961335
BLAST score	373
E value	0.0e+00
Match length	437
% identity	100
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F1N20 (ESSAII project)

Seq. No.	157585
Seq. ID	LIB3176-074-P1-K1-B2
Method	BLASTX
NCBI GI	g4538963
BLAST score	522
E value	3.0e-53
Match length	132
% identity	61
NCBI Description	(AL049488) chlorophyll a/b-binding protein-like [Arabidopsis thaliana] >gi_4741958_gb_AAD28776.1_AF134129_1 (AF134129) Lhcb5 protein [Arabidopsis thaliana]

Seq. No.	157586
Seq. ID	LIB3176-074-P1-K1-B3
Method	BLASTX
NCBI GI	g4679028
BLAST score	310
E value	3.0e-28
Match length	124
% identity	52
NCBI Description	(AF077207) HSPC021 [Homo sapiens]

Seq. No.	157587
Seq. ID	LIB3176-074-P1-K1-B4
Method	BLASTN
NCBI GI	g4580454
BLAST score	273
E value	1.0e-152
Match length	430
% identity	88
NCBI Description	Arabidopsis thaliana chromosome II BAC T2G17 genomic sequence, complete sequence

Seq. No.	157588
Seq. ID	LIB3176-074-P1-K1-B5
Method	BLASTN
NCBI GI	g4662609
BLAST score	365

E value	0.0e+00
Match length	406
% identity	97
NCBI Description	Genomic sequence for Arabidopsis thaliana BAC F10A5, complete sequence

Seq. No.	157589
Seq. ID	LIB3176-074-P1-K1-B6
Method	BLASTX
NCBI GI	g1345592
BLAST score	570
E value	8.0e-59
Match length	120
% identity	96
NCBI Description	14-3-3-LIKE PROTEIN GF14 EPSILON >gi_1022778 (U36446) GF14 epsilon isoform [Arabidopsis thaliana]

Seq. No.	157590
Seq. ID	LIB3176-074-P1-K1-B7
Method	BLASTX
NCBI GI	g1766046
BLAST score	558
E value	1.0e-57
Match length	112
% identity	97
NCBI Description	(U81993) NAD+ dependent isocitrate dehydrogenase subunit 1 [Arabidopsis thaliana]

Seq. No.	157591
Seq. ID	LIB3176-074-P1-K1-C1
Method	BLASTN
NCBI GI	g3080406
BLAST score	73
E value	5.0e-33
Match length	125
% identity	90
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F23E12 (ESSA project)

Seq. No.	157592
Seq. ID	LIB3176-074-P1-K1-C12
Method	BLASTX
NCBI GI	g464621
BLAST score	591
E value	3.0e-61
Match length	137
% identity	82
NCBI Description	60S RIBOSOMAL PROTEIN L6 (YL16-LIKE) >gi_280374_pir__S28586 ribosomal protein ML16 - common ice plant >gi_19539_emb_CAA49175_ (X69378) ribosomal protein YL16 [Mesembryanthemum crystallinum]

Seq. No.	157593
Seq. ID	LIB3176-074-P1-K1-C2
Method	BLASTX
NCBI GI	g2924520
BLAST score	624

E value	2.0e-76
Match length	146
% identity	99
NCBI Description	(AL022023) plasma membrane intrinsic protein (SIMIP) [Arabidopsis thaliana]

Seq. No.	157594
Seq. ID	LIB3176-074-P1-K1-C3
Method	BLASTX
NCBI GI	g1335862
BLAST score	539
E value	3.0e-55
Match length	158
% identity	71
NCBI Description	(U42608) clathrin heavy chain [Glycine max]

Seq. No.	157595
Seq. ID	LIB3176-074-P1-K1-C4
Method	BLASTX
NCBI GI	g4165488
BLAST score	623
E value	4.0e-65
Match length	115
% identity	100
NCBI Description	(AJ132399) alpha-tubulin 3 [Hordeum vulgare]

Seq. No.	157596
Seq. ID	LIB3176-074-P1-K1-C5
Method	BLASTX
NCBI GI	g113026
BLAST score	479
E value	3.0e-48
Match length	115
% identity	83
NCBI Description	ISOCITRATE LYASE (ISOCITRASE) (ISOCITRATASE) (ICL) >gi_68211_pir__WZRPI isocitrate lyase (EC 4.1.3.1) - rape >gi_255220_bbs_112862 isocitrate lyase, threo-D S-isocitrate glyoxylate-lyase, IL {EC 4.1.3.1} [Brassica napus, seedlings, Peptide, 576 aa] >gi_167144 (L08482) isocitrate lyase [Brassica napus] >gi_447142_prf__1913424A isocitrate lyase [Brassica napus]

Seq. No.	157597
Seq. ID	LIB3176-074-P1-K1-C7
Method	BLASTN
NCBI GI	g2252823
BLAST score	463
E value	0.0e+00
Match length	488
% identity	52
NCBI Description	Arabidopsis thaliana BAC IG005I10

Seq. No.	157598
Seq. ID	LIB3176-074-P1-K1-C8
Method	BLASTX
NCBI GI	g4335737
BLAST score	69

E value	1.0e-25
Match length	145
% identity	44
NCBI Description	(AC006248) putative serine/threonine kinase [Arabidopsis thaliana]

Seq. No.	157599
Seq. ID	LIB3176-074-P1-K1-C9
Method	BLASTX
NCBI GI	g132074
BLAST score	781
E value	1.0e-83
Match length	145
% identity	99
NCBI Description	RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN 1A PRECURSOR (RUBISCO SMALL SUBUNIT 1A) >gi_68063_pir__RKMUA1 ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain A1 precursor - Arabidopsis thaliana

Seq. No.	157600
Seq. ID	LIB3176-074-P1-K1-D1
Method	BLASTX
NCBI GI	g4544399
BLAST score	321
E value	2.0e-48
Match length	156
% identity	61
NCBI Description	(AC007047) putative beta-ketoacyl-CoA synthase [Arabidopsis thaliana]

Seq. No.	157601
Seq. ID	LIB3176-074-P1-K1-D11
Method	BLASTX
NCBI GI	g2341034
BLAST score	361
E value	1.0e-34
Match length	86
% identity	81
NCBI Description	(AC000104) F19P19.13 [Arabidopsis thaliana]

Seq. No.	157602
Seq. ID	LIB3176-074-P1-K1-D2
Method	BLASTX
NCBI GI	g3913733
BLAST score	680
E value	1.0e-71
Match length	141
% identity	91
NCBI Description	HYDROXYACYLGLUTATHIONE HYDROLASE CYTOPLASMIC ISOZYME (GLYOXALASE II) (GLX II) >gi_1924921_emb_CAA69644_ (Y08357) hydroxyacylglutathione hydrolase [Arabidopsis thaliana]

Seq. No.	157603
Seq. ID	LIB3176-074-P1-K1-D3
Method	BLASTX
NCBI GI	g2244750
BLAST score	759

E value	5.0e-81
Match length	150
% identity	99
NCBI Description	(Z97335) adenosylhomocysteinase [Arabidopsis thaliana] >gi_3088579 (AF059581) S-adenosyl-L-homocysteine hydrolase [Arabidopsis thaliana]

Seq. No.	157604
Seq. ID	LIB3176-074-P1-K1-D4
Method	BLASTX
NCBI GI	g4585882
BLAST score	406
E value	7.0e-40
Match length	85
% identity	96
NCBI Description	(AC005850) PSI type III chlorophyll a/b-binding protein [Arabidopsis thaliana]

Seq. No.	157605
Seq. ID	LIB3176-074-P1-K1-D5
Method	BLASTX
NCBI GI	g1256509
BLAST score	194
E value	4.0e-15
Match length	48
% identity	69
NCBI Description	(X92943) pectate lyase [Musa acuminata]

Seq. No.	157606
Seq. ID	LIB3176-074-P1-K1-D8
Method	BLASTX
NCBI GI	g1703108
BLAST score	685
E value	3.0e-72
Match length	130
% identity	98
NCBI Description	ACTIN 2/7 >gi_2129525_pir__S71210 actin 2 - Arabidopsis thaliana >gi_2129528_pir__S68107 actin 7 - Arabidopsis thaliana >gi_1049307 (U37281) actin-2 [Arabidopsis thaliana] >gi_1943863 (U27811) actin7 [Arabidopsis thaliana]

Seq. No.	157607
Seq. ID	LIB3176-074-P1-K1-D9
Method	BLASTX
NCBI GI	g2244852
BLAST score	701
E value	4.0e-74
Match length	147
% identity	98
NCBI Description	(Z97337) hypothetical protein [Arabidopsis thaliana]

Seq. No.	157608
Seq. ID	LIB3176-074-P1-K1-E12
Method	BLASTX
NCBI GI	g3122673
BLAST score	650

E value	3.0e-68
Match length	146
% identity	87
NCBI Description	60S RIBOSOMAL PROTEIN L15 >gi_2245027_emb_CAB10447_ (Z97341) ribosomal protein [Arabidopsis thaliana]

Seq. No.	157609
Seq. ID	LIB3176-074-P1-K1-E2
Method	BLASTX
NCBI GI	g1353157
BLAST score	251
E value	2.0e-21
Match length	130
% identity	38
NCBI Description	HYPOTHETICAL 108.5 KD PROTEIN R06F6.2 IN CHROMOSOME II >gi_3878900_emb_CAA86774_ (Z46794) similar to vacuolar biogenesis protein (pep5); cDNA EST EMBL:D27614 comes from this gene; cDNA EST EMBL:D34974 comes from this gene [Caenorhabditis elegans]

Seq. No.	157610
Seq. ID	LIB3176-074-P1-K1-E5
Method	BLASTX
NCBI GI	g232031
BLAST score	150
E value	1.0e-09
Match length	93
% identity	37
NCBI Description	ELONGATION FACTOR 1 BETA' >gi_322851_pir__S29224 translation elongation factor eEF-1 beta' chain - rice >gi_218161_dbj_BAA02253_ (D12821) elongation factor 1 beta' [Oryza sativa]

Seq. No.	157611
Seq. ID	LIB3176-074-P1-K1-E6
Method	BLASTX
NCBI GI	g416681
BLAST score	202
E value	1.0e-15
Match length	116
% identity	38
NCBI Description	ATP SYNTHASE DELTA CHAIN, CHLOROPLAST PRECURSOR >gi_280404_pir__S26198 H+-transporting ATP synthase (EC 3.6.1.34) delta chain precursor, chloroplast - common tobacco >gi_19787_emb_CAA45153_ (X63607) chloroplast ATP synthase (delta subunit) [Nicotiana tabacum]

Seq. No.	157612
Seq. ID	LIB3176-074-P1-K1-E9
Method	BLASTX
NCBI GI	g3549670
BLAST score	565
E value	3.0e-58
Match length	112
% identity	99
NCBI Description	(AL031394) putative protein [Arabidopsis thaliana]

Seq. No.	157613
Seq. ID	LIB3176-074-P1-K1-F1
Method	BLASTX
NCBI GI	g1657617
BLAST score	653
E value	1.0e-68
Match length	129
% identity	99
NCBI Description	(U72503) G2p [Arabidopsis thaliana] >gi_3068707 (AF049236) putative nuclear DNA-binding protein G2p [Arabidopsis thaliana]

Seq. No.	157614
Seq. ID	LIB3176-074-P1-K1-F10
Method	BLASTX
NCBI GI	g1346929
BLAST score	746
E value	2.0e-79
Match length	157
% identity	97
NCBI Description	ASPARTATE CARBAMOYLTRANSFERASE PRECURSOR (ASPARTATE TRANSCARBAMYLASE) (ATCASE) >gi_1076293_pir__S46441 aspartate carbamoyltransferase (EC 2.1.3.2) - Arabidopsis thaliana >gi_443820_emb_CAA50687_ (X71843) aspartate carbamoyltransferase [Arabidopsis thaliana]

Seq. No.	157615
Seq. ID	LIB3176-074-P1-K1-F11
Method	BLASTN
NCBI GI	g2337888
BLAST score	311
E value	1.0e-175
Match length	475
% identity	99
NCBI Description	Genomic sequence for Arabidopsis thaliana BAC F14J16, complete sequence [Arabidopsis thaliana]

Seq. No.	157616
Seq. ID	LIB3176-074-P1-K1-F12
Method	BLASTX
NCBI GI	g126766
BLAST score	77
E value	7.0e-51
Match length	126
% identity	83
NCBI Description	MALATE SYNTHASE, GLYOXYSOMAL >gi_68216_pir__SYRPMA malate synthase (EC 4.1.3.2), glyoxysomal - rape >gi_167150 (J04468) malate synthase (EC 4.1.3.2) [Brassica napus]

Seq. No.	157617
Seq. ID	LIB3176-074-P1-K1-F2
Method	BLASTX
NCBI GI	g1928991
BLAST score	648
E value	5.0e-68
Match length	146
% identity	90

NCBI Description	(U92815) heat shock protein 70 precursor [Citrullus lanatus]
Seq. No.	157618
Seq. ID	LIB3176-074-P1-K1-F3
Method	BLASTX
NCBI GI	g2980775
BLAST score	137
E value	2.0e-64
Match length	137
% identity	96
NCBI Description	(AL022198) leucyl aminopeptidase - like protein (partial) [Arabidopsis thaliana]
Seq. No.	157619
Seq. ID	LIB3176-074-P1-K1-F4
Method	BLASTX
NCBI GI	g1791309
BLAST score	487
E value	3.0e-49
Match length	102
% identity	96
NCBI Description	(U83500) cystathionine gamma-synthase [Arabidopsis thaliana] >gi_2852454_dbj_BAA24699_ (AB010888) cystathionine gamma-synthase [Arabidopsis thaliana]
Seq. No.	157620
Seq. ID	LIB3176-074-P1-K1-F5
Method	BLASTX
NCBI GI	g2078350
BLAST score	270
E value	1.0e-23
Match length	92
% identity	63
NCBI Description	(U95923) transaldolase [Solanum tuberosum]
Seq. No.	157621
Seq. ID	LIB3176-074-P1-K1-F6
Method	BLASTX
NCBI GI	g4582468
BLAST score	300
E value	7.0e-28
Match length	72
% identity	86
NCBI Description	(AC007071) putative 40S ribosomal protein; contains C-terminal domain [Arabidopsis thaliana]
Seq. No.	157622
Seq. ID	LIB3176-074-P1-K1-F7
Method	BLASTX
NCBI GI	g119143
BLAST score	395
E value	3.0e-58
Match length	139
% identity	86
NCBI Description	ELONGATION FACTOR 1-ALPHA (EF-1-ALPHA) >gi_81606_pir__S06724 translation elongation factor eEF-1

alpha chain - Arabidopsis thaliana >gi_295788_emb_CAA34453_ (X16430) elongation factor 1-alpha [Arabidopsis thaliana] >gi_1369927_emb_CAA34454_ (X16431) elongation factor 1-alpha [Arabidopsis thaliana] >gi_1369928_emb_CAA34455_ (X16431) elongation factor 1-alpha [Arabidopsis thaliana] >gi_1532172 (U63815) EF-1alpha-A1 [Arabidopsis thaliana] >gi_1532173 (U63815) EF-1alpha-A2 [Arabidopsis thaliana] >gi_1532174 (U63815) EF-1alpha-A3 [Arabidopsis thaliana]

Seq. No.	157623
Seq. ID	LIB3176-074-P1-K1-F8
Method	BLASTX
NCBI GI	g2583134
BLAST score	393
E value	4.0e-38
Match length	79
% identity	96
NCBI Description	(AC002387) putative proline-rich protein [Arabidopsis thaliana]

Seq. No.	157624
Seq. ID	LIB3176-074-P1-K1-F9
Method	BLASTX
NCBI GI	g4406780
BLAST score	572
E value	3.0e-59
Match length	129
% identity	84
NCBI Description	(AC006532) putative multispanning membrane protein [Arabidopsis thaliana]

Seq. No.	157625
Seq. ID	LIB3176-074-P1-K1-G10
Method	BLASTX
NCBI GI	g2894564
BLAST score	134
E value	1.0e-28
Match length	68
% identity	97
NCBI Description	(AL021890) putative protein [Arabidopsis thaliana]

Seq. No.	157626
Seq. ID	LIB3176-074-P1-K1-G11
Method	BLASTX
NCBI GI	g3193310
BLAST score	372
E value	1.0e-35
Match length	89
% identity	84
NCBI Description	(AF069300) contains similarity to Nicotiana tabacum hin1 (GB:Y07563) [Arabidopsis thaliana]

Seq. No.	157627
Seq. ID	LIB3176-074-P1-K1-G12
Method	BLASTX
NCBI GI	g115767
BLAST score	53

E value	2.0e-80
Match length	156
% identity	97
NCBI Description	CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR (CAB-165/180) (LHCP) >gi_81603_pir__A29280 chlorophyll a/b-binding protein ab165 - Arabidopsis thaliana >gi_16368_emb_CAA27540_ (X03907) chlorophyll a/b binding protein (LHCP AB 65) [Arabidopsis thaliana] >gi_16372_emb_CAA27541_ (X03908) chlorophyll a/b binding protein (LHCP AB 180) [Arabidopsis thaliana]

Seq. No.	157628
Seq. ID	LIB3176-074-P1-K1-G2
Method	BLASTX
NCBI GI	g4678261
BLAST score	713
E value	1.0e-75
Match length	154
% identity	94
NCBI Description	(AL049657) putative proteasome regulatory subunit [Arabidopsis thaliana]

Seq. No.	157629
Seq. ID	LIB3176-074-P1-K1-G4
Method	BLASTX
NCBI GI	g1172872
BLAST score	461
E value	3.0e-46
Match length	102
% identity	88
NCBI Description	CYSTEINE PROTEINASE RD19A PRECURSOR >gi_541856_pir__JN0718 drought-inducible cysteine proteinase (EC 3.4.22.-) RD19A precursor - Arabidopsis thaliana >gi_435618_dbj_BAA02373_ (D13042) thiol protease [Arabidopsis thaliana] >gi_4539328_emb_CAB38829.1_ (AL035679) drought-inducible cysteine proteinase RD19A precursor [Arabidopsis thaliana]

Seq. No.	157630
Seq. ID	LIB3176-074-P1-K1-G5
Method	BLASTX
NCBI GI	g3107931
BLAST score	663
E value	9.0e-70
Match length	150
% identity	86
NCBI Description	(AB013353) UDP-glucose pyrophosphorylase [Pyrus pyrifolia]

Seq. No.	157631
Seq. ID	LIB3176-074-P1-K1-G6
Method	BLASTX
NCBI GI	g3355475
BLAST score	498
E value	2.0e-50
Match length	139
% identity	72
NCBI Description	(AC004218) ribosomal protein L23a [Arabidopsis thaliana]

Seq. No.	157632
Seq. ID	LIB3176-074-P1-K1-G7
Method	BLASTX
NCBI GI	g2062158
BLAST score	615
E value	4.0e-64
Match length	151
% identity	42
NCBI Description	(AC001645) jasmonate inducible protein isolog [Arabidopsis thaliana]

Seq. No.	157633
Seq. ID	LIB3176-074-P1-K1-G8
Method	BLASTX
NCBI GI	g1173104
BLAST score	491
E value	6.0e-50
Match length	91
% identity	96
NCBI Description	RIBONUCLEASE 2 PRECURSOR >gi_289210 (M98336) ribonuclease [Arabidopsis thaliana] >gi_2642160 (AC003000) ribonuclease, RNS2 [Arabidopsis thaliana]

Seq. No.	157634
Seq. ID	LIB3176-074-P1-K1-G9
Method	BLASTX
NCBI GI	g2335099
BLAST score	286
E value	1.0e-25
Match length	99
% identity	56
NCBI Description	(AC002339) unknown protein [Arabidopsis thaliana]

Seq. No.	157635
Seq. ID	LIB3176-074-P1-K1-H1
Method	BLASTX
NCBI GI	g3043415
BLAST score	294
E value	2.0e-57
Match length	141
% identity	82
NCBI Description	(Y17053) At-hsc70-3 [Arabidopsis thaliana]

Seq. No.	157636
Seq. ID	LIB3176-074-P1-K1-H10
Method	BLASTX
NCBI GI	g1001430
BLAST score	277
E value	2.0e-24
Match length	130
% identity	49
NCBI Description	(D63999) ORF1 [Synechocystis sp.]

Seq. No.	157637
Seq. ID	LIB3176-074-P1-K1-H11
Method	BLASTN
NCBI GI	g3319339

BLAST score	38
E value	4.0e-12
Match length	58
% identity	91
NCBI Description	Arabidopsis thaliana BAC F9D12

Seq. No.	157638
Seq. ID	LIB3176-074-P1-K1-H12
Method	BLASTX
NCBI GI	g3236242
BLAST score	456
E value	2.0e-45
Match length	101
% identity	91
NCBI Description	(AC004684) putative ribosomal protein L36 [Arabidopsis thaliana]

Seq. No.	157639
Seq. ID	LIB3176-074-P1-K1-H3
Method	BLASTX
NCBI GI	g2262167
BLAST score	556
E value	2.0e-57
Match length	107
% identity	98
NCBI Description	(AC002329) cytosolic ribosomal protein S4 [Arabidopsis thaliana]

Seq. No.	157640
Seq. ID	LIB3176-074-P1-K1-H4
Method	BLASTX
NCBI GI	g267083
BLAST score	551
E value	1.0e-56
Match length	102
% identity	99
NCBI Description	TUBULIN BETA-9 CHAIN >gi_320190_pir__JQ1593 tubulin beta-9 chain - Arabidopsis thaliana >gi_166910 (M84706) beta-9 tubulin [Arabidopsis thaliana]

Seq. No.	157641
Seq. ID	LIB3176-074-P1-K1-H6
Method	BLASTN
NCBI GI	g4699904
BLAST score	259
E value	1.0e-144
Match length	279
% identity	98
NCBI Description	Genomic sequence for Arabidopsis thaliana BAC F1E22, complete sequence

Seq. No.	157642
Seq. ID	LIB3176-074-P1-K1-H7
Method	BLASTX
NCBI GI	g4587610
BLAST score	662
E value	1.0e-69

Match length	134
% identity	99
NCBI Description	(AC006951) putative indole-3-glycerol phosphate synthase precursor [Arabidopsis thaliana]

Seq. No.	157643
Seq. ID	LIB3176-074-P1-K1-H8
Method	BLASTX
NCBI GI	g2213584
BLAST score	81
E value	5.0e-60
Match length	133
% identity	83
NCBI Description	(AC000348) T7N9.4 [Arabidopsis thaliana]

Seq. No.	157644
Seq. ID	LIB3176-083-P1-K1-A1
Method	BLASTN
NCBI GI	g4371278
BLAST score	148
E value	1.0e-77
Match length	323
% identity	87
NCBI Description	Arabidopsis thaliana chromosome II BAC T2N18 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	157645
Seq. ID	LIB3176-083-P1-K1-A10
Method	BLASTX
NCBI GI	g464621
BLAST score	625
E value	2.0e-65
Match length	143
% identity	82
NCBI Description	60S RIBOSOMAL PROTEIN L6 (YL16-LIKE) >gi_280374_pir__S28586 ribosomal protein ML16 - common ice plant >gi_19539_emb_CAA49175_ (X69378) ribosomal protein YL16 [Mesembryanthemum crystallinum]

Seq. No.	157646
Seq. ID	LIB3176-083-P1-K1-A11
Method	BLASTX
NCBI GI	g481132
BLAST score	479
E value	2.0e-48
Match length	118
% identity	77
NCBI Description	sucrose transport protein SUC1 - Arabidopsis thaliana >gi_407094_emb_CAA53147_ (X75365) sucrose-proton symporter [Arabidopsis thaliana]

Seq. No.	157647
Seq. ID	LIB3176-083-P1-K1-A12
Method	BLASTX
NCBI GI	g132719
BLAST score	261
E value	1.0e-22

Match length	114
% identity	45
NCBI Description	50S RIBOSOMAL PROTEIN L17 >gi_71252_pir__R5EC17 ribosomal protein L17 - Escherichia coli >gi_42800_emb_CAA26396_ (X02543) ribosomal protein L17 (aa 1-127) [Escherichia coli] >gi_42808_emb_CAA25338_ (X00766) ribosomal component L17 [Escherichia coli] >gi_147716 (J01685) ribosomal protein L17 [Escherichia coli] >gi_606228 (U18997) 50S ribosomal subunit protein L17 [Escherichia coli] >gi_1789689 (AE000407) 50S ribosomal subunit protein L17 [Escherichia coli] >gi_223573_prf__0901236A protein L17 [Escherichia coli]
Seq. No.	157648
Seq. ID	LIB3176-083-P1-K1-A3
Method	BLASTX
NCBI GI	g1363489
BLAST score	611
E value	1.0e-63
Match length	138
% identity	82
NCBI Description	thioglucosidase (EC 3.2.3.1) 3D precursor - Arabidopsis thaliana >gi_984052_emb_CAA61592_ (X89413) thioglucoside glucohydrolase [Arabidopsis thaliana]
Seq. No.	157649
Seq. ID	LIB3176-083-P1-K1-A4
Method	BLASTX
NCBI GI	g1710581
BLAST score	644
E value	1.0e-67
Match length	133
% identity	95
NCBI Description	60S RIBOSOMAL PROTEIN L9 >gi_2129720_pir__S71255 ribosomal protein L9 - Arabidopsis thaliana >gi_1107489_emb_CAA63024_ (X91958) 60S ribosomal protein L9 [Arabidopsis thaliana]
Seq. No.	157650
Seq. ID	LIB3176-083-P1-K1-A6
Method	BLASTX
NCBI GI	g1709970
BLAST score	343
E value	2.0e-32
Match length	108
% identity	69
NCBI Description	60S RIBOSOMAL PROTEIN L10A
Seq. No.	157651
Seq. ID	LIB3176-083-P1-K1-A8
Method	BLASTX
NCBI GI	g1363489
BLAST score	751
E value	4.0e-80
Match length	135
% identity	100
NCBI Description	thioglucosidase (EC 3.2.3.1) 3D precursor - Arabidopsis thaliana >gi_984052_emb_CAA61592_ (X89413) thioglucoside

glucohydrolase [Arabidopsis thaliana]

Seq. No.	157652
Seq. ID	LIB3176-083-P1-K1-A9
Method	BLASTX
NCBI GI	g267073
BLAST score	447
E value	5.0e-58
Match length	130
% identity	90
NCBI Description	TUBULIN BETA-2/BETA-3 CHAIN >gi_320184_pir__JQ1587 tubulin beta chain - Arabidopsis thaliana >gi_166898 (M84700) beta-2 tubulin [Arabidopsis thaliana] >gi_166900 (M84701) beta-3 tubulin [Arabidopsis thaliana]

Seq. No.	157653
Seq. ID	LIB3176-083-P1-K1-B1
Method	BLASTX
NCBI GI	g1345592
BLAST score	665
E value	5.0e-70
Match length	142
% identity	93
NCBI Description	14-3-3-LIKE PROTEIN GF14 EPSILON >gi_1022778 (U36446) GF14 epsilon isoform [Arabidopsis thaliana]

Seq. No.	157654
Seq. ID	LIB3176-083-P1-K1-B10
Method	BLASTX
NCBI GI	g140508
BLAST score	417
E value	3.0e-66
Match length	133
% identity	90
NCBI Description	PROBABLE INTRON MATURASE >gi_99852_pir__S07168 probable maturase, 63K - white mustard chloroplast >gi_12220_emb_CAA28509_ (X04826) ycf14 (AA1-324) [Sinapis alba]

Seq. No.	157655
Seq. ID	LIB3176-083-P1-K1-B11
Method	BLASTX
NCBI GI	g4741948
BLAST score	242
E value	5.0e-21
Match length	49
% identity	100
NCBI Description	(AF134124) Lhcb2 protein [Arabidopsis thaliana]

Seq. No.	157656
Seq. ID	LIB3176-083-P1-K1-B12
Method	BLASTX
NCBI GI	g4049348
BLAST score	502
E value	6.0e-51
Match length	98
% identity	100

NCBI Description	(AL034567) putative protein [Arabidopsis thaliana]
Seq. No.	157657
Seq. ID	LIB3176-083-P1-K1-B3
Method	BLASTX
NCBI GI	g3176673
BLAST score	627
E value	1.0e-65
Match length	142
% identity	89
NCBI Description	(AC003671) Similar to serine/threonine kinase gb_Y12531 from Brassica oleracea. [Arabidopsis thaliana]
Seq. No.	157658
Seq. ID	LIB3176-083-P1-K1-B4
Method	BLASTX
NCBI GI	g3687249
BLAST score	581
E value	3.0e-60
Match length	122
% identity	89
NCBI Description	(AC005169) putative copia-like transposable element [Arabidopsis thaliana]
Seq. No.	157659
Seq. ID	LIB3176-083-P1-K1-B5
Method	BLASTX
NCBI GI	g4454056
BLAST score	597
E value	4.0e-62
Match length	141
% identity	89
NCBI Description	(AJ000930) ClpP [Arabidopsis thaliana]
Seq. No.	157660
Seq. ID	LIB3176-083-P1-K1-B6
Method	BLASTN
NCBI GI	g2244747
BLAST score	336
E value	0.0e+00
Match length	435
% identity	100
NCBI Description	Arabidopsis thaliana DNA chromosome 4, ESSA I contig fragment No
Seq. No.	157661
Seq. ID	LIB3176-083-P1-K1-B7
Method	BLASTN
NCBI GI	g2924733
BLAST score	48
E value	1.0e-18
Match length	102
% identity	93
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MUF9, complete sequence [Arabidopsis thaliana]
Seq. No.	157662

Seq. ID	LIB3176-083-P1-K1-B8
Method	BLASTX
NCBI GI	g1172873
BLAST score	431
E value	1.0e-42
Match length	133
% identity	68
NCBI Description	CYSTEINE PROTEINASE RD21A PRECURSOR >gi_541857_pir__JN0719 drought-inducible cysteine proteinase (EC 3.4.22.-) RD21A precursor - Arabidopsis thaliana >gi_435619_dbj_BAA02374_ (D13043) thiol protease [Arabidopsis thaliana]

Seq. No.	157663
Seq. ID	LIB3176-083-P1-K1-B9
Method	BLASTX
NCBI GI	g4587680
BLAST score	229
E value	1.0e-19
Match length	61
% identity	74
NCBI Description	(AC007197) putative cytochrome p450 [Arabidopsis thaliana]

Seq. No.	157664
Seq. ID	LIB3176-083-P1-K1-C1
Method	BLASTN
NCBI GI	g4159711
BLAST score	226
E value	1.0e-124
Match length	430
% identity	79
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MUD12, complete sequence

Seq. No.	157665
Seq. ID	LIB3176-083-P1-K1-C10
Method	BLASTX
NCBI GI	g1169599
BLAST score	398
E value	9.0e-39
Match length	92
% identity	83
NCBI Description	OMEGA-3 FATTY ACID DESATURASE, CHLOROPLAST PRECURSOR >gi_541883_pir__JQ2336 omega-3 fatty acid desaturase (EC 1.14.99.-) CFD - Arabidopsis thaliana >gi_408481 (L22961) omega-3 fatty acid desaturase [Arabidopsis thaliana] >gi_468434_dbj_BAA05040_ (D26019) plastid fatty acid desaturase [Arabidopsis thaliana] >gi_541653_dbj_BAA03106_ (D14007) omega-3-desaturase [Arabidopsis thaliana]

Seq. No.	157666
Seq. ID	LIB3176-083-P1-K1-C11
Method	BLASTX
NCBI GI	g2894564
BLAST score	133
E value	2.0e-28
Match length	66
% identity	100

NCBI Description	(AL021890) putative protein [Arabidopsis thaliana]
Seq. No.	157667
Seq. ID	LIB3176-083-P1-K1-C12
Method	BLASTN
NCBI GI	g4757397
BLAST score	405
E value	0.0e+00
Match length	413
% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MBG14, complete sequence
Seq. No.	157668
Seq. ID	LIB3176-083-P1-K1-C2
Method	BLASTN
NCBI GI	g2760829
BLAST score	194
E value	1.0e-105
Match length	384
% identity	100
NCBI Description	Arabidopsis thaliana chromosome II BAC F18A8 genomic sequence, complete sequence [Arabidopsis thaliana]
Seq. No.	157669
Seq. ID	LIB3176-083-P1-K1-C3
Method	BLASTX
NCBI GI	g1063415
BLAST score	664
E value	6.0e-70
Match length	124
% identity	100
NCBI Description	(L40948) K+ channel protein [Arabidopsis thaliana]
Seq. No.	157670
Seq. ID	LIB3176-083-P1-K1-C4
Method	BLASTX
NCBI GI	g3885331
BLAST score	736
E value	2.0e-78
Match length	142
% identity	100
NCBI Description	(AC005623) putative cytochrome p450 protein [Arabidopsis thaliana]
Seq. No.	157671
Seq. ID	LIB3176-083-P1-K1-C9
Method	BLASTN
NCBI GI	g2833627
BLAST score	420
E value	0.0e+00
Match length	420
% identity	100
NCBI Description	Arabidopsis thaliana chromosome 1 BAC F17O7 complete sequence [Arabidopsis thaliana]
Seq. No.	157672

Seq. ID	LIB3176-083-P1-K1-D1
Method	BLASTX
NCBI GI	g3738092
BLAST score	653
E value	1.0e-68
Match length	127
% identity	100
NCBI Description	(AC005617) similar to glyoxysomal malate dehydrogenase [Arabidopsis thaliana]

Seq. No.	157673
Seq. ID	LIB3176-083-P1-K1-D10
Method	BLASTX
NCBI GI	g2961372
BLAST score	727
E value	2.0e-77
Match length	139
% identity	99
NCBI Description	(AL022141) putative ribosomal protein L8 [Arabidopsis thaliana] >gi_3036817_emb_CAA18507_ (AL022373) ribosomal protein L2 [Arabidopsis thaliana]

Seq. No.	157674
Seq. ID	LIB3176-083-P1-K1-D12
Method	BLASTN
NCBI GI	g4757414
BLAST score	388
E value	0.0e+00
Match length	416
% identity	98
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MYF24, complete sequence

Seq. No.	157675
Seq. ID	LIB3176-083-P1-K1-D2
Method	BLASTX
NCBI GI	g2760362
BLAST score	613
E value	6.0e-64
Match length	120
% identity	100
NCBI Description	(AF016511) 15.9 kDa subunit of RNA polymerase II [Arabidopsis thaliana]

Seq. No.	157676
Seq. ID	LIB3176-083-P1-K1-D3
Method	BLASTX
NCBI GI	g3021506
BLAST score	49
E value	6.0e-29
Match length	88
% identity	75
NCBI Description	(X96727) isocitrate dehydrogenase (NAD+) [Nicotiana tabacum]

Seq. No.	157677
Seq. ID	LIB3176-083-P1-K1-D4

Method	BLASTX
NCBI GI	g1363489
BLAST score	645
E value	1.0e-67
Match length	118
% identity	100
NCBI Description	thioglucosidase (EC 3.2.3.1) 3D precursor - Arabidopsis thaliana >gi_984052_emb_CAA61592_ (X89413) thioglucoside glucohydrolase [Arabidopsis thaliana]

Seq. No.	157678
Seq. ID	LIB3176-083-P1-K1-D5
Method	BLASTX
NCBI GI	g4204285
BLAST score	754
E value	2.0e-80
Match length	141
% identity	98
NCBI Description	(AC003027) lcl_prt_seq No definition line found [Arabidopsis thaliana]

Seq. No.	157679
Seq. ID	LIB3176-083-P1-K1-D6
Method	BLASTX
NCBI GI	g3603353
BLAST score	594
E value	1.0e-61
Match length	136
% identity	83
NCBI Description	(AF074843) peroxisomal targeting signal type 1 receptor [Arabidopsis thaliana]

Seq. No.	157680
Seq. ID	LIB3176-083-P1-K1-D8
Method	BLASTX
NCBI GI	g3402487
BLAST score	707
E value	5.0e-75
Match length	138
% identity	100
NCBI Description	(AB015138) Vacuolar proton pyrophosphatase [Arabidopsis thaliana]

Seq. No.	157681
Seq. ID	LIB3176-083-P1-K1-D9
Method	BLASTN
NCBI GI	g2253009
BLAST score	333
E value	0.0e+00
Match length	337
% identity	100
NCBI Description	Arabidopsis thaliana mRNA for MAP3K delta-1 protein kinase, partial

Seq. No.	157682
Seq. ID	LIB3176-083-P1-K1-E1
Method	BLASTX

NCBI GI	g2292917
BLAST score	747
E value	1.0e-79
Match length	140
% identity	100
NCBI Description	(X99851) galactokinase [Arabidopsis thaliana]

Seq. No.	157683
Seq. ID	LIB3176-083-P1-K1-E10
Method	BLASTX
NCBI GI	g1363489
BLAST score	645
E value	1.0e-67
Match length	120
% identity	99
NCBI Description	thioglucosidase (EC 3.2.3.1) 3D precursor - Arabidopsis thaliana >gi_984052_emb_CAA61592_ (X89413) thioglucoside glucohydrolase [Arabidopsis thaliana]

Seq. No.	157684
Seq. ID	LIB3176-083-P1-K1-E12
Method	BLASTX
NCBI GI	g2739389
BLAST score	537
E value	5.0e-55
Match length	142
% identity	30
NCBI Description	(AC002505) Cf-2.2 like protein [Arabidopsis thaliana]

Seq. No.	157685
Seq. ID	LIB3176-083-P1-K1-E2
Method	BLASTN
NCBI GI	g2264314
BLAST score	65
E value	5.0e-28
Match length	197
% identity	83
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MQK4, complete sequence [Arabidopsis thaliana]

Seq. No.	157686
Seq. ID	LIB3176-083-P1-K1-E3
Method	BLASTN
NCBI GI	g2191157
BLAST score	254
E value	1.0e-141
Match length	412
% identity	94
NCBI Description	Arabidopsis thaliana BAC IG002P16

Seq. No.	157687
Seq. ID	LIB3176-083-P1-K1-E5
Method	BLASTX
NCBI GI	g1071912
BLAST score	601
E value	1.0e-62
Match length	131

% identity	92
NCBI Description	cysteine synthase (EC 4.2.99.8) cpACS1 - Arabidopsis thaliana >gi_572517_emb_CAA57344_ (X81698) cysteine synthase [Arabidopsis thaliana]

Seq. No.	157688
Seq. ID	LIB3176-083-P1-K1-E6
Method	BLASTX
NCBI GI	g625977
BLAST score	586
E value	8.0e-61
Match length	116
% identity	98
NCBI Description	p40 protein homolog - Arabidopsis thaliana >gi_402904 (U01955) laminin receptor-like protein [Arabidopsis thaliana]

Seq. No.	157689
Seq. ID	LIB3176-083-P1-K1-E7
Method	BLASTX
NCBI GI	g2262167
BLAST score	696
E value	1.0e-73
Match length	133
% identity	100
NCBI Description	(AC002329) cytosolic ribosomal protein S4 [Arabidopsis thaliana]

Seq. No.	157690
Seq. ID	LIB3176-083-P1-K1-E8
Method	BLASTX
NCBI GI	g1345132
BLAST score	710
E value	2.0e-75
Match length	138
% identity	100
NCBI Description	(U47029) ERECTA [Arabidopsis thaliana] >gi_1389566_dbj_BAA11869_ (D83257) receptor protein kinase [Arabidopsis thaliana] >gi_3075386 (AC004484) receptor protein kinase, ERECTA [Arabidopsis thaliana]

Seq. No.	157691
Seq. ID	LIB3176-083-P1-K1-E9
Method	BLASTX
NCBI GI	g1709798
BLAST score	690
E value	5.0e-73
Match length	139
% identity	97
NCBI Description	26S PROTEASE REGULATORY SUBUNIT 6B HOMOLOG >gi_1155334 (U43398) POTATP1 [Solanum tuberosum]

Seq. No.	157692
Seq. ID	LIB3176-083-P1-K1-F1
Method	BLASTX
NCBI GI	g66618
BLAST score	401

E value	4.0e-39
Match length	82
% identity	100
NCBI Description	3-phosphoshikimate 1-carboxyvinyltransferase (EC 2.5.1.19) precursor - Arabidopsis thaliana

Seq. No.	157693
Seq. ID	LIB3176-083-P1-K1-F10
Method	BLASTX
NCBI GI	g4567226
BLAST score	232
E value	3.0e-19
Match length	89
% identity	57
NCBI Description	(AC007119) unknown protein [Arabidopsis thaliana]

Seq. No.	157694
Seq. ID	LIB3176-083-P1-K1-F11
Method	BLASTX
NCBI GI	g113026
BLAST score	593
E value	1.0e-61
Match length	127
% identity	89
NCBI Description	ISOCITRATE LYASE (ISOCITRASE) (ISOCITRATASE) (ICL) >gi_68211_pir__WZRPI isocitrate lyase (EC 4.1.3.1) - rape >gi_255220_bbs_112862 isocitrate lyase, threo-D S-isocitrate glyoxylate-lyase, IL {EC 4.1.3.1} [Brassica napus, seedlings, Peptide, 576 aa] >gi_167144 (L08482) isocitrate lyase [Brassica napus] >gi_447142_prf__1913424A isocitrate lyase [Brassica napus]

Seq. No.	157695
Seq. ID	LIB3176-083-P1-K1-F12
Method	BLASTX
NCBI GI	g4454032
BLAST score	277
E value	2.0e-26
Match length	104
% identity	59
NCBI Description	(AL035394) putative protein [Arabidopsis thaliana]

Seq. No.	157696
Seq. ID	LIB3176-083-P1-K1-F2
Method	BLASTX
NCBI GI	g399013
BLAST score	601
E value	1.0e-62
Match length	122
% identity	98
NCBI Description	ADP,ATP CARRIER PROTEIN 1 PRECURSOR (ADP/ATP TRANSLOCASE 1) (ADENINE NUCLEOTIDE TRANSLOCATOR 1) (ANT 1) >gi_99658_pir__S21313 ADP,ATP carrier protein - Arabidopsis thaliana (fragment) >gi_16175_emb_CAA46518_ (X65549) adenylate translocator [Arabidopsis thaliana] >gi_445607_prf__1909354A adenylate translocator [Arabidopsis thaliana]

Seq. No.	157697
Seq. ID	LIB3176-083-P1-K1-F3
Method	BLASTX
NCBI GI	g70643
BLAST score	401
E value	4.0e-39
Match length	83
% identity	98
NCBI Description	ubiquitin precursor - soybean (fragment)

Seq. No.	157698
Seq. ID	LIB3176-083-P1-K1-F4
Method	BLASTX
NCBI GI	g399013
BLAST score	312
E value	6.0e-29
Match length	60
% identity	100
NCBI Description	ADP,ATP CARRIER PROTEIN 1 PRECURSOR (ADP/ATP TRANSLOCASE 1) (ADENINE NUCLEOTIDE TRANSLOCATOR 1) (ANT 1) >gi_99658_pir__S21313 ADP,ATP carrier protein - Arabidopsis thaliana (fragment) >gi_16175_emb_CAA46518_ (X65549) adenylate translocator [Arabidopsis thaliana] >gi_445607_prf__1909354A adenylate translocator [Arabidopsis thaliana]

Seq. No.	157699
Seq. ID	LIB3176-083-P1-K1-F5
Method	BLASTN
NCBI GI	g4220640
BLAST score	350
E value	0.0e+00
Match length	416
% identity	54
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MPE11, complete sequence [Arabidopsis thaliana]

Seq. No.	157700
Seq. ID	LIB3176-083-P1-K1-F6
Method	BLASTN
NCBI GI	g3805839
BLAST score	186
E value	1.0e-100
Match length	339
% identity	92
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F4B14 (ESSAII project)

Seq. No.	157701
Seq. ID	LIB3176-083-P1-K1-F7
Method	BLASTX
NCBI GI	g114335
BLAST score	206
E value	8.0e-17
Match length	54
% identity	72

NCBI Description	PLASMA MEMBRANE ATPASE 2 (PROTON PUMP) >gi_67973_pir__PXMUP2 H+-transporting ATPase (EC 3.6.1.35) type 2, plasma membrane - Arabidopsis thaliana >gi_166629 (J05570) H+-ATPase [Arabidopsis thaliana]

Seq. No.	157702
Seq. ID	LIB3176-083-P1-K1-F8
Method	BLASTN
NCBI GI	g1483217
BLAST score	361
E value	0.0e+00
Match length	421
% identity	100
NCBI Description	A.thaliana gene induced upon wounding stress

Seq. No.	157703
Seq. ID	LIB3176-083-P1-K1-F9
Method	BLASTN
NCBI GI	g4096078
BLAST score	48
E value	7.0e-18
Match length	175
% identity	93
NCBI Description	Arabidopsis thaliana chromosome I BAC T5A14 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	157704
Seq. ID	LIB3176-083-P1-K1-G12
Method	BLASTX
NCBI GI	g4585988
BLAST score	738
E value	1.0e-78
Match length	144
% identity	95
NCBI Description	(AC005287) Similar to phosphoprotein phosphatase 2A regulatory subunit [Arabidopsis thaliana]

Seq. No.	157705
Seq. ID	LIB3176-083-P1-K1-G2
Method	BLASTX
NCBI GI	g4371297
BLAST score	716
E value	5.0e-76
Match length	143
% identity	98
NCBI Description	(AC006260) phenylalanine ammonia-lyase 1, 3' partial [Arabidopsis thaliana]

Seq. No.	157706
Seq. ID	LIB3176-083-P1-K1-G3
Method	BLASTX
NCBI GI	g2529682
BLAST score	191
E value	9.0e-15
Match length	88
% identity	49
NCBI Description	(AC002535) unknown protein [Arabidopsis thaliana]

Seq. No.	157707
Seq. ID	LIB3176-083-P1-K1-G4
Method	BLASTX
NCBI GI	g4678328
BLAST score	454
E value	1.0e-45
Match length	92
% identity	99
NCBI Description	(AL049658) aldehyde dehydrogenase (NAD+)-like protein [Arabidopsis thaliana]

Seq. No.	157708
Seq. ID	LIB3176-083-P1-K1-G5
Method	BLASTX
NCBI GI	g730526
BLAST score	355
E value	7.0e-34
Match length	93
% identity	72
NCBI Description	60S RIBOSOMAL PROTEIN L13 (BBC1 PROTEIN HOMOLOG) >gi_480787_pir__S37271 ribosomal protein L13 - Arabidopsis thaliana >gi_404166_emb_CAA53005_ (X75162) BBC1 protein [Arabidopsis thaliana]

Seq. No.	157709
Seq. ID	LIB3176-083-P1-K1-G8
Method	BLASTX
NCBI GI	g4204258
BLAST score	461
E value	4.0e-46
Match length	140
% identity	62
NCBI Description	(AC005223) 14409 [Arabidopsis thaliana]

Seq. No.	157710
Seq. ID	LIB3176-083-P1-K1-G9
Method	BLASTX
NCBI GI	g2335094
BLAST score	577
E value	1.0e-59
Match length	111
% identity	99
NCBI Description	(AC002339) putative polygalacturonase [Arabidopsis thaliana]

Seq. No.	157711
Seq. ID	LIB3176-083-P1-K1-H10
Method	BLASTX
NCBI GI	g2583135
BLAST score	251
E value	1.0e-21
Match length	49
% identity	94
NCBI Description	(AC002387) hypothetical protein [Arabidopsis thaliana] >gi_3822216 (AF074948) FIL [Arabidopsis thaliana] >gi_4322477_gb_AAD16053_ (AF087015) abnormal floral organs

protein [Arabidopsis thaliana]

Seq. No.	157712
Seq. ID	LIB3176-083-P1-K1-H11
Method	BLASTN
NCBI GI	g4757411
BLAST score	167
E value	6.0e-89
Match length	392
% identity	95
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MXC7, complete sequence

Seq. No.	157713
Seq. ID	LIB3176-083-P1-K1-H12
Method	BLASTX
NCBI GI	g4587595
BLAST score	211
E value	8.0e-17
Match length	82
% identity	49
NCBI Description	(AC006951) putative proline-rich protein APG [Arabidopsis thaliana]

Seq. No.	157714
Seq. ID	LIB3176-083-P1-K1-H2
Method	BLASTX
NCBI GI	g1170040
BLAST score	706
E value	7.0e-75
Match length	143
% identity	97
NCBI Description	GLUTATHIONE REDUCTASE, CHLOROPLAST PRECURSOR (GR) (GRASE) >gi_451198_dbj_BAA03137_ (D14049) glutathione reductase precursor [Arabidopsis thaliana] >gi_1944448_dbj_BAA19653_ (D89620) glutathione reductase precursor [Arabidopsis thaliana] >gi_740576_prf__2005376A glutathione reductase [Arabidopsis thaliana]

Seq. No.	157715
Seq. ID	LIB3176-083-P1-K1-H3
Method	BLASTX
NCBI GI	g2119848
BLAST score	664
E value	6.0e-70
Match length	139
% identity	91
NCBI Description	chlorophyll a/b-binding protein type I precursor Lhb1B1 - Arabidopsis thaliana >gi_16366_emb_CAA45789_ (X64459) photosystem II type I chlorophyll a /b binding protein [Arabidopsis thaliana] >gi_3128229 (AC004077) putative photosystem II type I chlorophyll a/b binding protein [Arabidopsis thaliana] >gi_3337372 (AC004481) putative photosystem II type I chlorophyll a/b binding protein [Arabidopsis thaliana]

Seq. No.	157716

Seq. ID	LIB3176-083-P1-K1-H4
Method	BLASTX
NCBI GI	g4490329
BLAST score	325
E value	8.0e-31
Match length	73
% identity	85
NCBI Description	(AL035656) extensin-like protein [Arabidopsis thaliana]

Seq. No.	157717
Seq. ID	LIB3176-083-P1-K1-H5
Method	BLASTX
NCBI GI	g3377843
BLAST score	345
E value	9.0e-33
Match length	84
% identity	82
NCBI Description	(AF076274) contains similarity to rat p47 protein (GB:AB002086) [Arabidopsis thaliana]

Seq. No.	157718
Seq. ID	LIB3176-083-P1-K1-H6
Method	BLASTX
NCBI GI	g3201632
BLAST score	247
E value	3.0e-21
Match length	96
% identity	53
NCBI Description	(AC004669) putative 2A6 protein [Arabidopsis thaliana]

Seq. No.	157719
Seq. ID	LIB3176-083-P1-K1-H7
Method	BLASTX
NCBI GI	g2341034
BLAST score	584
E value	1.0e-60
Match length	120
% identity	98
NCBI Description	(AC000104) F19P19.13 [Arabidopsis thaliana]

Seq. No.	157720
Seq. ID	LIB3176-083-P1-K1-H8
Method	BLASTX
NCBI GI	g2894445
BLAST score	647
E value	6.0e-68
Match length	140
% identity	88
NCBI Description	(Y14333) transketolase [Arabidopsis thaliana]

Seq. No.	157721
Seq. ID	LIB3176-083-P1-K1-H9
Method	BLASTX
NCBI GI	g731284
BLAST score	181
E value	3.0e-13
Match length	117

% identity	39
NCBI Description	HYPOTHETICAL 75.2 KD PROTEIN IN ACS1-GCV3 INTERGENIC REGION >gi_1077482_pir__S51971 probable membrane protein YAL048c - yeast (Saccharomyces cerevisiae) >gi_595536 (U12980) Yal048cp [Saccharomyces cerevisiae]
Seq. No.	157722
Seq. ID	LIB3176-084-P1-K1-A1
Method	BLASTX
NCBI GI	g3096931
BLAST score	577
E value	9.0e-60
Match length	113
% identity	99
NCBI Description	(AL023094) putative ribosomal protein S16 [Arabidopsis thaliana]
Seq. No.	157723
Seq. ID	LIB3176-084-P1-K1-A10
Method	BLASTN
NCBI GI	g4753195
BLAST score	229
E value	1.0e-126
Match length	372
% identity	99
NCBI Description	Arabidopsis thaliana BAC F15A18 from chromosome V near 68.5 cM, complete sequence
Seq. No.	157724
Seq. ID	LIB3176-084-P1-K1-A11
Method	BLASTX
NCBI GI	g4263712
BLAST score	497
E value	2.0e-50
Match length	124
% identity	78
NCBI Description	(AC006223) putative ribosomal protein S12 [Arabidopsis thaliana]
Seq. No.	157725
Seq. ID	LIB3176-084-P1-K1-A12
Method	BLASTX
NCBI GI	g2088654
BLAST score	723
E value	8.0e-77
Match length	154
% identity	94
NCBI Description	(AF002109) 60S acidic ribosomal protein P0 isolog [Arabidopsis thaliana]
Seq. No.	157726
Seq. ID	LIB3176-084-P1-K1-A3
Method	BLASTN
NCBI GI	g2160155
BLAST score	75
E value	2.0e-34
Match length	139

% identity	89
NCBI Description	Sequence of BAC F21M12 from Arabidopsis thaliana chromosome 1, complete sequence [Arabidopsis thaliana]

Seq. No.	157727
Seq. ID	LIB3176-084-P1-K1-A4
Method	BLASTX
NCBI GI	g399940
BLAST score	706
E value	9.0e-75
Match length	157
% identity	89
NCBI Description	MITOCHONDRIAL HEAT SHOCK 70 KD PROTEIN PRECURSOR >gi_100004_pir__S25005 heat shock protein, 70K - kidney bean >gi_22636_emb_CAA47345_ (X66874) 70 kDa heat shock protein [Phaseolus vulgaris]

Seq. No.	157728
Seq. ID	LIB3176-084-P1-K1-A5
Method	BLASTX
NCBI GI	g4567268
BLAST score	730
E value	1.0e-77
Match length	152
% identity	93
NCBI Description	(AC006841) putative fructose biphosphate aldolase [Arabidopsis thaliana]

Seq. No.	157729
Seq. ID	LIB3176-084-P1-K1-A6
Method	BLASTN
NCBI GI	g4678371
BLAST score	257
E value	1.0e-142
Match length	341
% identity	99
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone T6G15 (ESSA project)

Seq. No.	157730
Seq. ID	LIB3176-084-P1-K1-A7
Method	BLASTX
NCBI GI	g2246621
BLAST score	254
E value	3.0e-22
Match length	68
% identity	78
NCBI Description	(AF004393) salt-stress induced tonoplast intrinsic protein [Arabidopsis thaliana]

Seq. No.	157731
Seq. ID	LIB3176-084-P1-K1-A8
Method	BLASTX
NCBI GI	g2851508
BLAST score	361
E value	9.0e-35
Match length	79

% identity	89
NCBI Description	60S RIBOSOMAL PROTEIN L21 >gi_2160162 (AC000132) Similar to ribosomal protein L21 (gb_L38826). ESTs gb_AA395597,gb_ATTS5197 come from this gene. [Arabidopsis thaliana] >gi_3482935 (AC003970) Putative ribosomal protein L21 [Arabidopsis thaliana]

Seq. No.	157732
Seq. ID	LIB3176-084-P1-K1-A9
Method	BLASTN
NCBI GI	g4376087
BLAST score	162
E value	5.0e-86
Match length	292
% identity	96
NCBI Description	Arabidopsis thaliana DNA chromosome 4, ESSA I AP2 contig fragment No

Seq. No.	157733
Seq. ID	LIB3176-084-P1-K1-B10
Method	BLASTX
NCBI GI	g3377808
BLAST score	602
E value	1.0e-62
Match length	133
% identity	88
NCBI Description	(AF075597) contains similarity to Nicotiana alata pistil extensin-like protein (GB:U45958) [Arabidopsis thaliana]

Seq. No.	157734
Seq. ID	LIB3176-084-P1-K1-B11
Method	BLASTX
NCBI GI	g3169180
BLAST score	823
E value	2.0e-88
Match length	152
% identity	99
NCBI Description	(AC004401) putative casein kinase II catalytic subunit [Arabidopsis thaliana]

Seq. No.	157735
Seq. ID	LIB3176-084-P1-K1-B12
Method	BLASTN
NCBI GI	g3785992
BLAST score	206
E value	1.0e-112
Match length	459
% identity	98
NCBI Description	Arabidopsis thaliana chromosome II BAC T6A23 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	157736
Seq. ID	LIB3176-084-P1-K1-B2
Method	BLASTN
NCBI GI	g4079614
BLAST score	47
E value	2.0e-17

Match length	139
% identity	83
NCBI Description	Arabidopsis thaliana chromosome I BAC F21M11 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	157737
Seq. ID	LIB3176-084-P1-K1-B3
Method	BLASTX
NCBI GI	g3869088
BLAST score	598
E value	3.0e-62
Match length	119
% identity	95
NCBI Description	(AB019427) elongation factor-1 alpha [Nicotiana paniculata]

Seq. No.	157738
Seq. ID	LIB3176-084-P1-K1-B4
Method	BLASTX
NCBI GI	g4455203
BLAST score	224
E value	2.0e-18
Match length	144
% identity	5
NCBI Description	(AL035440) putative protein [Arabidopsis thaliana]

Seq. No.	157739
Seq. ID	LIB3176-084-P1-K1-B5
Method	BLASTX
NCBI GI	g119194
BLAST score	561
E value	3.0e-58
Match length	125
% identity	95
NCBI Description	ELONGATION FACTOR TU, CHLOROPLAST PRECURSOR (EF-TU) >gi_81607_pir__S09152 translation elongation factor Tu precursor, chloroplast - Arabidopsis thaliana >gi_22565_emb_CAA36498_ (X52256) elongation factor Tu precursor [Arabidopsis thaliana] >gi_226817_prf__1607332A elongation factor Tu [Arabidopsis thaliana]

Seq. No.	157740
Seq. ID	LIB3176-084-P1-K1-B6
Method	BLASTX
NCBI GI	g3292815
BLAST score	190
E value	3.0e-14
Match length	135
% identity	42
NCBI Description	(AL031018) hypothetical protein [Arabidopsis thaliana]

Seq. No.	157741
Seq. ID	LIB3176-084-P1-K1-B7
Method	BLASTX
NCBI GI	g3236246
BLAST score	369
E value	2.0e-41
Match length	102

% identity	86
NCBI Description	(AC004684) putative expansin protein [Arabidopsis thaliana]

Seq. No.	157742
Seq. ID	LIB3176-084-P1-K1-B8
Method	BLASTN
NCBI GI	g2098816
BLAST score	305
E value	1.0e-171
Match length	412
% identity	96
NCBI Description	Arabidopsis thaliana BAC F19G10, complete sequence

Seq. No.	157743
Seq. ID	LIB3176-084-P1-K1-B9
Method	BLASTN
NCBI GI	g4467094
BLAST score	438
E value	0.0e+00
Match length	478
% identity	97
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F20D10 (ESSA project)

Seq. No.	157744
Seq. ID	LIB3176-084-P1-K1-C1
Method	BLASTX
NCBI GI	g119350
BLAST score	633
E value	3.0e-66
Match length	127
% identity	98
NCBI Description	ENOLASE (2-PHOSPHOGLYCERATE DEHYDRATASE) (2-PHOSPHO-D-GLYCERATE HYDRO-LYASE) >gi_81608_pir__JQ1187 phosphopyruvate hydratase (EC 4.2.1.11) - Arabidopsis thaliana >gi_16271_emb_CAA41114_ (X58107) enolase [Arabidopsis thaliana] >gi_4581151_gb_AAD24635.1_AC006919_13 (AC006919) enolase (2-phospho-D-glycerate hydroylase);identical to P25696 [Arabidopsis thaliana]

Seq. No.	157745
Seq. ID	LIB3176-084-P1-K1-C10
Method	BLASTX
NCBI GI	g3004560
BLAST score	428
E value	3.0e-42
Match length	127
% identity	69
NCBI Description	(AC003673) putative ATP binding protein [Arabidopsis thaliana]

Seq. No.	157746
Seq. ID	LIB3176-084-P1-K1-C11
Method	BLASTX
NCBI GI	g4732123
BLAST score	422

E value	2.0e-41
Match length	127
% identity	63
NCBI Description	(AF129087) mitogen-activated protein kinase homologue [Medicago sativa]

Seq. No.	157747
Seq. ID	LIB3176-084-P1-K1-C2
Method	BLASTX
NCBI GI	g1067224
BLAST score	153
E value	6.0e-10
Match length	91
% identity	37
NCBI Description	(Z67999) serine palmitoyltransferase 2 [Schizosaccharomyces pombe]

Seq. No.	157748
Seq. ID	LIB3176-084-P1-K1-C3
Method	BLASTX
NCBI GI	g4582787
BLAST score	444
E value	4.0e-44
Match length	112
% identity	76
NCBI Description	(AJ012281) adenosine kinase [Zea mays]

Seq. No.	157749
Seq. ID	LIB3176-084-P1-K1-C5
Method	BLASTX
NCBI GI	g3367522
BLAST score	270
E value	1.0e-23
Match length	89
% identity	63
NCBI Description	(AC004392) EST gb_T04691 comes from this gene. [Arabidopsis thaliana]

Seq. No.	157750
Seq. ID	LIB3176-084-P1-K1-C6
Method	BLASTX
NCBI GI	g2129636
BLAST score	647
E value	5.0e-74
Match length	146
% identity	95
NCBI Description	lipase - Arabidopsis thaliana >gi_1145627 (U38916) lipase [Arabidopsis thaliana]

Seq. No.	157751
Seq. ID	LIB3176-084-P1-K1-C7
Method	BLASTX
NCBI GI	g133440
BLAST score	545
E value	6.0e-56
Match length	127
% identity	86

NCBI Description DNA-DIRECTED RNA POLYMERASE BETA' CHAIN

Seq. No. 157752
Seq. ID LIB3176-084-P1-K1-C8
Method BLASTX
NCBI GI g2961389
BLAST score 240
E value 3.0e-20
Match length 79
% identity 53
NCBI Description (AL022141) purple acid phosphatase like protein [Arabidopsis thaliana] >gi_4006925_emb_CAB16853.1_ (Z99708) purple acid phosphatase like protein [Arabidopsis thaliana]

Seq. No. 157753
Seq. ID LIB3176-084-P1-K1-C9
Method BLASTX
NCBI GI g2244792
BLAST score 234
E value 2.0e-19
Match length 50
% identity 80
NCBI Description (Z97336) ankyrin homolog [Arabidopsis thaliana]

Seq. No. 157754
Seq. ID LIB3176-084-P1-K1-D10
Method BLASTX
NCBI GI g2262167
BLAST score 616
E value 3.0e-64
Match length 119
% identity 99
NCBI Description (AC002329) cytosolic ribosomal protein S4 [Arabidopsis thaliana]

Seq. No. 157755
Seq. ID LIB3176-084-P1-K1-D11
Method BLASTX
NCBI GI g336392
BLAST score 276
E value 7.0e-25
Match length 54
% identity 100
NCBI Description (J05215) ribosomal protein S17 [Arabidopsis thaliana]

Seq. No. 157756
Seq. ID LIB3176-084-P1-K1-D12
Method BLASTX
NCBI GI g4406816
BLAST score 722
E value 9.0e-77
Match length 141
% identity 98
NCBI Description (AC006201) 60S ribosomal protein L2 [Arabidopsis thaliana]

Seq. No. 157757
Seq. ID LIB3176-084-P1-K1-D4

Method	BLASTX
NCBI GI	g3915866
BLAST score	551
E value	1.0e-56
Match length	155
% identity	70
NCBI Description	GLUTAMINYL-TRNA SYNTHETASE (GLUTAMINE--TRNA LIGASE) (GLNRS) >gi_2995455_emb_CAA62901_ (X91787) tRNA-glutamine synthetase [Lupinus luteus]

Seq. No.	157758
Seq. ID	LIB3176-084-P1-K1-D5
Method	BLASTX
NCBI GI	g4587542
BLAST score	194
E value	2.0e-15
Match length	39
% identity	97
NCBI Description	(AC006577) Belongs to the PF_00657 Lipase/Acylhydrolase with GDSL-motif family. ESTs gb_T45815, gb_T45130 and gb_Z38046 come from this gene. [Arabidopsis thaliana]

Seq. No.	157759
Seq. ID	LIB3176-084-P1-K1-D6
Method	BLASTN
NCBI GI	g3492855
BLAST score	258
E value	1.0e-143
Match length	431
% identity	98
NCBI Description	Genomic sequence for Arabidopsis thaliana BAC F20N2, complete sequence [Arabidopsis thaliana]

Seq. No.	157760
Seq. ID	LIB3176-084-P1-K1-D8
Method	BLASTX
NCBI GI	g1169201
BLAST score	545
E value	6.0e-56
Match length	136
% identity	83
NCBI Description	DNA-DAMAGE-REPAIR/TOLERATION PROTEIN DRT112 PRECURSOR >gi_421830_pir__S33707 DRT112 protein - Arabidopsis thaliana >gi_166696 (M98456) DRT112 [Arabidopsis thaliana]

Seq. No.	157761
Seq. ID	LIB3176-084-P1-K1-D9
Method	BLASTX
NCBI GI	g3176668
BLAST score	290
E value	1.0e-26
Match length	77
% identity	79
NCBI Description	(AC004393) Similar to ribosomal protein L17 gb_X62724 from Hordeum vulgare. ESTs gb_Z34728, gb_F19974, gb_T75677 and gb_Z33937 come from this gene. [Arabidopsis thaliana]

Seq. No.	157762
Seq. ID	LIB3176-084-P1-K1-E10
Method	BLASTX
NCBI GI	g3335516
BLAST score	104
E value	3.0e-04
Match length	151
% identity	83
NCBI Description	(AF053941) nonphototropic hypocotyl 2 [Arabidopsis thaliana]

Seq. No.	157763
Seq. ID	LIB3176-084-P1-K1-E12
Method	BLASTN
NCBI GI	g3548797
BLAST score	98
E value	6.0e-48
Match length	256
% identity	95
NCBI Description	Arabidopsis thaliana chromosome II BAC T18E12 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	157764
Seq. ID	LIB3176-084-P1-K1-E2
Method	BLASTX
NCBI GI	g1531758
BLAST score	231
E value	4.0e-19
Match length	76
% identity	63
NCBI Description	(X98772) AUX1 [Arabidopsis thaliana] >gi_3335360 (AC003028) unknown protein [Arabidopsis thaliana]

Seq. No.	157765
Seq. ID	LIB3176-084-P1-K1-E3
Method	BLASTN
NCBI GI	g3386593
BLAST score	68
E value	9.0e-30
Match length	144
% identity	87
NCBI Description	Arabidopsis thaliana chromosome II BAC F4I18 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	157766
Seq. ID	LIB3176-084-P1-K1-E4
Method	BLASTX
NCBI GI	g4490704
BLAST score	392
E value	9.0e-39
Match length	107
% identity	80
NCBI Description	(AL035680) putative protein [Arabidopsis thaliana]

Seq. No.	157767
Seq. ID	LIB3176-084-P1-K1-E5
Method	BLASTN

NCBI GI	g4468801
BLAST score	439
E value	0.0e+00
Match length	455
% identity	99
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F6G17 (ESSA project)

Seq. No.	157768
Seq. ID	LIB3176-084-P1-K1-E7
Method	BLASTX
NCBI GI	g2511590
BLAST score	245
E value	2.0e-21
Match length	55
% identity	85
NCBI Description	(Y13692) multicatalytic endopeptidase complex, proteasome component, beta subunit [Arabidopsis thaliana] >gi_3421111 (AF043534) 20S proteasome beta subunit PBD1 [Arabidopsis thaliana]

Seq. No.	157769
Seq. ID	LIB3176-084-P1-K1-E8
Method	BLASTN
NCBI GI	g1483149
BLAST score	34
E value	1.0e-09
Match length	89
% identity	86
NCBI Description	Arabidopsis thaliana mRNA for monodehydroascorbate reductase, complete cds

Seq. No.	157770
Seq. ID	LIB3176-084-P1-K1-E9
Method	BLASTX
NCBI GI	g126766
BLAST score	438
E value	1.0e-43
Match length	94
% identity	86
NCBI Description	MALATE SYNTHASE, GLYOXYSOMAL >gi_68216_pir__SYRPMA malate synthase (EC 4.1.3.2), glyoxysomal - rape >gi_167150 (J04468) malate synthase (EC 4.1.3.2) [Brassica napus]

Seq. No.	157771
Seq. ID	LIB3176-084-P1-K1-F1
Method	BLASTX
NCBI GI	g100490
BLAST score	668
E value	2.0e-70
Match length	136
% identity	28
NCBI Description	polyubiquitin - garden snapdragon (fragment) >gi_16071_emb_CAA48140_ (X67957) ubiquitin [Antirrhinum majus]

Seq. No.	157772

Seq. ID	LIB3176-084-P1-K1-F10
Method	BLASTX
NCBI GI	g113024
BLAST score	732
E value	7.0e-78
Match length	145
% identity	97
NCBI Description	ISOCITRATE LYASE (ISOCITRASE) (ISOCITRATASE) (ICL) >gi_553043 (M83534) isocitrate lyase [Arabidopsis thaliana]

Seq. No.	157773
Seq. ID	LIB3176-084-P1-K1-F12
Method	BLASTX
NCBI GI	g3335516
BLAST score	543
E value	6.0e-56
Match length	106
% identity	98
NCBI Description	(AF053941) nonphototropic hypocotyl 2 [Arabidopsis thaliana]

Seq. No.	157774
Seq. ID	LIB3176-084-P1-K1-F3
Method	BLASTX
NCBI GI	g3402711
BLAST score	311
E value	5.0e-29
Match length	75
% identity	49
NCBI Description	(AC004261) putative RNA-binding protein [Arabidopsis thaliana]

Seq. No.	157775
Seq. ID	LIB3176-084-P1-K1-F4
Method	BLASTX
NCBI GI	g224293
BLAST score	433
E value	9.0e-43
Match length	86
% identity	100
NCBI Description	histone H4 [Triticum aestivum]

Seq. No.	157776
Seq. ID	LIB3176-084-P1-K1-F6
Method	BLASTX
NCBI GI	g1363489
BLAST score	148
E value	3.0e-17
Match length	49
% identity	90
NCBI Description	thioglucosidase (EC 3.2.3.1) 3D precursor - Arabidopsis thaliana >gi_984052_emb_CAA61592_ (X89413) thioglucoside glucohydrolase [Arabidopsis thaliana]

Seq. No.	157777
Seq. ID	LIB3176-084-P1-K1-F7
Method	BLASTX

NCBI GI	g126766
BLAST score	341
E value	2.0e-32
Match length	91
% identity	73
NCBI Description	MALATE SYNTHASE, GLYOXYSOMAL >gi_68216_pir__SYRPMA malate synthase (EC 4.1.3.2), glyoxysomal - rape >gi_167150 (J04468) malate synthase (EC 4.1.3.2) [Brassica napus]

Seq. No.	157778
Seq. ID	LIB3176-084-P1-K1-F8
Method	BLASTN
NCBI GI	g2342717
BLAST score	78
E value	1.0e-35
Match length	322
% identity	64
NCBI Description	Arabidopsis thaliana chromosome II BAC T14G11 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	157779
Seq. ID	LIB3176-084-P1-K1-F9
Method	BLASTN
NCBI GI	g2760316
BLAST score	35
E value	4.0e-11
Match length	57
% identity	89
NCBI Description	The sequence of BAC F1N21 from Arabidopsis thaliana chromosome 1, complete sequence [Arabidopsis thaliana]

Seq. No.	157780
Seq. ID	LIB3176-084-P1-K1-G1
Method	BLASTN
NCBI GI	g3702730
BLAST score	143
E value	1.0e-74
Match length	269
% identity	97
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MAB16, complete sequence [Arabidopsis thaliana]

Seq. No.	157781
Seq. ID	LIB3176-084-P1-K1-G10
Method	BLASTX
NCBI GI	g166867
BLAST score	275
E value	1.0e-24
Match length	85
% identity	66
NCBI Description	(J05216) ribosomal protein S11 (probable start codon at bp 67) [Arabidopsis thaliana]

Seq. No.	157782
Seq. ID	LIB3176-084-P1-K1-G11
Method	BLASTX
NCBI GI	g3286693

BLAST score	524
E value	1.0e-53
Match length	112
% identity	94
NCBI Description	(Y15433) 33 kDa polypeptide of oxygen-evolving complex (OEC) in photosystem II [Arabidopsis thaliana]

Seq. No.	157783
Seq. ID	LIB3176-084-P1-K1-G12
Method	BLASTX
NCBI GI	g1350930
BLAST score	458
E value	4.0e-46
Match length	91
% identity	98
NCBI Description	40S RIBOSOMAL PROTEIN S13

Seq. No.	157784
Seq. ID	LIB3176-084-P1-K1-G2
Method	BLASTX
NCBI GI	g1170503
BLAST score	226
E value	1.0e-18
Match length	48
% identity	92
NCBI Description	EUKARYOTIC INITIATION FACTOR 4A-1 (EIF-4A-1) >gi_322503_pir__JC1452 translation initiation factor eIF-4A1 - Arabidopsis thaliana >gi_16554_emb_CAA46188_ (X65052) eukaryotic translation initiation factor 4A-1 [Arabidopsis thaliana]

Seq. No.	157785
Seq. ID	LIB3176-084-P1-K1-G3
Method	BLASTX
NCBI GI	g4559372
BLAST score	701
E value	3.0e-74
Match length	141
% identity	95
NCBI Description	(AC006585) putative CONSTANS protein [Arabidopsis thaliana] >gi_4646235_gb_AAD26898.1_AC007266_6 (AC007266) putative CONSTANS protein [Arabidopsis thaliana]

Seq. No.	157786
Seq. ID	LIB3176-084-P1-K1-G4
Method	BLASTN
NCBI GI	g4371278
BLAST score	211
E value	1.0e-115
Match length	263
% identity	95
NCBI Description	Arabidopsis thaliana chromosome II BAC T2N18 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	157787
Seq. ID	LIB3176-084-P1-K1-G6
Method	BLASTN

NCBI GI	g4581084
BLAST score	178
E value	8.0e-96
Match length	190
% identity	98
NCBI Description	Arabidopsis thaliana chromosome I BAC T30F21 genomic sequence, complete sequence

Seq. No.	157788
Seq. ID	LIB3176-084-P1-K1-G7
Method	BLASTX
NCBI GI	g2244750
BLAST score	483
E value	7.0e-49
Match length	94
% identity	100
NCBI Description	(Z97335) adenosylhomocysteinase [Arabidopsis thaliana] >gi_3088579 (AF059581) S-adenosyl-L-homocysteine hydrolase [Arabidopsis thaliana]

Seq. No.	157789
Seq. ID	LIB3176-084-P1-K1-G9
Method	BLASTX
NCBI GI	g4337027
BLAST score	196
E value	1.0e-15
Match length	45
% identity	84
NCBI Description	(AF123254) MFP2 [Arabidopsis thaliana]

Seq. No.	157790
Seq. ID	LIB3176-084-P1-K1-H1
Method	BLASTX
NCBI GI	g2529665
BLAST score	619
E value	1.0e-64
Match length	147
% identity	85
NCBI Description	(AC002535) putative ribosomal protein L7A [Arabidopsis thaliana]

Seq. No.	157791
Seq. ID	LIB3176-084-P1-K1-H10
Method	BLASTX
NCBI GI	g405617
BLAST score	222
E value	1.0e-18
Match length	55
% identity	78
NCBI Description	(X61610) LHCII Type III chlorophyll a/b binding protein [Brassica napus]

Seq. No.	157792
Seq. ID	LIB3176-084-P1-K1-H11
Method	BLASTX
NCBI GI	g99752
BLAST score	355

E value	6.0e-34
Match length	95
% identity	81
NCBI Description	protochlorophyllide reductase (EC 1.3.1.33) precursor - Arabidopsis thaliana

Seq. No.	157793
Seq. ID	LIB3176-084-P1-K1-H12
Method	BLASTN
NCBI GI	g4206764
BLAST score	292
E value	1.0e-163
Match length	333
% identity	96
NCBI Description	Arabidopsis thaliana putative type 1 membrane protein (PMP) mRNA, complete cds

Seq. No.	157794
Seq. ID	LIB3176-084-P1-K1-H3
Method	BLASTX
NCBI GI	g2088654
BLAST score	518
E value	9.0e-53
Match length	118
% identity	83
NCBI Description	(AF002109) 60S acidic ribosomal protein P0 isolog [Arabidopsis thaliana]

Seq. No.	157795
Seq. ID	LIB3176-084-P1-K1-H4
Method	BLASTX
NCBI GI	g1483150
BLAST score	374
E value	5.0e-41
Match length	85
% identity	86
NCBI Description	(D84417) monodehydroascorbate reductase [Arabidopsis thaliana]

Seq. No.	157796
Seq. ID	LIB3176-084-P1-K1-H5
Method	BLASTN
NCBI GI	g3985931
BLAST score	225
E value	1.0e-123
Match length	233
% identity	99
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K21H1, complete sequence [Arabidopsis thaliana]

Seq. No.	157797
Seq. ID	LIB3176-084-P1-K1-H6
Method	BLASTX
NCBI GI	g1483150
BLAST score	374
E value	2.0e-36
Match length	80

% identity	95
NCBI Description	(D84417) monodehydroascorbate reductase [Arabidopsis thaliana]
Seq. No.	157798
Seq. ID	LIB3176-084-P1-K1-H7
Method	BLASTX
NCBI GI	g132110
BLAST score	49
E value	6.0e-55
Match length	117
% identity	92
NCBI Description	RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN 3B PRECURSOR (RUBISCO SMALL SUBUNIT 3B) >gi_68060_pir__RKMUB3 ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain B3 precursor - Arabidopsis thaliana >gi_16195_emb_CAA32702_ (X14564) ribulose bisphosphate carboxylase [Arabidopsis thaliana]
Seq. No.	157799
Seq. ID	LIB3176-084-P1-K1-H8
Method	BLASTX
NCBI GI	g3929649
BLAST score	585
E value	1.0e-60
Match length	119
% identity	100
NCBI Description	(AJ131205) mitochondrial NAD-dependent malate dehydrogenase [Arabidopsis thaliana]
Seq. No.	157800
Seq. ID	LIB3176-084-P1-K1-H9
Method	BLASTX
NCBI GI	g1076303
BLAST score	457
E value	1.0e-45
Match length	90
% identity	52
NCBI Description	RNA-binding protein cp29 precursor - Arabidopsis thaliana >gi_681902_dbj_BAA06518_ (D31710) cp29 [Arabidopsis thaliana]
Seq. No.	157801
Seq. ID	LIB3176-085-P1-K1-A1
Method	BLASTX
NCBI GI	g2129538
BLAST score	367
E value	4.0e-35
Match length	71
% identity	100
NCBI Description	AT103 protein - Arabidopsis thaliana >gi_1033195 (U38232) AT103 [Arabidopsis thaliana]
Seq. No.	157802
Seq. ID	LIB3176-085-P1-K1-A11
Method	BLASTX
NCBI GI	g4539408

BLAST score	383
E value	6.0e-37
Match length	131
% identity	65
NCBI Description	(AL049524) putative alpha NAC [Arabidopsis thaliana]

Seq. No.	157803
Seq. ID	LIB3176-085-P1-K1-A12
Method	BLASTX
NCBI GI	g399013
BLAST score	564
E value	4.0e-58
Match length	111
% identity	100
NCBI Description	ADP,ATP CARRIER PROTEIN 1 PRECURSOR (ADP/ATP TRANSLOCASE 1) (ADENINE NUCLEOTIDE TRANSLOCATOR 1) (ANT 1) >gi_99658_pir__S21313 ADP,ATP carrier protein - Arabidopsis thaliana (fragment) >gi_16175_emb_CAA46518_ (X65549) adenylate translocator [Arabidopsis thaliana] >gi_445607_prf__1909354A adenylate translocator [Arabidopsis thaliana]

Seq. No.	157804
Seq. ID	LIB3176-085-P1-K1-A2
Method	BLASTN
NCBI GI	g3869068
BLAST score	75
E value	1.0e-34
Match length	87
% identity	97
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MDC16, complete sequence [Arabidopsis thaliana]

Seq. No.	157805
Seq. ID	LIB3176-085-P1-K1-A3
Method	BLASTX
NCBI GI	g2062164
BLAST score	615
E value	3.0e-64
Match length	117
% identity	63
NCBI Description	(AC001645) jasmonate inducible protein isolog [Arabidopsis thaliana]

Seq. No.	157806
Seq. ID	LIB3176-085-P1-K1-A4
Method	BLASTX
NCBI GI	g4417278
BLAST score	102
E value	3.0e-11
Match length	93
% identity	37
NCBI Description	(AC007019) hypothetical protein [Arabidopsis thaliana]

Seq. No.	157807
Seq. ID	LIB3176-085-P1-K1-A5
Method	BLASTN

NCBI GI	g1149572
BLAST score	368
E value	0.0e+00
Match length	388
% identity	99
NCBI Description	A.thaliana rpl21 mRNA for chloroplast ribosomal large subunit protein L21

Seq. No.	157808
Seq. ID	LIB3176-085-P1-K1-A6
Method	BLASTN
NCBI GI	g4539402
BLAST score	46
E value	9.0e-17
Match length	72
% identity	99
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F7L13 (ESSA project)

Seq. No.	157809
Seq. ID	LIB3176-085-P1-K1-A8
Method	BLASTN
NCBI GI	g3869068
BLAST score	398
E value	0.0e+00
Match length	438
% identity	97
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MDC16, complete sequence [Arabidopsis thaliana]

Seq. No.	157810
Seq. ID	LIB3176-085-P1-K1-A9
Method	BLASTX
NCBI GI	g2809238
BLAST score	258
E value	3.0e-22
Match length	72
% identity	62
NCBI Description	(AC002560) F21B7.7 [Arabidopsis thaliana]

Seq. No.	157811
Seq. ID	LIB3176-085-P1-K1-B1
Method	BLASTX
NCBI GI	g113026
BLAST score	636
E value	1.0e-66
Match length	138
% identity	88
NCBI Description	ISOCITRATE LYASE (ISOCITRASE) (ISOCITRATASE) (ICL) >gi_68211_pir__WZRPI isocitrate lyase (EC 4.1.3.1) - rape >gi_255220_bbs_112862 isocitrate lyase, threo-D S-isocitrate glyoxylate-lyase, IL {EC 4.1.3.1} [Brassica napus, seedlings, Peptide, 576 aa] >gi_167144 (L08482) isocitrate lyase [Brassica napus] >gi_447142_prf__1913424A isocitrate lyase [Brassica napus]

Seq. No.	157812

Seq. ID	LIB3176-085-P1-K1-B10
Method	BLASTN
NCBI GI	g572605
BLAST score	129
E value	3.0e-66
Match length	433
% identity	89
NCBI Description	B.napus ACCg8 gene

Seq. No.	157813
Seq. ID	LIB3176-085-P1-K1-B11
Method	BLASTX
NCBI GI	g3413709
BLAST score	663
E value	9.0e-70
Match length	127
% identity	100
NCBI Description	(AC004747) hypothetical protein [Arabidopsis thaliana]

Seq. No.	157814
Seq. ID	LIB3176-085-P1-K1-B2
Method	BLASTX
NCBI GI	g548847
BLAST score	419
E value	4.0e-41
Match length	82
% identity	100
NCBI Description	CHLOROPLAST 30S RIBOSOMAL PROTEIN S12 >gi_1086182_pir__S39501 ribosomal protein S12 - curled-leaved tobacco >gi_225248_prf__1211235CG ribosomal protein S12 [Nicotiana tabacum]

Seq. No.	157815
Seq. ID	LIB3176-085-P1-K1-B3
Method	BLASTX
NCBI GI	g3980396
BLAST score	57
E value	3.0e-27
Match length	129
% identity	60
NCBI Description	(AC004561) putative C-4 sterol methyl oxidase [Arabidopsis thaliana]

Seq. No.	157816
Seq. ID	LIB3176-085-P1-K1-B4
Method	BLASTX
NCBI GI	g4038043
BLAST score	428
E value	3.0e-42
Match length	88
% identity	88
NCBI Description	(AC005936) putative DNA-binding protein [Arabidopsis thaliana]

Seq. No.	157817
Seq. ID	LIB3176-085-P1-K1-B5
Method	BLASTN

NCBI GI	g12219
BLAST score	115
E value	8.0e-58
Match length	360
% identity	91
NCBI Description	Mustard chloroplast trnk gene for tRNA-Lys(UUU)

Seq. No.	157818
Seq. ID	LIB3176-085-P1-K1-B6
Method	BLASTX
NCBI GI	g1710424
BLAST score	676
E value	3.0e-71
Match length	136
% identity	99
NCBI Description	50S RIBOSOMAL PROTEIN L21, CHLOROPLAST PRECURSOR (CL21) >gi_2129718_pir__S71282 ribosomal protein L21 - Arabidopsis thaliana >gi_1149573_emb_CAA89887_ (Z49787) chloroplast ribosomal large subunit protein L21 [Arabidopsis thaliana]

Seq. No.	157819
Seq. ID	LIB3176-085-P1-K1-B7
Method	BLASTX
NCBI GI	g3962377
BLAST score	455
E value	2.0e-45
Match length	119
% identity	84
NCBI Description	(AJ002551) heat shock protein 70 [Arabidopsis thaliana]

Seq. No.	157820
Seq. ID	LIB3176-085-P1-K1-B8
Method	BLASTX
NCBI GI	g399013
BLAST score	574
E value	2.0e-59
Match length	115
% identity	99
NCBI Description	ADP,ATP CARRIER PROTEIN 1 PRECURSOR (ADP/ATP TRANSLOCASE 1) (ADENINE NUCLEOTIDE TRANSLOCATOR 1) (ANT 1) >gi_99658_pir__S21313 ADP,ATP carrier protein - Arabidopsis thaliana (fragment) >gi_16175_emb_CAA46518_ (X65549) adenylate translocator [Arabidopsis thaliana] >gi_445607_prf__1909354A adenylate translocator [Arabidopsis thaliana]

Seq. No.	157821
Seq. ID	LIB3176-085-P1-K1-B9
Method	BLASTX
NCBI GI	g1175013
BLAST score	548
E value	2.0e-56
Match length	122
% identity	89
NCBI Description	PLASMA MEMBRANE INTRINSIC PROTEIN 2A >gi_629542_pir__S44084 plasma membrane intrinsic protein 2a - Arabidopsis thaliana >gi_472877_emb_CAA53477_ (X75883) plasma membrane intrinsic

protein 2a [Arabidopsis thaliana]

Seq. No.	157822
Seq. ID	LIB3176-085-P1-K1-C10
Method	BLASTX
NCBI GI	g3176668
BLAST score	762
E value	2.0e-81
Match length	146
% identity	99
NCBI Description	(AC004393) Similar to ribosomal protein L17 gb_X62724 from Hordeum vulgare. ESTs gb_Z34728, gb_F19974, gb_T75677 and gb_Z33937 come from this gene. [Arabidopsis thaliana]

Seq. No.	157823
Seq. ID	LIB3176-085-P1-K1-C11
Method	BLASTX
NCBI GI	g1076289
BLAST score	340
E value	7.0e-32
Match length	65
% identity	100
NCBI Description	amino acid permease AAP5 - Arabidopsis thaliana >gi_608673_emb_CAA54632_ (X77501) amino acid permease [Arabidopsis thaliana]

Seq. No.	157824
Seq. ID	LIB3176-085-P1-K1-C12
Method	BLASTN
NCBI GI	g2947056
BLAST score	256
E value	1.0e-142
Match length	435
% identity	91
NCBI Description	Arabidopsis thaliana chromosome II BAC T20F6 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	157825
Seq. ID	LIB3176-085-P1-K1-C2
Method	BLASTX
NCBI GI	g1363489
BLAST score	809
E value	7.0e-87
Match length	150
% identity	100
NCBI Description	thioglucosidase (EC 3.2.3.1) 3D precursor - Arabidopsis thaliana >gi_984052_emb_CAA61592_ (X89413) thioglucoside glucohydrolase [Arabidopsis thaliana]

Seq. No.	157826
Seq. ID	LIB3176-085-P1-K1-C3
Method	BLASTX
NCBI GI	g3687251
BLAST score	79
E value	1.0e-71
Match length	143
% identity	92

NCBI Description	(AC005169) unknown protein [Arabidopsis thaliana]

Seq. No.	157827
Seq. ID	LIB3176-085-P1-K1-C4
Method	BLASTX
NCBI GI	g1524280
BLAST score	201
E value	1.0e-15
Match length	77
% identity	53
NCBI Description	(Z79702) rocE [Mycobacterium tuberculosis]

Seq. No.	157828
Seq. ID	LIB3176-085-P1-K1-C5
Method	BLASTX
NCBI GI	g3913518
BLAST score	401
E value	5.0e-39
Match length	87
% identity	97
NCBI Description	3'(2'),5'-BISPHOSPHATE NUCLEOTIDASE (3'(2'),5-BISPHOSPHONUCLEOSIDE 3'(2')-PHOSPHOHYDROLASE) (DPNPASE) >gi_1103921 (U40433) 3'(2'),5'-bisphosphate nucleotidase [Arabidopsis thaliana]

Seq. No.	157829
Seq. ID	LIB3176-085-P1-K1-C6
Method	BLASTX
NCBI GI	g4469020
BLAST score	711
E value	2.0e-75
Match length	152
% identity	91
NCBI Description	(AL035602) putative protein (fragment) [Arabidopsis thaliana]

Seq. No.	157830
Seq. ID	LIB3176-085-P1-K1-C7
Method	BLASTX
NCBI GI	g1172873
BLAST score	736
E value	2.0e-78
Match length	140
% identity	99
NCBI Description	CYSTEINE PROTEINASE RD21A PRECURSOR >gi_541857_pir__JN0719 drought-inducible cysteine proteinase (EC 3.4.22.-) RD21A precursor - Arabidopsis thaliana >gi_435619_dbj_BAA02374_ (D13043) thiol protease [Arabidopsis thaliana]

Seq. No.	157831
Seq. ID	LIB3176-085-P1-K1-C9
Method	BLASTX
NCBI GI	g832876
BLAST score	567
E value	2.0e-58
Match length	151
% identity	70

NCBI Description	(L41345) ascorbate free radical reductase [Solanum lycopersicum] >gi_1097368_prf__2113407A ascorbate free radical reductase [Lycopersicon esculentum]
Seq. No.	157832
Seq. ID	LIB3176-085-P1-K1-D1
Method	BLASTX
NCBI GI	g3193323
BLAST score	606
E value	4.0e-63
Match length	123
% identity	98
NCBI Description	(AF069299) similar to ribosomal protein S13 (Pfam; S15.hmm, score: 78.35); identical to Arabidopsis 40S ribosomal protein S13 (fragment) (SW: P49203A) except the first 32 amino acids are different [Arabidopsis thaliana]
Seq. No.	157833
Seq. ID	LIB3176-085-P1-K1-D3
Method	BLASTX
NCBI GI	g2393724
BLAST score	144
E value	7.0e-09
Match length	70
% identity	41
NCBI Description	(U80819) glutathione-S-transferase homolog [Mus musculus]
Seq. No.	157834
Seq. ID	LIB3176-085-P1-K1-D5
Method	BLASTX
NCBI GI	g170354
BLAST score	549
E value	2.0e-56
Match length	111
% identity	22
NCBI Description	(M74156) pentameric polyubiquitin [Nicotiana sylvestris]
Seq. No.	157835
Seq. ID	LIB3176-085-P1-K1-D6
Method	BLASTX
NCBI GI	g3860167
BLAST score	476
E value	8.0e-48
Match length	132
% identity	77
NCBI Description	(AF098964) disease resistance protein RPP1-WsC [Arabidopsis thaliana]
Seq. No.	157836
Seq. ID	LIB3176-085-P1-K1-D7
Method	BLASTX
NCBI GI	g2506496
BLAST score	544
E value	6.0e-56
Match length	105
% identity	100
NCBI Description	GLUTATHIONE S-TRANSFERASE ERD11 (CLASS PHI)

	>gi_1890156_emb_CAA72413_ (Y11727) gluthatione S-transferase [Arabidopsis thaliana]
Seq. No.	157837
Seq. ID	LIB3176-085-P1-K1-D8
Method	BLASTX
NCBI GI	g119194
BLAST score	763
E value	2.0e-81
Match length	152
% identity	99
NCBI Description	ELONGATION FACTOR TU, CHLOROPLAST PRECURSOR (EF-TU) >gi_81607_pir__S09152 translation elongation factor Tu precursor, chloroplast - Arabidopsis thaliana >gi_22565_emb_CAA36498_ (X52256) elongation factor Tu precursor [Arabidopsis thaliana] >gi_226817_prf__1607332A elongation factor Tu [Arabidopsis thaliana]
Seq. No.	157838
Seq. ID	LIB3176-085-P1-K1-E1
Method	BLASTX
NCBI GI	g4262180
BLAST score	109
E value	3.0e-67
Match length	132
% identity	97
NCBI Description	(AC005508) 29621 [Arabidopsis thaliana]
Seq. No.	157839
Seq. ID	LIB3176-085-P1-K1-E10
Method	BLASTX
NCBI GI	g1279640
BLAST score	280
E value	7.0e-25
Match length	71
% identity	70
NCBI Description	(X92204) NAM [Petunia x hybrida]
Seq. No.	157840
Seq. ID	LIB3176-085-P1-K1-E11
Method	BLASTX
NCBI GI	g3023802
BLAST score	141
E value	1.0e-08
Match length	130
% identity	28
NCBI Description	ALPHA-(1,3)-FUCOSYLTRANSFERASE (GALACTOSIDE 3-L-FUCOSYLTRANSFERASE) (FUCOSYLTRANSFERASE 6) (FUCT-VI) >gi_2655932_emb_CAA74362_ (Y14035) alpha-3-L-fucosyltransferase [Pan troglodytes]
Seq. No.	157841
Seq. ID	LIB3176-085-P1-K1-E12
Method	BLASTX
NCBI GI	g3319350
BLAST score	398
E value	4.0e-39

Match length	87
% identity	90
NCBI Description	(AF077407) No definition line found [Arabidopsis thaliana]

Seq. No.	157842
Seq. ID	LIB3176-085-P1-K1-E2
Method	BLASTX
NCBI GI	g267069
BLAST score	640
E value	4.0e-67
Match length	124
% identity	97
NCBI Description	TUBULIN ALPHA-2/ALPHA-4 CHAIN >gi_320183_pir__JQ1594 tubulin alpha chain - Arabidopsis thaliana >gi_166914 (M84696) apha-2 tubulin [Arabidopsis thaliana] >gi_166916 (M84697) alpha-4 tubulin [Arabidopsis thaliana]

Seq. No.	157843
Seq. ID	LIB3176-085-P1-K1-E3
Method	BLASTX
NCBI GI	g280386
BLAST score	628
E value	1.0e-65
Match length	123
% identity	99
NCBI Description	ubiquitin / ribosomal protein CEP52 - Arabidopsis thaliana >gi_166930 (J05507) ubiquitin extension protein (UBQ1) [Arabidopsis thaliana] >gi_166932 (J05508) ubiquitin extension protein (UBQ2) [Arabidopsis thaliana] >gi_4678227_gb_AAD26972.1_AC007135_8 (AC007135) ubiquitin/ribosomal protein CEP52 [Arabidopsis thaliana]

Seq. No.	157844
Seq. ID	LIB3176-085-P1-K1-E4
Method	BLASTX
NCBI GI	g99742
BLAST score	600
E value	2.0e-62
Match length	134
% identity	89
NCBI Description	2-dehydro-3-deoxyphosphoheptonate aldolase (EC 4.1.2.15) 1 - Arabidopsis thaliana

Seq. No.	157845
Seq. ID	LIB3176-085-P1-K1-E5
Method	BLASTX
NCBI GI	g99742
BLAST score	593
E value	1.0e-61
Match length	133
% identity	88
NCBI Description	2-dehydro-3-deoxyphosphoheptonate aldolase (EC 4.1.2.15) 1 - Arabidopsis thaliana

Seq. No.	157846
Seq. ID	LIB3176-085-P1-K1-E6
Method	BLASTX

NCBI GI	g4262180
BLAST score	103
E value	4.0e-78
Match length	147
% identity	99
NCBI Description	(AC005508) 29621 [Arabidopsis thaliana]

Seq. No.	157847
Seq. ID	LIB3176-085-P1-K1-E8
Method	BLASTX
NCBI GI	g4165861
BLAST score	255
E value	6.0e-22
Match length	114
% identity	23
NCBI Description	(AF006603) histone deacetylase mHDA2 [Mus musculus]

Seq. No.	157848
Seq. ID	LIB3176-085-P1-K1-F1
Method	BLASTX
NCBI GI	g1707364
BLAST score	416
E value	8.0e-41
Match length	140
% identity	66
NCBI Description	(X94626) AATP2 [Arabidopsis thaliana]

Seq. No.	157849
Seq. ID	LIB3176-085-P1-K1-F10
Method	BLASTX
NCBI GI	g2398531
BLAST score	544
E value	8.0e-56
Match length	119
% identity	90
NCBI Description	(Y13726) Transcription factor [Arabidopsis thaliana]

Seq. No.	157850
Seq. ID	LIB3176-085-P1-K1-F12
Method	BLASTN
NCBI GI	g3337347
BLAST score	254
E value	1.0e-141
Match length	342
% identity	99
NCBI Description	Arabidopsis thaliana chromosome II BAC F13P17 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	157851
Seq. ID	LIB3176-085-P1-K1-F2
Method	BLASTX
NCBI GI	g4567207
BLAST score	775
E value	8.0e-83
Match length	148
% identity	99
NCBI Description	(AC007168) unknown protein [Arabidopsis thaliana]

Seq. No.	157852
Seq. ID	LIB3176-085-P1-K1-F3
Method	BLASTX
NCBI GI	g4678349
BLAST score	526
E value	1.0e-53
Match length	137
% identity	24
NCBI Description	(AL049659) putative protein [Arabidopsis thaliana]

Seq. No.	157853
Seq. ID	LIB3176-085-P1-K1-F4
Method	BLASTN
NCBI GI	g1707006
BLAST score	352
E value	0.0e+00
Match length	396
% identity	99
NCBI Description	Arabidopsis thaliana chromosome II BAC T1B8 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	157854
Seq. ID	LIB3176-085-P1-K1-F5
Method	BLASTX
NCBI GI	g135860
BLAST score	582
E value	3.0e-60
Match length	109
% identity	65
NCBI Description	TONOPLAST INTRINSIC PROTEIN, GAMMA (GAMMA TIP) (AQUAPORIN-TIP) >gi_99761_pir__S22202 tonoplast intrinsic protein gamma - Arabidopsis thaliana >gi_16312_emb_CAA45115_ (X63552) tonoplast intrinsic protein, gamma-TIP(Ara). [Arabidopsis thaliana] >gi_166732 (M84344) tonoplast intrinsic protein [Arabidopsis thaliana] >gi_445129_prf__1908432B tonoplast intrinsic protein gamma [Arabidopsis thaliana]

Seq. No.	157855
Seq. ID	LIB3176-085-P1-K1-F6
Method	BLASTX
NCBI GI	g2398531
BLAST score	531
E value	3.0e-54
Match length	119
% identity	89
NCBI Description	(Y13726) Transcription factor [Arabidopsis thaliana]

Seq. No.	157856
Seq. ID	LIB3176-085-P1-K1-F7
Method	BLASTX
NCBI GI	g3337091
BLAST score	468
E value	6.0e-47
Match length	123
% identity	70

NCBI Description	(AB016204) polygalacturonase inhibitor (PGIP) [Citrus unshiu]

Seq. No.	157857
Seq. ID	LIB3176-085-P1-K1-F9
Method	BLASTX
NCBI GI	g3121825
BLAST score	368
E value	3.0e-35
Match length	115
% identity	64
NCBI Description	2-CYS PEROXIREDOXIN BAS1 PRECURSOR (THIOL-SPECIFIC ANTIOXIDANT PROTEIN) >gi_1498247_emb_CAA63910_ (X94219) bas1 protein [Spinacia oleracea]

Seq. No.	157858
Seq. ID	LIB3176-085-P1-K1-G1
Method	BLASTX
NCBI GI	g416681
BLAST score	209
E value	1.0e-16
Match length	138
% identity	38
NCBI Description	ATP SYNTHASE DELTA CHAIN, CHLOROPLAST PRECURSOR >gi_280404_pir__S26198 H+-transporting ATP synthase (EC 3.6.1.34) delta chain precursor, chloroplast - common tobacco >gi_19787_emb_CAA45153_ (X63607) chloroplast ATP synthase (delta subunit) [Nicotiana tabacum]

Seq. No.	157859
Seq. ID	LIB3176-085-P1-K1-G10
Method	BLASTX
NCBI GI	g2062161
BLAST score	538
E value	3.0e-55
Match length	137
% identity	42
NCBI Description	(AC001645) jasmonate inducible protein isolog [Arabidopsis thaliana]

Seq. No.	157860
Seq. ID	LIB3176-085-P1-K1-G11
Method	BLASTX
NCBI GI	g4467139
BLAST score	77
E value	2.0e-12
Match length	56
% identity	57
NCBI Description	(AL035540) putative protein phosphatase-2c [Arabidopsis thaliana]

Seq. No.	157861
Seq. ID	LIB3176-085-P1-K1-G12
Method	BLASTX
NCBI GI	g3386621
BLAST score	370
E value	2.0e-35

Match length	81
% identity	88
NCBI Description	(AC004665) unknown protein [Arabidopsis thaliana]

Seq. No.	157862
Seq. ID	LIB3176-085-P1-K1-G2
Method	BLASTX
NCBI GI	g2495365
BLAST score	743
E value	4.0e-79
Match length	147
% identity	100
NCBI Description	HEAT SHOCK PROTEIN 81-2 (HSP81-2) >gi_445127_prf__1908431B heat shock protein HSP81-2 [Arabidopsis thaliana]

Seq. No.	157863
Seq. ID	LIB3176-085-P1-K1-G3
Method	BLASTX
NCBI GI	g3298443
BLAST score	321
E value	1.0e-29
Match length	81
% identity	73
NCBI Description	(AB010880) chloroplast ribosomal protein L17 [Nicotiana tabacum]

Seq. No.	157864
Seq. ID	LIB3176-085-P1-K1-G4
Method	BLASTX
NCBI GI	g119350
BLAST score	688
E value	1.0e-72
Match length	138
% identity	97
NCBI Description	ENOLASE (2-PHOSPHOGLYCERATE DEHYDRATASE) (2-PHOSPHO-D-GLYCERATE HYDRO-LYASE) >gi_81608_pir__JQ1187 phosphopyruvate hydratase (EC 4.2.1.11) - Arabidopsis thaliana >gi_16271_emb_CAA41114_ (X58107) enolase [Arabidopsis thaliana] >gi_4581151_gb_AAD24635.1_AC006919_13 (AC006919) enolase (2-phospho-D-glycerate hydroylase);identical to P25696 [Arabidopsis thaliana]

Seq. No.	157865
Seq. ID	LIB3176-085-P1-K1-G5
Method	BLASTX
NCBI GI	g4097690
BLAST score	585
E value	1.0e-60
Match length	115
% identity	98
NCBI Description	(U66592) prohibitin 2 [Arabidopsis thaliana] >gi_4099801 (U89791) prohibitin-like protein [Arabidopsis thaliana] >gi_4204301 (AC003027) prohibitin 2 [Arabidopsis thaliana]

Seq. No.	157866
Seq. ID	LIB3176-085-P1-K1-G6

Method	BLASTX
NCBI GI	g267070
BLAST score	620
E value	1.0e-64
Match length	116
% identity	99
NCBI Description	TUBULIN ALPHA-6 CHAIN >gi_282852_pir__JQ1597 tubulin alpha-6 chain - Arabidopsis thaliana >gi_166920 (M84699) TUA6 [Arabidopsis thaliana] >gi_2244853_emb_CAB10275_ (Z97337) tubulin alpha-6 chain (TUA6) [Arabidopsis thaliana]

Seq. No.	157867
Seq. ID	LIB3176-085-P1-K1-G7
Method	BLASTX
NCBI GI	g2281089
BLAST score	390
E value	9.0e-38
Match length	87
% identity	86
NCBI Description	(AC002333) Sm protein F isolog [Arabidopsis thaliana]

Seq. No.	157868
Seq. ID	LIB3176-085-P1-K1-G8
Method	BLASTX
NCBI GI	g4504909
BLAST score	364
E value	1.0e-34
Match length	135
% identity	51
NCBI Description	karyopherin (importin) beta 3 >gi_2102696 (U72761) karyopherin beta 3 [Homo sapiens]

Seq. No.	157869
Seq. ID	LIB3176-085-P1-K1-G9
Method	BLASTX
NCBI GI	g3047082
BLAST score	729
E value	1.0e-77
Match length	140
% identity	97
NCBI Description	(AF058914) similar to Vigna radiata pectinacetylesterase precursor (GB:X99348) [Arabidopsis thaliana]

Seq. No.	157870
Seq. ID	LIB3176-085-P1-K1-H1
Method	BLASTX
NCBI GI	g4336752
BLAST score	650
E value	3.0e-68
Match length	134
% identity	93
NCBI Description	(AF104451) catalase [Brassica juncea]

Seq. No.	157871
Seq. ID	LIB3176-085-P1-K1-H11
Method	BLASTX

NCBI GI	g135406
BLAST score	568
E value	1.0e-58
Match length	112
% identity	96
NCBI Description	TUBULIN ALPHA-3/ALPHA-5 CHAIN >gi_99768_pir__A32712 tubulin alpha-5 chain - Arabidopsis thaliana >gi_166912 (M17189) alpha-tubulin [Arabidopsis thaliana] >gi_166918 (M84698) alpha-5 tubulin [Arabidopsis thaliana]

Seq. No.	157872
Seq. ID	LIB3176-085-P1-K1-H12
Method	BLASTN
NCBI GI	g3449326
BLAST score	413
E value	0.0e+00
Match length	437
% identity	99
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K19M22, complete sequence [Arabidopsis thaliana]

Seq. No.	157873
Seq. ID	LIB3176-085-P1-K1-H4
Method	BLASTN
NCBI GI	g4587641
BLAST score	253
E value	1.0e-140
Match length	439
% identity	98
NCBI Description	Arabidopsis thaliana chromosome I BAC F20D21 genomic sequence, complete sequence

Seq. No.	157874
Seq. ID	LIB3176-085-P1-K1-H5
Method	BLASTX
NCBI GI	g2369714
BLAST score	650
E value	3.0e-68
Match length	143
% identity	90
NCBI Description	(Z97178) elongation factor 2 [Beta vulgaris]

Seq. No.	157875
Seq. ID	LIB3176-085-P1-K1-H6
Method	BLASTN
NCBI GI	g3228389
BLAST score	266
E value	1.0e-148
Match length	354
% identity	94
NCBI Description	Genomic sequence for Arabidopsis thaliana BAC F17L21, complete sequence [Arabidopsis thaliana]

Seq. No.	157876
Seq. ID	LIB3176-085-P1-K1-H7
Method	BLASTX
NCBI GI	g132110

BLAST score	334
E value	2.0e-31
Match length	76
% identity	87
NCBI Description	RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN 3B PRECURSOR (RUBISCO SMALL SUBUNIT 3B) >gi_68060_pir__RKMUB3 ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain B3 precursor - Arabidopsis thaliana >gi_16195_emb_CAA32702_ (X14564) ribulose bisphosphate carboxylase [Arabidopsis thaliana]

Seq. No.	157877
Seq. ID	LIB3176-085-P1-K1-H9
Method	BLASTN
NCBI GI	g4455290
BLAST score	92
E value	2.0e-44
Match length	227
% identity	99
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F18A5 (ESSAII project)

Seq. No.	157878
Seq. ID	LIB3176-086-P1-K1-A10
Method	BLASTX
NCBI GI	g4006883
BLAST score	645
E value	1.0e-67
Match length	142
% identity	88
NCBI Description	(Z99707) cysteine proteinase [Arabidopsis thaliana]

Seq. No.	157879
Seq. ID	LIB3176-086-P1-K1-A11
Method	BLASTX
NCBI GI	g1703220
BLAST score	238
E value	5.0e-20
Match length	87
% identity	51
NCBI Description	AIG2 PROTEIN >gi_1127806 (U40857) AIG2 [Arabidopsis thaliana]

Seq. No.	157880
Seq. ID	LIB3176-086-P1-K1-A12
Method	BLASTX
NCBI GI	g1346106
BLAST score	506
E value	2.0e-51
Match length	93
% identity	100
NCBI Description	GUANINE NUCLEOTIDE-BINDING PROTEIN BETA SUBUNIT >gi_557694 (U12232) GTP binding protein beta subunit [Arabidopsis thaliana] >gi_3096915_emb_CAA18825.1_ (AL023094) GTP binding protein beta subunit [Arabidopsis thaliana]

Seq. No.	157881

Seq. ID	LIB3176-086-P1-K1-A2
Method	BLASTX
NCBI GI	g3482976
BLAST score	712
E value	1.0e-75
Match length	138
% identity	99
NCBI Description	(AL031369) cytochrome P450-like protein [Arabidopsis thaliana]

Seq. No.	157882
Seq. ID	LIB3176-086-P1-K1-A3
Method	BLASTX
NCBI GI	g1469888
BLAST score	189
E value	3.0e-14
Match length	103
% identity	42
NCBI Description	(D63487) The KIAA0153 gene product is related to a putative C.elegans gene encoded in cosmid F42A8. [Homo sapiens]

Seq. No.	157883
Seq. ID	LIB3176-086-P1-K1-A4
Method	BLASTN
NCBI GI	g3882354
BLAST score	171
E value	3.0e-91
Match length	303
% identity	96
NCBI Description	Arabidopsis thaliana 12-oxophytodienoate reductase OPR1 and 12-oxophytodienoate reductase OPR2 genes, complete cds

Seq. No.	157884
Seq. ID	LIB3176-086-P1-K1-A5
Method	BLASTX
NCBI GI	g4455253
BLAST score	93
E value	7.0e-69
Match length	135
% identity	96
NCBI Description	(AL035523) superoxide dismutase (EC 1.15.1.1) (Fe)(fragment) [Arabidopsis thaliana]

Seq. No.	157885
Seq. ID	LIB3176-086-P1-K1-A6
Method	BLASTX
NCBI GI	g3915865
BLAST score	432
E value	7.0e-43
Match length	87
% identity	94
NCBI Description	40S RIBOSOMAL PROTEIN S4

Seq. No.	157886
Seq. ID	LIB3176-086-P1-K1-A7
Method	BLASTX
NCBI GI	g1170373

BLAST score	513
E value	3.0e-52
Match length	98
% identity	100
NCBI Description	HEAT SHOCK COGNATE 70 KD PROTEIN 1 >gi_1072473_pir__S46302 heat shock cognate protein 70-1 - Arabidopsis thaliana >gi_397482_emb_CAA52684_ (X74604) heat shock protein 70 cognate [Arabidopsis thaliana]

Seq. No.	157887
Seq. ID	LIB3176-086-P1-K1-A8
Method	BLASTX
NCBI GI	g99696
BLAST score	365
E value	5.0e-35
Match length	95
% identity	78
NCBI Description	glutamate--ammonia ligase (EC 6.3.1.2) precursor, chloroplast (clone lambdaAtgsl1) - Arabidopsis thaliana >gi_240070_bbs_69728 (S69727) light-regulated glutamine synthetase isoenzyme [Arabidopsis thaliana, Peptide, 430 aa] [Arabidopsis thaliana] >gi_228453_prf__1804333A Gln synthetase [Arabidopsis thaliana]

Seq. No.	157888
Seq. ID	LIB3176-086-P1-K1-A9
Method	BLASTX
NCBI GI	g2842487
BLAST score	285
E value	2.0e-25
Match length	57
% identity	96
NCBI Description	(AL021749) SOF1 protein-like protein [Arabidopsis thaliana]

Seq. No.	157889
Seq. ID	LIB3176-086-P1-K1-B1
Method	BLASTX
NCBI GI	g3024697
BLAST score	606
E value	4.0e-63
Match length	121
% identity	97
NCBI Description	T-COMPLEX PROTEIN 1, EPSILON SUBUNIT (TCP-1-EPSILON) (CCT-EPSILON) >gi_2213618 (AC000103) F21J9.12 [Arabidopsis thaliana]

Seq. No.	157890
Seq. ID	LIB3176-086-P1-K1-B10
Method	BLASTN
NCBI GI	g4309683
BLAST score	261
E value	1.0e-145
Match length	305
% identity	97
NCBI Description	Arabidopsis thaliana chromosome 1 BAC T31J12 sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	157891
Seq. ID	LIB3176-086-P1-K1-B11
Method	BLASTX
NCBI GI	g3193316
BLAST score	77
E value	1.0e-39
Match length	126
% identity	63
NCBI Description	(AF069299) contains similarity to nucleotide sugar epimerases [Arabidopsis thaliana]

Seq. No.	157892
Seq. ID	LIB3176-086-P1-K1-B12
Method	BLASTX
NCBI GI	g4587542
BLAST score	580
E value	4.0e-60
Match length	126
% identity	90
NCBI Description	(AC006577) Belongs to the PF_00657 Lipase/Acylhydrolase with GDSL-motif family. ESTs gb_T45815, gb_T45130 and gb_Z38046 come from this gene. [Arabidopsis thaliana]

Seq. No.	157893
Seq. ID	LIB3176-086-P1-K1-B2
Method	BLASTX
NCBI GI	g2781394
BLAST score	691
E value	4.0e-73
Match length	139
% identity	99
NCBI Description	(U70424) O-methyltransferase 1 [Arabidopsis thaliana]

Seq. No.	157894
Seq. ID	LIB3176-086-P1-K1-B3
Method	BLASTX
NCBI GI	g2459435
BLAST score	616
E value	3.0e-64
Match length	141
% identity	81
NCBI Description	(AC002332) putative serine carboxypeptidase [Arabidopsis thaliana]

Seq. No.	157895
Seq. ID	LIB3176-086-P1-K1-B4
Method	BLASTX
NCBI GI	g113024
BLAST score	577
E value	9.0e-60
Match length	139
% identity	79
NCBI Description	ISOCITRATE LYASE (ISOCITRASE) (ISOCITRATASE) (ICL) >gi_553043 (M83534) isocitrate lyase [Arabidopsis thaliana]

Seq. No.	157896
Seq. ID	LIB3176-086-P1-K1-B5

Method	BLASTX
NCBI GI	g2688299
BLAST score	214
E value	3.0e-17
Match length	66
% identity	53
NCBI Description	(AE001145) prolyl-tRNA synthetase (proS) [Borrelia burgdorferi]

Seq. No.	157897
Seq. ID	LIB3176-086-P1-K1-B6
Method	BLASTX
NCBI GI	g115767
BLAST score	622
E value	5.0e-71
Match length	135
% identity	98
NCBI Description	CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR (CAB-165/180) (LHCP) >gi_81603_pir__A29280 chlorophyll a/b-binding protein ab165 - Arabidopsis thaliana >gi_16368_emb_CAA27540_ (X03907) chlorophyll a/b binding protein (LHCP AB 65) [Arabidopsis thaliana] >gi_16372_emb_CAA27541_ (X03908) chlorophyll a/b binding protein (LHCP AB 180) [Arabidopsis thaliana]

Seq. No.	157898
Seq. ID	LIB3176-086-P1-K1-B7
Method	BLASTX
NCBI GI	g3776575
BLAST score	544
E value	6.0e-56
Match length	124
% identity	86
NCBI Description	(AC005388) Similar to Schizosaccharomyces CCAAT-binding factor F7G19.16 gi_1922964 from Arabidopsis thaliana BAC gb_AC000106. EST gb_H36963 comes from this gene. [Arabidopsis thaliana]

Seq. No.	157899
Seq. ID	LIB3176-086-P1-K1-B8
Method	BLASTX
NCBI GI	g4337027
BLAST score	437
E value	2.0e-43
Match length	88
% identity	98
NCBI Description	(AF123254) MFP2 [Arabidopsis thaliana]

Seq. No.	157900
Seq. ID	LIB3176-086-P1-K1-B9
Method	BLASTX
NCBI GI	g2501056
BLAST score	606
E value	4.0e-66
Match length	137
% identity	97
NCBI Description	SERYL-TRNA SYNTHETASE (SERINE--TRNA LIGASE) (SERRS)

	>gi_2129737_pir__S71293 seryl-tRNA synthetase - Arabidopsis thaliana >gi_1359497_emb_CAA94388_ (Z70313) seryl-tRNA Synthetase [Arabidopsis thaliana]
Seq. No.	157901
Seq. ID	LIB3176-086-P1-K1-C1
Method	BLASTX
NCBI GI	g2262167
BLAST score	600
E value	2.0e-62
Match length	123
% identity	94
NCBI Description	(AC002329) cytosolic ribosomal protein S4 [Arabidopsis thaliana]
Seq. No.	157902
Seq. ID	LIB3176-086-P1-K1-C10
Method	BLASTX
NCBI GI	g421826
BLAST score	267
E value	1.0e-23
Match length	98
% identity	54
NCBI Description	chlorophyll a/b-binding protein CP29 - Arabidopsis thaliana >gi_298036_emb_CAA50712_ (X71878) CP29 [Arabidopsis thaliana]
Seq. No.	157903
Seq. ID	LIB3176-086-P1-K1-C11
Method	BLASTX
NCBI GI	g1076678
BLAST score	348
E value	3.0e-33
Match length	76
% identity	92
NCBI Description	ubiquitin / ribosomal protein S27a - potato (fragment)
Seq. No.	157904
Seq. ID	LIB3176-086-P1-K1-C12
Method	BLASTX
NCBI GI	g3738291
BLAST score	336
E value	1.0e-31
Match length	64
% identity	100
NCBI Description	(AC005309) unknown protein [Arabidopsis thaliana]
Seq. No.	157905
Seq. ID	LIB3176-086-P1-K1-C2
Method	BLASTN
NCBI GI	g3426033
BLAST score	307
E value	1.0e-172
Match length	423
% identity	96
NCBI Description	Arabidopsis thaliana chromosome II BAC F12C20 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	157906
Seq. ID	LIB3176-086-P1-K1-C3
Method	BLASTX
NCBI GI	g399013
BLAST score	525
E value	1.0e-53
Match length	105
% identity	99
NCBI Description	ADP,ATP CARRIER PROTEIN 1 PRECURSOR (ADP/ATP TRANSLOCASE 1) (ADENINE NUCLEOTIDE TRANSLOCATOR 1) (ANT 1) >gi_99658_pir__S21313 ADP,ATP carrier protein - Arabidopsis thaliana (fragment) >gi_16175_emb_CAA46518_ (X65549) adenylate translocator [Arabidopsis thaliana] >gi_445607_prf__1909354A adenylate translocator [Arabidopsis thaliana]

Seq. No.	157907
Seq. ID	LIB3176-086-P1-K1-C4
Method	BLASTX
NCBI GI	g2811028
BLAST score	537
E value	5.0e-55
Match length	125
% identity	89
NCBI Description	HYPOTHETICAL 47.9 KD PROTEIN M021B04.12 >gi_2191188 (AF007271) similar to S. cerevisiae SIK1P (PID:g984964) [Arabidopsis thaliana]

Seq. No.	157908
Seq. ID	LIB3176-086-P1-K1-C6
Method	BLASTN
NCBI GI	g16367
BLAST score	73
E value	7.0e-33
Match length	177
% identity	93
NCBI Description	A.thaliana gene (LHCP AB 165) for chlorophyll a/b binding protein

Seq. No.	157909
Seq. ID	LIB3176-086-P1-K1-C7
Method	BLASTN
NCBI GI	g2351067
BLAST score	364
E value	0.0e+00
Match length	420
% identity	97
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MPO12, complete sequence [Arabidopsis thaliana]

Seq. No.	157910
Seq. ID	LIB3176-086-P1-K1-C8
Method	BLASTN
NCBI GI	g4757417
BLAST score	260
E value	1.0e-144

Match length	437
% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: T30G6, complete sequence

Seq. No.	157911
Seq. ID	LIB3176-086-P1-K1-D10
Method	BLASTX
NCBI GI	g3318617
BLAST score	274
E value	2.0e-40
Match length	101
% identity	90
NCBI Description	(AB016066) mitochondrial phosphate transporter [Arabidopsis thaliana]

Seq. No.	157912
Seq. ID	LIB3176-086-P1-K1-D11
Method	BLASTN
NCBI GI	g3738275
BLAST score	406
E value	0.0e+00
Match length	418
% identity	99
NCBI Description	Arabidopsis thaliana chromosome II BAC F17A22 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	157913
Seq. ID	LIB3176-086-P1-K1-D12
Method	BLASTX
NCBI GI	g1350680
BLAST score	479
E value	2.0e-48
Match length	98
% identity	97
NCBI Description	60S RIBOSOMAL PROTEIN L1

Seq. No.	157914
Seq. ID	LIB3176-086-P1-K1-D3
Method	BLASTX
NCBI GI	g1402908
BLAST score	656
E value	5.0e-69
Match length	133
% identity	95
NCBI Description	(X98315) peroxidase [Arabidopsis thaliana] >gi_1429221_emb_CAA67313_ (X98777) peroxidase ATP16a [Arabidopsis thaliana] >gi_4455802_emb_CAB37193_ (AJ133036) peroxidase [Arabidopsis thaliana]

Seq. No.	157915
Seq. ID	LIB3176-086-P1-K1-D4
Method	BLASTX
NCBI GI	g481815
BLAST score	179
E value	4.0e-13
Match length	84

% identity	42
NCBI Description	vegetative storage protein - western balsam poplar x cottonwood >gi_309839 (L20233) vegetative storage protein [Populus trichocarpa x Populus deltoides]

Seq. No.	157916
Seq. ID	LIB3176-086-P1-K1-D7
Method	BLASTX
NCBI GI	g2281088
BLAST score	678
E value	1.0e-71
Match length	131
% identity	98
NCBI Description	(AC002333) indole-3-acetate beta-glucosyltransferase isolog [Arabidopsis thaliana]

Seq. No.	157917
Seq. ID	LIB3176-086-P1-K1-D8
Method	BLASTX
NCBI GI	g4586021
BLAST score	706
E value	7.0e-75
Match length	141
% identity	97
NCBI Description	(AC007170) putative cytoplasmic aconitate hydratase [Arabidopsis thaliana]

Seq. No.	157918
Seq. ID	LIB3176-086-P1-K1-D9
Method	BLASTX
NCBI GI	g2244750
BLAST score	46
E value	6.0e-57
Match length	120
% identity	96
NCBI Description	(Z97335) adenosylhomocysteinase [Arabidopsis thaliana] >gi_3088579 (AF059581) S-adenosyl-L-homocysteine hydrolase [Arabidopsis thaliana]

Seq. No.	157919
Seq. ID	LIB3176-086-P1-K1-E1
Method	BLASTN
NCBI GI	g4490734
BLAST score	109
E value	2.0e-54
Match length	125
% identity	97
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone (ESSA project)

Seq. No.	157920
Seq. ID	LIB3176-086-P1-K1-E11
Method	BLASTN
NCBI GI	g3927822
BLAST score	236
E value	1.0e-130
Match length	399

% identity	97
NCBI Description	Arabidopsis thaliana chromosome II BAC F8N16 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	157921
Seq. ID	LIB3176-086-P1-K1-E12
Method	BLASTN
NCBI GI	g2244788
BLAST score	46
E value	8.0e-17
Match length	124
% identity	85
NCBI Description	Arabidopsis thaliana DNA chromosome 4, ESSA I contig fragment No

Seq. No.	157922
Seq. ID	LIB3176-086-P1-K1-E2
Method	BLASTX
NCBI GI	g3510249
BLAST score	365
E value	2.0e-52
Match length	136
% identity	80
NCBI Description	(AC005310) unknown protein [Arabidopsis thaliana]

Seq. No.	157923
Seq. ID	LIB3176-086-P1-K1-E3
Method	BLASTN
NCBI GI	g3297806
BLAST score	31
E value	1.0e-07
Match length	316
% identity	81
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F17I5 (ESSA project)

Seq. No.	157924
Seq. ID	LIB3176-086-P1-K1-E4
Method	BLASTX
NCBI GI	g1172977
BLAST score	250
E value	1.0e-21
Match length	82
% identity	67
NCBI Description	60S RIBOSOMAL PROTEIN L18 >gi_606970 (U15741) cytoplasmic ribosomal protein L18 [Arabidopsis thaliana]

Seq. No.	157925
Seq. ID	LIB3176-086-P1-K1-E6
Method	BLASTX
NCBI GI	g2341032
BLAST score	483
E value	6.0e-52
Match length	116
% identity	93
NCBI Description	(AC000104) EST gb_ATTS0956 comes from this gene. [Arabidopsis thaliana]

Seq. No.	157926
Seq. ID	LIB3176-086-P1-K1-E7
Method	BLASTN
NCBI GI	g3046855
BLAST score	230
E value	1.0e-126
Match length	258
% identity	98
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MSL1, complete sequence [Arabidopsis thaliana]

Seq. No.	157927
Seq. ID	LIB3176-086-P1-K1-E8
Method	BLASTX
NCBI GI	g1621268
BLAST score	416
E value	6.0e-41
Match length	102
% identity	75
NCBI Description	(Z81012) unknown [Ricinus communis]

Seq. No.	157928
Seq. ID	LIB3176-086-P1-K1-E9
Method	BLASTN
NCBI GI	g1877523
BLAST score	100
E value	6.0e-49
Match length	377
% identity	98
NCBI Description	Arabidopsis thaliana BAC T7I23, complete sequence [Arabidopsis thaliana]

Seq. No.	157929
Seq. ID	LIB3176-086-P1-K1-F1
Method	BLASTX
NCBI GI	g2244750
BLAST score	412
E value	2.0e-40
Match length	102
% identity	77
NCBI Description	(Z97335) adenosylhomocysteinase [Arabidopsis thaliana] >gi_3088579 (AF059581) S-adenosyl-L-homocysteine hydrolase [Arabidopsis thaliana]

Seq. No.	157930
Seq. ID	LIB3176-086-P1-K1-F10
Method	BLASTX
NCBI GI	g462013
BLAST score	582
E value	2.0e-60
Match length	132
% identity	86
NCBI Description	ENDOPLASMIN HOMOLOG PRECURSOR (GRP94 HOMOLOG) >gi_542022_pir__S39558 HSP90 homolog - Madagascar periwinkle >gi_348696 (L14594) heat shock protein 90 [Catharanthus roseus]

Seq. No.	157931
Seq. ID	LIB3176-086-P1-K1-F11
Method	BLASTX
NCBI GI	g132939
BLAST score	604
E value	6.0e-63
Match length	125
% identity	91
NCBI Description	60S RIBOSOMAL PROTEIN L3 >gi_81657_pir__JQ0771 ribosomal protein L3 (ARP1) - Arabidopsis thaliana >gi_166858 (M32654) ribosomal protein [Arabidopsis thaliana]

Seq. No.	157932
Seq. ID	LIB3176-086-P1-K1-F12
Method	BLASTN
NCBI GI	g3063438
BLAST score	190
E value	1.0e-103
Match length	205
% identity	99
NCBI Description	Complete sequence of Arabidopsis F22O13, complete sequence [Arabidopsis thaliana]

Seq. No.	157933
Seq. ID	LIB3176-086-P1-K1-F2
Method	BLASTX
NCBI GI	g1769905
BLAST score	475
E value	9.0e-48
Match length	130
% identity	71
NCBI Description	(X98108) 23 kDa polypeptide of oxygen-evolving comlex (OEC) [Arabidopsis thaliana]

Seq. No.	157934
Seq. ID	LIB3176-086-P1-K1-F4
Method	BLASTX
NCBI GI	g1170939
BLAST score	654
E value	9.0e-69
Match length	135
% identity	91
NCBI Description	S-ADENOSYLMETHIONINE SYNTHETASE 3 (METHIONINE ADENOSYLTRANSFERASE 3) (ADOMET SYNTHETASE 3) >gi_1084408_pir__S46540 methionine adenosyltransferase (EC 2.5.1.6) - tomato >gi_429108_emb_CAA80867_ (Z24743) S-adenosyl-L-methionine synthetase [Lycopersicon esculentum]

Seq. No.	157935
Seq. ID	LIB3176-086-P1-K1-F6
Method	BLASTN
NCBI GI	g2645198
BLAST score	395
E value	0.0e+00
Match length	399

% identity	100
NCBI Description	Arabidopsis thaliana chromosome I BAC T26J12 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	157936
Seq. ID	LIB3176-086-P1-K1-F7
Method	BLASTX
NCBI GI	g399091
BLAST score	360
E value	1.0e-34
Match length	76
% identity	91
NCBI Description	PYROPHOSPHATE-ENERGIZED VACUOLAR MEMBRANE PROTON PUMP (PYROPHOSPHATE-ENERGIZED INORGANIC PYROPHOSPHATASE) (H+-PPASE) >gi_282878_pir__A38230 inorganic pyrophosphatase (EC 3.6.1.1), H+-translocating pyrophosphate-energized - Arabidopsis thaliana >gi_166634 (M81892) vacuolar H+-phosphatase [Arabidopsis thaliana]

Seq. No.	157937
Seq. ID	LIB3176-086-P1-K1-F8
Method	BLASTX
NCBI GI	g4651204
BLAST score	182
E value	2.0e-13
Match length	47
% identity	62
NCBI Description	(AB026262) ring finger protein [Cicer arietinum]

Seq. No.	157938
Seq. ID	LIB3176-086-P1-K1-G1
Method	BLASTX
NCBI GI	g4503515
BLAST score	234
E value	2.0e-19
Match length	125
% identity	48
NCBI Description	UNKNOWN >gi_2351380 (U54559) translation initiation factor eIF3 p40 subunit [Homo sapiens]

Seq. No.	157939
Seq. ID	LIB3176-086-P1-K1-G10
Method	BLASTX
NCBI GI	g3286693
BLAST score	644
E value	1.0e-67
Match length	130
% identity	99
NCBI Description	(Y15433) 33 kDa polypeptide of oxygen-evolving complex (OEC) in photosystem II [Arabidopsis thaliana]

Seq. No.	157940
Seq. ID	LIB3176-086-P1-K1-G12
Method	BLASTX
NCBI GI	g2245085
BLAST score	698
E value	6.0e-74

Match length	142
% identity	99
NCBI Description	(Z97343) lactate dehydrogenase [Arabidopsis thaliana]

Seq. No.	157941
Seq. ID	LIB3176-086-P1-K1-G2
Method	BLASTX
NCBI GI	g4006934
BLAST score	507
E value	2.0e-51
Match length	121
% identity	78
NCBI Description	(AJ012571) glutathione transferase [Arabidopsis thaliana]

Seq. No.	157942
Seq. ID	LIB3176-086-P1-K1-G3
Method	BLASTN
NCBI GI	g499159
BLAST score	373
E value	0.0e+00
Match length	412
% identity	98
NCBI Description	A.thaliana mRNA Athb-5

Seq. No.	157943
Seq. ID	LIB3176-086-P1-K1-G4
Method	BLASTX
NCBI GI	g231587
BLAST score	529
E value	4.0e-54
Match length	137
% identity	76
NCBI Description	ATP SYNTHASE BETA CHAIN, MITOCHONDRIAL PRECURSOR >gi_283001_pir__S25304 H+-transporting ATP synthase (EC 3.6.1.34) beta chain precursor, mitochondrial - rice >gi_218147_dbj_BAA01372_ (D10491) mitochondrial F1-ATPase [Oryza sativa]

Seq. No.	157944
Seq. ID	LIB3176-086-P1-K1-G6
Method	BLASTX
NCBI GI	g1864017
BLAST score	628
E value	1.0e-65
Match length	122
% identity	98
NCBI Description	(D63396) elongation factor-1 alpha [Nicotiana tabacum]

Seq. No.	157945
Seq. ID	LIB3176-086-P1-K1-G8
Method	BLASTX
NCBI GI	g1946690
BLAST score	522
E value	2.0e-53
Match length	103
% identity	97
NCBI Description	(U94495) glutathione peroxidase [Arabidopsis thaliana]

>gi_4582452_gb_AAD24836.1_AC007071_8 (AC007071) putative glutathione peroxidase [Arabidopsis thaliana]

Seq. No.	157946
Seq. ID	LIB3176-086-P1-K1-G9
Method	BLASTX
NCBI GI	g120667
BLAST score	339
E value	5.0e-32
Match length	86
% identity	78
NCBI Description	GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE, CYTOSOLIC >gi_81622_pir__JQ1287 glyceraldehyde-3-phosphate dehydrogenase (EC 1.2.1.12), cytosolic - Arabidopsis thaliana >gi_166706 (M64116) cystolic glyceraldehyde-3-phosphate dehydrogenase [Arabidopsis thaliana] >gi_166710 (M64119) glyceraldehyde-3-phosphate dehydrogenase [Arabidopsis thaliana]

Seq. No.	157947
Seq. ID	LIB3176-086-P1-K1-H10
Method	BLASTX
NCBI GI	g4115379
BLAST score	307
E value	4.0e-28
Match length	110
% identity	57
NCBI Description	(AC005967) putative carbonyl reductase [Arabidopsis thaliana]

Seq. No.	157948
Seq. ID	LIB3176-086-P1-K1-H2
Method	BLASTX
NCBI GI	g4406759
BLAST score	148
E value	2.0e-09
Match length	99
% identity	38
NCBI Description	(AC006836) hypothetical protein [Arabidopsis thaliana]

Seq. No.	157949
Seq. ID	LIB3176-086-P1-K1-H3
Method	BLASTN
NCBI GI	g166810
BLAST score	376
E value	0.0e+00
Match length	405
% identity	98
NCBI Description	Arabidopsis thaliana Columbia protein kinase mRNA, complete cds

Seq. No.	157950
Seq. ID	LIB3176-086-P1-K1-H4
Method	BLASTN
NCBI GI	g2358139
BLAST score	199
E value	1.0e-108

Match length	437
% identity	98
NCBI Description	Arabidopsis thaliana chromosome 1 YAC yUP8H12 complete sequence [Arabidopsis thaliana]

Seq. No.	157951
Seq. ID	LIB3176-086-P1-K1-H5
Method	BLASTX
NCBI GI	g3763916
BLAST score	371
E value	1.0e-35
Match length	113
% identity	64
NCBI Description	(AC004450) unknown protein [Arabidopsis thaliana] >gi_4531439_gb_AAD22124.1_AC006224_6 (AC006224) unknown protein [Arabidopsis thaliana]

Seq. No.	157952
Seq. ID	LIB3176-086-P1-K1-H7
Method	BLASTX
NCBI GI	g2244749
BLAST score	377
E value	1.0e-47
Match length	104
% identity	96
NCBI Description	(Z97335) hydroxymethyltransferase [Arabidopsis thaliana]

Seq. No.	157953
Seq. ID	LIB3176-086-P1-K1-H8
Method	BLASTX
NCBI GI	g4206210
BLAST score	626
E value	1.0e-65
Match length	121
% identity	65
NCBI Description	(AF071527) putative calcium channel [Arabidopsis thaliana] >gi_4263043_gb_AAD15312_ (AC005142) putative calcium channel [Arabidopsis thaliana]

Seq. No.	157954
Seq. ID	LIB3176-086-P1-K1-H9
Method	BLASTX
NCBI GI	g4678319
BLAST score	504
E value	3.0e-51
Match length	98
% identity	100
NCBI Description	(AL049658) putative protein [Arabidopsis thaliana]

Seq. No.	157955
Seq. ID	LIB3176-087-P1-K1-A11
Method	BLASTN
NCBI GI	g3738088
BLAST score	225
E value	1.0e-123
Match length	351
% identity	100

NCBI Description	Arabidopsis thaliana chromosome II BAC T30L20 genomic sequence, complete sequence [Arabidopsis thaliana]
Seq. No.	157956
Seq. ID	LIB3176-087-P1-K1-A12
Method	BLASTX
NCBI GI	g4336752
BLAST score	651
E value	2.0e-68
Match length	122
% identity	100
NCBI Description	(AF104451) catalase [Brassica juncea]
Seq. No.	157957
Seq. ID	LIB3176-087-P1-K1-A2
Method	BLASTN
NCBI GI	g2275194
BLAST score	224
E value	1.0e-123
Match length	320
% identity	97
NCBI Description	Arabidopsis thaliana chromosome II BAC T08I13 genomic sequence, complete sequence [Arabidopsis thaliana]
Seq. No.	157958
Seq. ID	LIB3176-087-P1-K1-A3
Method	BLASTX
NCBI GI	g4336752
BLAST score	446
E value	1.0e-44
Match length	83
% identity	100
NCBI Description	(AF104451) catalase [Brassica juncea]
Seq. No.	157959
Seq. ID	LIB3176-087-P1-K1-A4
Method	BLASTX
NCBI GI	g440953
BLAST score	479
E value	3.0e-48
Match length	110
% identity	83
NCBI Description	(S66866) cytochrome c1 [Solanum tuberosum=potatoes, Desiree, monohaploid line AM 80/5793, Peptide Mitochondrial, 320 aa] [Solanum tuberosum]
Seq. No.	157960
Seq. ID	LIB3176-087-P1-K1-A5
Method	BLASTX
NCBI GI	g131398
BLAST score	522
E value	3.0e-53
Match length	133
% identity	80
NCBI Description	PHOTOSYSTEM II 10 KD POLYPEPTIDE PRECURSOR >gi_72714_pir__F2MU10 photosystem II 10K protein precursor - Arabidopsis thaliana >gi_16447_emb_CAA39441_ (X55970)

photosystem II 10 kDa polypeptide [Arabidopsis thaliana] >gi_3152571 (AC002986) Match to photosystem II 10kDa polypeptide gb_X55970. ESTs gb_Z17693, gb_N37616, gb_T41858, gb_T88021, gb_R37531, gb_T04679, gb_N37520, gb_N64965, gb_Z17592 and gb_N65338, gb_N37466 and gb_T45400 come from this gene. [Arabidopsis

Seq. No.	157961
Seq. ID	LIB3176-087-P1-K1-A6
Method	BLASTX
NCBI GI	g2827529
BLAST score	390
E value	8.0e-38
Match length	103
% identity	83
NCBI Description	(AL021633) putative protein [Arabidopsis thaliana]

Seq. No.	157962
Seq. ID	LIB3176-087-P1-K1-A7
Method	BLASTX
NCBI GI	g4755193
BLAST score	282
E value	2.0e-25
Match length	59
% identity	95
NCBI Description	(AC007018) putative ribosomal protein S17 [Arabidopsis thaliana]

Seq. No.	157963
Seq. ID	LIB3176-087-P1-K1-A8
Method	BLASTX
NCBI GI	g4371295
BLAST score	393
E value	2.0e-38
Match length	78
% identity	99
NCBI Description	(AC006260) putative CCAAT-binding transcription factor [Arabidopsis thaliana]

Seq. No.	157964
Seq. ID	LIB3176-087-P1-K1-B10
Method	BLASTN
NCBI GI	g2924730
BLAST score	403
E value	0.0e+00
Match length	415
% identity	99
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MPI7, complete sequence [Arabidopsis thaliana]

Seq. No.	157965
Seq. ID	LIB3176-087-P1-K1-B11
Method	BLASTX
NCBI GI	g483057
BLAST score	174
E value	2.0e-12
Match length	136

% identity	35
NCBI Description	hypothetical protein (xylB 5' region) - Butyrivibrio fibrisolvens (fragment) >gi_144165 (M55537) ORF1 [Butyrivibrio fibrisolvens]
Seq. No.	157966
Seq. ID	LIB3176-087-P1-K1-B12
Method	BLASTX
NCBI GI	g1546698
BLAST score	331
E value	5.0e-31
Match length	95
% identity	68
NCBI Description	(X98808) peroxidase ATP3a [Arabidopsis thaliana]
Seq. No.	157967
Seq. ID	LIB3176-087-P1-K1-B2
Method	BLASTX
NCBI GI	g2129562
BLAST score	620
E value	7.0e-65
Match length	121
% identity	97
NCBI Description	class III ADH, glutathione-dependent formaldehyde dehydrogenase. - Arabidopsis thaliana >gi_1143388_emb_CAA57973_ (X82647) class III ADH, glutathione-dependent formaldehyde dehydrogenase. [Arabidopsis thaliana]
Seq. No.	157968
Seq. ID	LIB3176-087-P1-K1-B3
Method	BLASTX
NCBI GI	g2500376
BLAST score	513
E value	3.0e-52
Match length	119
% identity	74
NCBI Description	60S RIBOSOMAL PROTEIN L34 >gi_4262177_gb_AAD14494_ (AC005508) 23552 [Arabidopsis thaliana]
Seq. No.	157969
Seq. ID	LIB3176-087-P1-K1-B4
Method	BLASTX
NCBI GI	g3688799
BLAST score	627
E value	1.0e-65
Match length	126
% identity	99
NCBI Description	(AF057137) gamma tonoplast intrinsic protein 2 [Arabidopsis thaliana]
Seq. No.	157970
Seq. ID	LIB3176-087-P1-K1-B5
Method	BLASTX
NCBI GI	g3757519
BLAST score	653
E value	1.0e-68

Match length	140
% identity	94
NCBI Description	(AC005167) hypothetical protein [Arabidopsis thaliana]

Seq. No.	157971
Seq. ID	LIB3176-087-P1-K1-B6
Method	BLASTX
NCBI GI	g2062161
BLAST score	587
E value	6.0e-61
Match length	115
% identity	48
NCBI Description	(AC001645) jasmonate inducible protein isolog [Arabidopsis thaliana]

Seq. No.	157972
Seq. ID	LIB3176-087-P1-K1-B7
Method	BLASTX
NCBI GI	g2529682
BLAST score	535
E value	5.0e-55
Match length	103
% identity	68
NCBI Description	(AC002535) unknown protein [Arabidopsis thaliana]

Seq. No.	157973
Seq. ID	LIB3176-087-P1-K1-B8
Method	BLASTN
NCBI GI	g3212102
BLAST score	98
E value	7.0e-48
Match length	284
% identity	92
NCBI Description	Arabidopsis Thaliana BAC F6A4, Chromosome IV, near 60.5 cM, complete sequence [Arabidopsis thaliana]

Seq. No.	157974
Seq. ID	LIB3176-087-P1-K1-B9
Method	BLASTX
NCBI GI	g132659
BLAST score	405
E value	1.0e-39
Match length	91
% identity	81
NCBI Description	50S RIBOSOMAL PROTEIN L13, CHLOROPLAST PRECURSOR (CL13) >gi_81483_pir__A32033 ribosomal protein L13 precursor, chloroplast - spinach >gi_170133 (J04461) ribosomal protein L13 [Spinacia oleracea]

Seq. No.	157975
Seq. ID	LIB3176-087-P1-K1-C1
Method	BLASTX
NCBI GI	g3738287
BLAST score	610
E value	1.0e-63
Match length	119
% identity	100

NCBI Description	(AC005309) glutathione s-transferase, GST6 [Arabidopsis thaliana]

Seq. No.	157976
Seq. ID	LIB3176-087-P1-K1-C10
Method	BLASTX
NCBI GI	g1732570
BLAST score	695
E value	1.0e-73
Match length	139
% identity	95
NCBI Description	(U72153) beta-glucosidase [Arabidopsis thaliana]

Seq. No.	157977
Seq. ID	LIB3176-087-P1-K1-C11
Method	BLASTX
NCBI GI	g4337175
BLAST score	502
E value	5.0e-51
Match length	119
% identity	84
NCBI Description	(AC006416) ESTs gb_T20589, gb_T04648, gb_AA597906, gb_T04111, gb_R84180, gb_R65428, gb_T44439, gb_T76570, gb_R90004, gb_T45020, gb_T42457, gb_T20921, gb_AA042762 and gb_AA720210 come from this gene. [Arabidopsis thaliana]

Seq. No.	157978
Seq. ID	LIB3176-087-P1-K1-C12
Method	BLASTX
NCBI GI	g3212849
BLAST score	424
E value	7.0e-42
Match length	107
% identity	81
NCBI Description	(AC004005) unknown protein [Arabidopsis thaliana]

Seq. No.	157979
Seq. ID	LIB3176-087-P1-K1-C2
Method	BLASTX
NCBI GI	g4678226
BLAST score	588
E value	5.0e-61
Match length	120
% identity	97
NCBI Description	(AC007135) putative 40S ribosomal protein S14 [Arabidopsis thaliana]

Seq. No.	157980
Seq. ID	LIB3176-087-P1-K1-C3
Method	BLASTX
NCBI GI	g4204265
BLAST score	340
E value	5.0e-32
Match length	117
% identity	57
NCBI Description	(AC005223) 45643 [Arabidopsis thaliana]

Seq. No.	157981
Seq. ID	LIB3176-087-P1-K1-C4
Method	BLASTN
NCBI GI	g4159703
BLAST score	149
E value	4.0e-78
Match length	361
% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K5F14, complete sequence

Seq. No.	157982
Seq. ID	LIB3176-087-P1-K1-C5
Method	BLASTX
NCBI GI	g4091080
BLAST score	390
E value	8.0e-38
Match length	117
% identity	60
NCBI Description	(AF045571) nucleic acid binding protein [Oryza sativa]

Seq. No.	157983
Seq. ID	LIB3176-087-P1-K1-C6
Method	BLASTX
NCBI GI	g3046703
BLAST score	363
E value	1.0e-34
Match length	70
% identity	100
NCBI Description	(AL021749) protein kinase ADK1-like protein [Arabidopsis thaliana]

Seq. No.	157984
Seq. ID	LIB3176-087-P1-K1-C7
Method	BLASTN
NCBI GI	g3885325
BLAST score	357
E value	0.0e+00
Match length	410
% identity	96
NCBI Description	Arabidopsis thaliana chromosome II BAC T20P8 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	157985
Seq. ID	LIB3176-087-P1-K1-C8
Method	BLASTX
NCBI GI	g548653
BLAST score	502
E value	6.0e-51
Match length	124
% identity	84
NCBI Description	50S RIBOSOMAL PROTEIN L12-A, CHLOROPLAST PRECURSOR (CL12-A) >gi_541895_pir__A53394 ribosomal protein L12.A, chloroplast - Arabidopsis thaliana >gi_468771_emb_CAA48181_ (X68046) ribosomal protein L12 [Arabidopsis thaliana]

Seq. No.	157986

Seq. ID	LIB3176-087-P1-K1-C9
Method	BLASTX
NCBI GI	g1546688
BLAST score	270
E value	5.0e-24
Match length	78
% identity	73
NCBI Description	(X98802) peroxidase ATP11a [Arabidopsis thaliana] >gi_2388572 (AC000098) Strong similarity to Arabidopsis peroxidase ATP11A (gb_X98802). [Arabidopsis thaliana] >gi_2388573 (AC000098) Strong similarity to Arabidopsis peroxidase ATP11A (gb_X98802). [Arabidopsis thaliana]

Seq. No.	157987
Seq. ID	LIB3176-087-P1-K1-D1
Method	BLASTX
NCBI GI	g2369714
BLAST score	657
E value	4.0e-69
Match length	130
% identity	95
NCBI Description	(Z97178) elongation factor 2 [Beta vulgaris]

Seq. No.	157988
Seq. ID	LIB3176-087-P1-K1-D10
Method	BLASTX
NCBI GI	g4056456
BLAST score	308
E value	3.0e-28
Match length	61
% identity	100
NCBI Description	(AC005990) Strong similarity to gb_U20808 auxin-induced protein from Vigna radiata and a member of the zinc-binding dehydrogenase family PF_00107. ESTs gb_T43674, gb_H77006 and gb_AA395179 come from this gene. [Arabidopsis thaliana]

Seq. No.	157989
Seq. ID	LIB3176-087-P1-K1-D11
Method	BLASTX
NCBI GI	g541858
BLAST score	664
E value	6.0e-70
Match length	126
% identity	100
NCBI Description	endoxyloglucan transferase - Arabidopsis thaliana >gi_469484_dbj_BAA03921_ (D16454) endo-xyloglucan transferase [Arabidopsis thaliana] >gi_4063757 (AC005561) endo-xyloglucan transferase [Arabidopsis thaliana]

Seq. No.	157990
Seq. ID	LIB3176-087-P1-K1-D2
Method	BLASTN
NCBI GI	g4757408
BLAST score	166
E value	3.0e-88
Match length	170
% identity	99

NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MQO24, complete sequence
Seq. No.	157991
Seq. ID	LIB3176-087-P1-K1-D3
Method	BLASTX
NCBI GI	g2739046
BLAST score	158
E value	1.0e-10
Match length	60
% identity	43
NCBI Description	(AF024652) polyphosphoinositide binding protein Ssh2p [Glycine max]
Seq. No.	157992
Seq. ID	LIB3176-087-P1-K1-D4
Method	BLASTX
NCBI GI	g2062164
BLAST score	256
E value	6.0e-35
Match length	102
% identity	81
NCBI Description	(AC001645) jasmonate inducible protein isolog [Arabidopsis thaliana]
Seq. No.	157993
Seq. ID	LIB3176-087-P1-K1-D5
Method	BLASTN
NCBI GI	g4581084
BLAST score	271
E value	1.0e-151
Match length	428
% identity	100
NCBI Description	Arabidopsis thaliana chromosome I BAC T30F21 genomic sequence, complete sequence
Seq. No.	157994
Seq. ID	LIB3176-087-P1-K1-D7
Method	BLASTX
NCBI GI	g544285
BLAST score	485
E value	4.0e-49
Match length	113
% identity	81
NCBI Description	FIBRILLARIN >gi_422056_pir__S33690 fibrillarin - fission yeast (Schizosaccharomyces pombe) >gi_296704_emb_CAA49550_ (X69930) fibrillarin [Schizosaccharomyces pombe] >gi_3687500_emb_CAA21168_ (AL031788) fibrillarin [Schizosaccharomyces pombe]
Seq. No.	157995
Seq. ID	LIB3176-087-P1-K1-D8
Method	BLASTX
NCBI GI	g2499811
BLAST score	371
E value	1.0e-35
Match length	98

% identity	74
NCBI Description	PROFILIN 2 >gi_1353766 (U43323) profilin 2 [Arabidopsis thaliana] >gi_1353772 (U43326) profilin 2 [Arabidopsis thaliana]

Seq. No.	157996
Seq. ID	LIB3176-087-P1-K1-D9
Method	BLASTX
NCBI GI	g3881780
BLAST score	163
E value	2.0e-11
Match length	105
% identity	36
NCBI Description	(Z48638) similar to lipid transfer protein [Caenorhabditis elegans]

Seq. No.	157997
Seq. ID	LIB3176-087-P1-K1-E1
Method	BLASTX
NCBI GI	g3776561
BLAST score	492
E value	8.0e-50
Match length	121
% identity	86
NCBI Description	(AC005388) Identical to DNA for acyl carrier protein (ACP) gene A2 gb_X57699 from A. thaliana. ESTs gb_W43252, gb_T42821, gb_N65229, gb_N97267, gb_F15491 and gb_AA040955 come from this gene. [Arabidopsis thaliana]

Seq. No.	157998
Seq. ID	LIB3176-087-P1-K1-E10
Method	BLASTX
NCBI GI	g4538930
BLAST score	691
E value	4.0e-73
Match length	136
% identity	99
NCBI Description	(AL049483) putative peroxidase [Arabidopsis thaliana]

Seq. No.	157999
Seq. ID	LIB3176-087-P1-K1-E11
Method	BLASTX
NCBI GI	g4589980
BLAST score	624
E value	3.0e-65
Match length	130
% identity	91
NCBI Description	(AC007195) cyclophilin, 3' partial [Arabidopsis thaliana]

Seq. No.	158000
Seq. ID	LIB3176-087-P1-K1-E12
Method	BLASTX
NCBI GI	g2129569
BLAST score	220
E value	7.0e-18
Match length	83
% identity	57

NCBI Description	cytosolic cyclophilin ROC3 - Arabidopsis thaliana >gi_1305455 (U40399) cytosolic cyclophilin [Arabidopsis thaliana] >gi_4581104_gb_AAD24594.1_AC005825_1 (AC005825) cytosolic cyclophilin (ROC3) [Arabidopsis thaliana]
Seq. No.	158001
Seq. ID	LIB3176-087-P1-K1-E2
Method	BLASTX
NCBI GI	g1169278
BLAST score	222
E value	3.0e-18
Match length	61
% identity	77
NCBI Description	DEHYDRIN ERD14 >gi_556474_dbj_BAA04569_ (D17715) ERD14 protein [Arabidopsis thaliana]
Seq. No.	158002
Seq. ID	LIB3176-087-P1-K1-E3
Method	BLASTX
NCBI GI	g445612
BLAST score	562
E value	6.0e-58
Match length	119
% identity	90
NCBI Description	ribosomal protein S19 [Solanum tuberosum]
Seq. No.	158003
Seq. ID	LIB3176-087-P1-K1-E6
Method	BLASTN
NCBI GI	g3985931
BLAST score	357
E value	0.0e+00
Match length	412
% identity	93
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K21H1, complete sequence [Arabidopsis thaliana]
Seq. No.	158004
Seq. ID	LIB3176-087-P1-K1-E7
Method	BLASTX
NCBI GI	g1363489
BLAST score	698
E value	6.0e-74
Match length	132
% identity	97
NCBI Description	thioglucosidase (EC 3.2.3.1) 3D precursor - Arabidopsis thaliana >gi_984052_emb_CAA61592_ (X89413) thioglucoside glucohydrolase [Arabidopsis thaliana]
Seq. No.	158005
Seq. ID	LIB3176-087-P1-K1-E9
Method	BLASTX
NCBI GI	g3318611
BLAST score	227
E value	1.0e-18
Match length	55
% identity	80

NCBI Description	(AB016063) mitochondrial phosphate transporter [Glycine max]

Seq. No.	158006
Seq. ID	LIB3176-087-P1-K1-F1
Method	BLASTX
NCBI GI	g114086
BLAST score	501
E value	8.0e-51
Match length	112
% identity	88
NCBI Description	RAS-RELATED PROTEIN ARA-2 >gi_320559_pir__JS0639 GTP-binding protein ara-2 - Arabidopsis thaliana >gi_217835_dbj_BAA00829_ (D01024) small GTP-binding protein [Arabidopsis thaliana]

Seq. No.	158007
Seq. ID	LIB3176-087-P1-K1-F10
Method	BLASTX
NCBI GI	g119975
BLAST score	560
E value	9.0e-58
Match length	139
% identity	83
NCBI Description	FERREDOXIN PRECURSOR >gi_99692_pir__S09979 ferredoxin [2Fe-2S] precursor - Arabidopsis thaliana >gi_16437_emb_CAA35754_ (X51370) ferredoxin precursor [Arabidopsis thaliana] >gi_166698 (M35868) ferrodoxin A [Arabidopsis thaliana]

Seq. No.	158008
Seq. ID	LIB3176-087-P1-K1-F11
Method	BLASTX
NCBI GI	g2781394
BLAST score	735
E value	3.0e-78
Match length	139
% identity	99
NCBI Description	(U70424) O-methyltransferase 1 [Arabidopsis thaliana]

Seq. No.	158009
Seq. ID	LIB3176-087-P1-K1-F12
Method	BLASTX
NCBI GI	g4502315
BLAST score	183
E value	2.0e-13
Match length	119
% identity	33
NCBI Description	ATPase, H+ transporting, lysosomal (vacuolar proton pump) 42kD >gi_401329_sp_P21283_VATC_HUMAN VACUOLAR ATP SYNTHASE SUBUNIT C (V-ATPASE C SUBUNIT) >gi_542836_pir__JN0907 H+-transporting ATPase (EC 3.6.1.35) chain C, vacuolar - human >gi_37643_emb_CAA48903_ (X69151) vacuolar proton-ATPase [Homo sapiens]

Seq. No.	158010
Seq. ID	LIB3176-087-P1-K1-F2

Method	BLASTN
NCBI GI	g4467131
BLAST score	232
E value	1.0e-127
Match length	372
% identity	100
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F20M13 (ESSA project)

Seq. No.	158011
Seq. ID	LIB3176-087-P1-K1-F4
Method	BLASTX
NCBI GI	g2827715
BLAST score	115
E value	1.0e-05
Match length	140
% identity	8
NCBI Description	(AL021684) receptor protein kinase - like protein [Arabidopsis thaliana]

Seq. No.	158012
Seq. ID	LIB3176-087-P1-K1-F5
Method	BLASTX
NCBI GI	g2462825
BLAST score	418
E value	4.0e-41
Match length	141
% identity	64
NCBI Description	(AF000657) contains Procite 'RNP1' putative RNA-binding region [Arabidopsis thaliana]

Seq. No.	158013
Seq. ID	LIB3176-087-P1-K1-F6
Method	BLASTX
NCBI GI	g3420004
BLAST score	230
E value	5.0e-19
Match length	92
% identity	45
NCBI Description	(AF000305) steroid sulfotransferase 1 [Brassica napus]

Seq. No.	158014
Seq. ID	LIB3176-087-P1-K1-F7
Method	BLASTX
NCBI GI	g2062167
BLAST score	587
E value	6.0e-61
Match length	110
% identity	100
NCBI Description	(AC001645) Proline-rich protein APG isolog [Arabidopsis thaliana]

Seq. No.	158015
Seq. ID	LIB3176-087-P1-K1-F8
Method	BLASTX
NCBI GI	g3273757
BLAST score	413

E value	1.0e-40
Match length	100
% identity	79
NCBI Description	(AF061852) iron superoxide dismutase 3 [Arabidopsis thaliana]

Seq. No.	158016
Seq. ID	LIB3176-087-P1-K1-F9
Method	BLASTN
NCBI GI	g4468976
BLAST score	402
E value	0.0e+00
Match length	414
% identity	99
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F19F18 (ESSA project)

Seq. No.	158017
Seq. ID	LIB3176-087-P1-K1-G1
Method	BLASTN
NCBI GI	g4589440
BLAST score	231
E value	1.0e-127
Match length	235
% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MSD21, complete sequence

Seq. No.	158018
Seq. ID	LIB3176-087-P1-K1-G10
Method	BLASTX
NCBI GI	g3482967
BLAST score	503
E value	4.0e-51
Match length	96
% identity	100
NCBI Description	(AL031369) Protein phosphatase 2C-like protein [Arabidopsis thaliana] >gi_4559345_gb_AAD23006.1_AC006585_1 (AC006585) protein phosphatase 2C [Arabidopsis thaliana]

Seq. No.	158019
Seq. ID	LIB3176-087-P1-K1-G11
Method	BLASTX
NCBI GI	g464986
BLAST score	575
E value	2.0e-59
Match length	107
% identity	99
NCBI Description	UBIQUITIN-CONJUGATING ENZYME E2-17 KD 9 (UBIQUITIN-PROTEIN LIGASE 9) (UBIQUITIN CARRIER PROTEIN 9) (UBCAT4B) >gi_421857_pir__S32674 ubiquitin--protein ligase (EC 6.3.2.19) UBC9 - Arabidopsis thaliana >gi_297884_emb_CAA78714_ (Z14990) ubiquitin conjugating enzyme homolog [Arabidopsis thaliana] >gi_349211 (L00639) ubiquitin conjugating enzyme [Arabidopsis thaliana] >gi_600391_emb_CAA51201_ (X72626) ubiquitin conjugating enzyme E2 [Arabidopsis thaliana]

>gi_4455355_emb_CAB36765.1_ (AL035524) ubiquitin-protein ligase UBC9 [Arabidopsis thaliana]

Seq. No.	158020
Seq. ID	LIB3176-087-P1-K1-G12
Method	BLASTX
NCBI GI	g531829
BLAST score	170
E value	2.0e-12
Match length	76
% identity	50
NCBI Description	(U12390) beta-galactosidase alpha peptide [cloning vector pSport1]

Seq. No.	158021
Seq. ID	LIB3176-087-P1-K1-G2
Method	BLASTX
NCBI GI	g3548808
BLAST score	241
E value	2.0e-71
Match length	136
% identity	100
NCBI Description	(AC005313) unknown protein [Arabidopsis thaliana]

Seq. No.	158022
Seq. ID	LIB3176-087-P1-K1-G3
Method	BLASTN
NCBI GI	g2244991
BLAST score	152
E value	6.0e-80
Match length	429
% identity	99
NCBI Description	Arabidopsis thaliana DNA chromosome 4, ESSA I contig fragment No

Seq. No.	158023
Seq. ID	LIB3176-087-P1-K1-G4
Method	BLASTX
NCBI GI	g2129579
BLAST score	740
E value	8.0e-79
Match length	141
% identity	100
NCBI Description	Dwarf1 protein - Arabidopsis thaliana >gi_516043 (U12400) Dwarf1 [Arabidopsis thaliana]

Seq. No.	158024
Seq. ID	LIB3176-087-P1-K1-G5
Method	BLASTX
NCBI GI	g3786324
BLAST score	211
E value	8.0e-17
Match length	61
% identity	59
NCBI Description	(AB015139) chlorophyll a oxygenase [Chlamydomonas reinhardtii]

Seq. No.	158025
Seq. ID	LIB3176-087-P1-K1-G6
Method	BLASTX
NCBI GI	g3242722
BLAST score	623
E value	4.0e-65
Match length	133
% identity	90
NCBI Description	(AC003040) putative acetone-cyanohydrin lyase [Arabidopsis thaliana]

Seq. No.	158026
Seq. ID	LIB3176-087-P1-K1-G7
Method	BLASTX
NCBI GI	g1174162
BLAST score	686
E value	2.0e-72
Match length	122
% identity	100
NCBI Description	(U44976) ubiquitin-conjugating enzyme [Arabidopsis thaliana] >gi_3746915 (AF091106) E2 ubiquitin-conjugating-like enzyme [Arabidopsis thaliana]

Seq. No.	158027
Seq. ID	LIB3176-087-P1-K1-G8
Method	BLASTX
NCBI GI	g3023216
BLAST score	672
E value	7.0e-71
Match length	134
% identity	100
NCBI Description	14-3-3-LIKE PROTEIN GF14 MU >gi_1531629 (U60444) GF14 mu [Arabidopsis thaliana]

Seq. No.	158028
Seq. ID	LIB3176-087-P1-K1-G9
Method	BLASTX
NCBI GI	g4587544
BLAST score	548
E value	2.0e-56
Match length	138
% identity	81
NCBI Description	(AC006577) Belongs to the PF_00657 Lipase/Acylhydrolase with GDSL-motif family. ESTs gb_T75865, gb_R30449, gb_AI239373, gb_F19931 and gb_F19930 come from this gene. [Arabidopsis thaliana]

Seq. No.	158029
Seq. ID	LIB3176-087-P1-K1-H1
Method	BLASTX
NCBI GI	g113024
BLAST score	580
E value	4.0e-60
Match length	141
% identity	82
NCBI Description	ISOCITRATE LYASE (ISOCITRASE) (ISOCITRATASE) (ICL) >gi_553043 (M83534) isocitrate lyase [Arabidopsis thaliana]

Seq. No.	158030
Seq. ID	LIB3176-087-P1-K1-H10
Method	BLASTX
NCBI GI	g399013
BLAST score	515
E value	2.0e-52
Match length	101
% identity	100
NCBI Description	ADP,ATP CARRIER PROTEIN 1 PRECURSOR (ADP/ATP TRANSLOCASE 1) (ADENINE NUCLEOTIDE TRANSLOCATOR 1) (ANT 1) >gi_99658_pir__S21313 ADP,ATP carrier protein - Arabidopsis thaliana (fragment) >gi_16175_emb_CAA46518_ (X65549) adenylate translocator [Arabidopsis thaliana] >gi_445607_prf__1909354A adenylate translocator [Arabidopsis thaliana]

Seq. No.	158031
Seq. ID	LIB3176-087-P1-K1-H11
Method	BLASTX
NCBI GI	g3929649
BLAST score	525
E value	1.0e-53
Match length	108
% identity	100
NCBI Description	(AJ131205) mitochondrial NAD-dependent malate dehydrogenase [Arabidopsis thaliana]

Seq. No.	158032
Seq. ID	LIB3176-087-P1-K1-H12
Method	BLASTX
NCBI GI	g4097565
BLAST score	434
E value	6.0e-43
Match length	82
% identity	100
NCBI Description	(U64920) ATGP3 [Arabidopsis thaliana]

Seq. No.	158033
Seq. ID	LIB3176-087-P1-K1-H4
Method	BLASTX
NCBI GI	g1173218
BLAST score	629
E value	9.0e-66
Match length	123
% identity	100
NCBI Description	40S RIBOSOMAL PROTEIN S15A >gi_440824 (L27461) ribosomal protein S15 [Arabidopsis thaliana] >gi_2150130 (AF001412) cytoplasmic ribosomal protein S15a [Arabidopsis thaliana]

Seq. No.	158034
Seq. ID	LIB3176-087-P1-K1-H5
Method	BLASTN
NCBI GI	g2264367
BLAST score	257
E value	1.0e-142
Match length	394

% identity	100
NCBI Description	Arabidopsis thaliana BAC F6P23 from chromosome IV, top arm, complete sequence [Arabidopsis thaliana]
Seq. No.	158035
Seq. ID	LIB3176-087-P1-K1-H6
Method	BLASTX
NCBI GI	g2583125
BLAST score	268
E value	1.0e-23
Match length	90
% identity	62
NCBI Description	(AC002387) putative transketolase precursor [Arabidopsis thaliana]
Seq. No.	158036
Seq. ID	LIB3176-087-P1-K1-H7
Method	BLASTX
NCBI GI	g3212849
BLAST score	564
E value	3.0e-58
Match length	124
% identity	90
NCBI Description	(AC004005) unknown protein [Arabidopsis thaliana]
Seq. No.	158037
Seq. ID	LIB3176-087-P1-K1-H8
Method	BLASTX
NCBI GI	g132110
BLAST score	619
E value	1.0e-64
Match length	114
% identity	99
NCBI Description	RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN 3B PRECURSOR (RUBISCO SMALL SUBUNIT 3B) >gi_68060_pir__RKMUB3 ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain B3 precursor - Arabidopsis thaliana >gi_16195_emb_CAA32702_ (X14564) ribulose bisphosphate carboxylase [Arabidopsis thaliana]
Seq. No.	158038
Seq. ID	LIB3176-088-P1-K1-A1
Method	BLASTN
NCBI GI	g4249393
BLAST score	191
E value	1.0e-103
Match length	265
% identity	100
NCBI Description	Arabidopsis thaliana chromosome II BAC T9J23 genomic sequence, complete sequence [Arabidopsis thaliana]
Seq. No.	158039
Seq. ID	LIB3176-088-P1-K1-A10
Method	BLASTN
NCBI GI	g4699904
BLAST score	135
E value	9.0e-70

Match length	422
% identity	98
NCBI Description	Genomic sequence for Arabidopsis thaliana BAC F1E22, complete sequence

Seq. No.	158040
Seq. ID	LIB3176-088-P1-K1-A11
Method	BLASTX
NCBI GI	g2738248
BLAST score	410
E value	2.0e-40
Match length	79
% identity	97
NCBI Description	(U97200) cobalamin-independent methionine synthase [Arabidopsis thaliana]

Seq. No.	158041
Seq. ID	LIB3176-088-P1-K1-A12
Method	BLASTX
NCBI GI	g2791834
BLAST score	370
E value	8.0e-40
Match length	100
% identity	93
NCBI Description	(AF041463) elongation factor 1-alpha [Manihot esculenta]

Seq. No.	158042
Seq. ID	LIB3176-088-P1-K1-A3
Method	BLASTX
NCBI GI	g119143
BLAST score	63
E value	2.0e-41
Match length	90
% identity	98
NCBI Description	ELONGATION FACTOR 1-ALPHA (EF-1-ALPHA) >gi_81606_pir__S06724 translation elongation factor eEF-1 alpha chain - Arabidopsis thaliana >gi_295788_emb_CAA34453_ (X16430) elongation factor 1-alpha [Arabidopsis thaliana] >gi_1369927_emb_CAA34454_ (X16431) elongation factor 1-alpha [Arabidopsis thaliana] >gi_1369928_emb_CAA34455_ (X16431) elongation factor 1-alpha [Arabidopsis thaliana] >gi_1532172 (U63815) EF-1alpha-A1 [Arabidopsis thaliana] >gi_1532173 (U63815) EF-1alpha-A2 [Arabidopsis thaliana] >gi_1532174 (U63815) EF-1alpha-A3 [Arabidopsis thaliana]

Seq. No.	158043
Seq. ID	LIB3176-088-P1-K1-A4
Method	BLASTX
NCBI GI	g3482928
BLAST score	578
E value	5.0e-60
Match length	115
% identity	98
NCBI Description	(AC003970) Unknown protein [Arabidopsis thaliana] >gi_3929586 (AF100166) phytochrome interacting factor 3 [Arabidopsis thaliana]

Seq. No.	158044
Seq. ID	LIB3176-088-P1-K1-A5
Method	BLASTX
NCBI GI	g418854
BLAST score	433
E value	5.0e-43
Match length	87
% identity	17
NCBI Description	ubiquitin precursor - parsley >gi_288112_emb_CAA45621_ (X64344) polyubiquitin [Petroselinum crispum] >gi_288114_emb_CAA45622_ (X64345) polyubiquitin [Petroselinum crispum]

Seq. No.	158045
Seq. ID	LIB3176-088-P1-K1-A7
Method	BLASTX
NCBI GI	g4587564
BLAST score	581
E value	3.0e-60
Match length	117
% identity	98
NCBI Description	(AC006550) Strong similarity to gb_X14017 photosystem I reaction centre subunit II precursor (psaD) from Spinacia oleracea. ESTs gb_R30423, gb_T42998, gb_Z18178, gb_T14133, gb_N65521, gb_T42498, gb_T41918, gb_N38024

Seq. No.	158046
Seq. ID	LIB3176-088-P1-K1-A8
Method	BLASTX
NCBI GI	g126766
BLAST score	246
E value	3.0e-21
Match length	51
% identity	90
NCBI Description	MALATE SYNTHASE, GLYOXYSOMAL >gi_68216_pir__SYRPMA malate synthase (EC 4.1.3.2), glyoxysomal - rape >gi_167150 (J04468) malate synthase (EC 4.1.3.2) [Brassica napus]

Seq. No.	158047
Seq. ID	LIB3176-088-P1-K1-A9
Method	BLASTX
NCBI GI	g1173218
BLAST score	403
E value	2.0e-39
Match length	80
% identity	99
NCBI Description	40S RIBOSOMAL PROTEIN S15A >gi_440824 (L27461) ribosomal protein S15 [Arabidopsis thaliana] >gi_2150130 (AF001412) cytoplasmic ribosomal protein S15a [Arabidopsis thaliana]

Seq. No.	158048
Seq. ID	LIB3176-088-P1-K1-B1
Method	BLASTX
NCBI GI	g4006877
BLAST score	276
E value	1.0e-24
Match length	52

% identity	51
NCBI Description	(Z99707) RNA-binding like protein [Arabidopsis thaliana]

Seq. No.	158049
Seq. ID	LIB3176-088-P1-K1-B10
Method	BLASTN
NCBI GI	g4689466
BLAST score	242
E value	1.0e-133
Match length	354
% identity	99
NCBI Description	Arabidopsis thaliana chromosome II BAC T23O15 genomic sequence, complete sequence

Seq. No.	158050
Seq. ID	LIB3176-088-P1-K1-B11
Method	BLASTN
NCBI GI	g3510343
BLAST score	365
E value	0.0e+00
Match length	369
% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MJC20, complete sequence [Arabidopsis thaliana]

Seq. No.	158051
Seq. ID	LIB3176-088-P1-K1-B2
Method	BLASTX
NCBI GI	g1864017
BLAST score	541
E value	1.0e-55
Match length	104
% identity	99
NCBI Description	(D63396) elongation factor-1 alpha [Nicotiana tabacum]

Seq. No.	158052
Seq. ID	LIB3176-088-P1-K1-B3
Method	BLASTN
NCBI GI	g3860243
BLAST score	119
E value	2.0e-60
Match length	295
% identity	98
NCBI Description	Arabidopsis thaliana chromosome II BAC F15K20 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	158053
Seq. ID	LIB3176-088-P1-K1-B4
Method	BLASTX
NCBI GI	g4218120
BLAST score	279
E value	5.0e-25
Match length	69
% identity	80
NCBI Description	(AL035353) Proline-rich APG-like protein [Arabidopsis thaliana]

Seq. No.	158054
Seq. ID	LIB3176-088-P1-K1-B7
Method	BLASTX
NCBI GI	g2313340
BLAST score	205
E value	4.0e-16
Match length	115
% identity	37
NCBI Description	(AE000544) ATP-dependent RNA helicase, DEAD-box family (deaD) [Helicobacter pylori 26695]

Seq. No.	158055
Seq. ID	LIB3176-088-P1-K1-B8
Method	BLASTN
NCBI GI	g4063706
BLAST score	297
E value	1.0e-166
Match length	297
% identity	100
NCBI Description	Arabidopsis thaliana extensin-like protein (ELP) mRNA, complete cds

Seq. No.	158056
Seq. ID	LIB3176-088-P1-K1-B9
Method	BLASTN
NCBI GI	g4581084
BLAST score	176
E value	1.0e-94
Match length	216
% identity	95
NCBI Description	Arabidopsis thaliana chromosome I BAC T30F21 genomic sequence, complete sequence

Seq. No.	158057
Seq. ID	LIB3176-088-P1-K1-C1
Method	BLASTN
NCBI GI	g4567300
BLAST score	365
E value	0.0e+00
Match length	417
% identity	98
NCBI Description	Arabidopsis thaliana chromosome II P1 MHK10 genomic sequence, complete sequence

Seq. No.	158058
Seq. ID	LIB3176-088-P1-K1-C10
Method	BLASTN
NCBI GI	g2961370
BLAST score	92
E value	3.0e-44
Match length	356
% identity	45
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F23E13 (ESSAII project)

Seq. No.	158059
Seq. ID	LIB3176-088-P1-K1-C11

Method	BLASTX
NCBI GI	g126766
BLAST score	454
E value	2.0e-45
Match length	93
% identity	90
NCBI Description	MALATE SYNTHASE, GLYOXYSOMAL >gi_68216_pir__SYRPMA malate synthase (EC 4.1.3.2), glyoxysomal - rape >gi_167150 (J04468) malate synthase (EC 4.1.3.2) [Brassica napus]

Seq. No.	158060
Seq. ID	LIB3176-088-P1-K1-C12
Method	BLASTX
NCBI GI	g477819
BLAST score	395
E value	1.0e-38
Match length	92
% identity	80
NCBI Description	mitochondrial processing peptidase (EC 3.4.99.41) beta chain precursor - potato >gi_410634_bbs_136741 cytochrome c reductase-processing peptidase subunit II, MPP subunit II, P53 [potatoes, var. Marfona, tuber, Peptide Mitochondrial, 530 aa]

Seq. No.	158061
Seq. ID	LIB3176-088-P1-K1-C2
Method	BLASTX
NCBI GI	g1170503
BLAST score	310
E value	1.0e-28
Match length	59
% identity	100
NCBI Description	EUKARYOTIC INITIATION FACTOR 4A-1 (EIF-4A-1) >gi_322503_pir__JC1452 translation initiation factor eIF-4A1 - Arabidopsis thaliana >gi_16554_emb_CAA46188_ (X65052) eukaryotic translation initiation factor 4A-1 [Arabidopsis thaliana]

Seq. No.	158062
Seq. ID	LIB3176-088-P1-K1-C3
Method	BLASTN
NCBI GI	g4164472
BLAST score	35
E value	4.0e-10
Match length	83
% identity	86
NCBI Description	Vernicia fordii negatively light-regulated protein mRNA, complete cds

Seq. No.	158063
Seq. ID	LIB3176-088-P1-K1-C4
Method	BLASTN
NCBI GI	g2760164
BLAST score	295
E value	1.0e-165
Match length	380
% identity	99

NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K18P6, complete sequence [Arabidopsis thaliana]
Seq. No.	158064
Seq. ID	LIB3176-088-P1-K1-C5
Method	BLASTX
NCBI GI	g4204274
BLAST score	173
E value	1.0e-12
Match length	32
% identity	100
NCBI Description	(AC004146) ribulose bisphosphate carboxylase, small subunit [Arabidopsis thaliana]
Seq. No.	158065
Seq. ID	LIB3176-088-P1-K1-C6
Method	BLASTX
NCBI GI	g135467
BLAST score	524
E value	1.0e-53
Match length	118
% identity	86
NCBI Description	TUBULIN BETA-4 CHAIN >gi_2129546_pir__S68122 beta-tubulin 4 - Arabidopsis thaliana >gi_166640 (M21415) beta-tubulin [Arabidopsis thaliana]
Seq. No.	158066
Seq. ID	LIB3176-088-P1-K1-C7
Method	BLASTX
NCBI GI	g4587544
BLAST score	606
E value	4.0e-63
Match length	141
% identity	87
NCBI Description	(AC006577) Belongs to the PF_00657 Lipase/Acylhydrolase with GDSL-motif family. ESTs gb_T75865, gb_R30449, gb_AI239373, gb_F19931 and gb_F19930 come from this gene. [Arabidopsis thaliana]
Seq. No.	158067
Seq. ID	LIB3176-088-P1-K1-C8
Method	BLASTN
NCBI GI	g2088638
BLAST score	307
E value	1.0e-172
Match length	311
% identity	100
NCBI Description	Arabidopsis thaliana chromosome II BAC T28M21 genomic sequence, complete sequence [Arabidopsis thaliana]
Seq. No.	158068
Seq. ID	LIB3176-088-P1-K1-C9
Method	BLASTN
NCBI GI	g3149951
BLAST score	89
E value	2.0e-42
Match length	97

% identity	98
NCBI Description	Arabidopsis thaliana mRNA for DRH1, complete cds

Seq. No.	158069
Seq. ID	LIB3176-088-P1-K1-D1
Method	BLASTX
NCBI GI	g4220527
BLAST score	439
E value	1.0e-43
Match length	123
% identity	60
NCBI Description	(AL035356) putative protein [Arabidopsis thaliana]

Seq. No.	158070
Seq. ID	LIB3176-088-P1-K1-D10
Method	BLASTN
NCBI GI	g3869066
BLAST score	329
E value	0.0e+00
Match length	329
% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MBM17, complete sequence [Arabidopsis thaliana]

Seq. No.	158071
Seq. ID	LIB3176-088-P1-K1-D11
Method	BLASTX
NCBI GI	g841208
BLAST score	133
E value	3.0e-10
Match length	82
% identity	51
NCBI Description	(U18995) trypsin inhibitor propeptide [Brassica oleracea]

Seq. No.	158072
Seq. ID	LIB3176-088-P1-K1-D12
Method	BLASTX
NCBI GI	g4630748
BLAST score	292
E value	1.0e-26
Match length	67
% identity	81
NCBI Description	(AC007236) putative anion exchange protein 3 [Arabidopsis thaliana]

Seq. No.	158073
Seq. ID	LIB3176-088-P1-K1-D2
Method	BLASTX
NCBI GI	g3335371
BLAST score	488
E value	2.0e-49
Match length	103
% identity	98
NCBI Description	(AC003028) putative ethylene-inducible protein [Arabidopsis thaliana]

Seq. No.	158074

Seq. ID	LIB3176-088-P1-K1-D3
Method	BLASTX
NCBI GI	g4406772
BLAST score	341
E value	1.0e-32
Match length	113
% identity	70
NCBI Description	(AC006836) putative nitrilase-associated protein [Arabidopsis thaliana]

Seq. No.	158075
Seq. ID	LIB3176-088-P1-K1-D4
Method	BLASTX
NCBI GI	g1709794
BLAST score	512
E value	4.0e-52
Match length	112
% identity	89
NCBI Description	26S PROTEASOME REGULATORY SUBUNIT S5A (MULTIUBIQUITIN CHAIN BINDING PROTEIN) >gi_1165206 (U33269) MBP1 [Arabidopsis thaliana] >gi_4467150_emb_CAB37519_ (AL035540) multiubiquitin chain binding protein (MBP1) [Arabidopsis thaliana]

Seq. No.	158076
Seq. ID	LIB3176-088-P1-K1-D6
Method	BLASTX
NCBI GI	g2983997
BLAST score	154
E value	2.0e-10
Match length	53
% identity	53
NCBI Description	(AE000749) hypothetical protein [Aquifex aeolicus]

Seq. No.	158077
Seq. ID	LIB3176-088-P1-K1-D7
Method	BLASTX
NCBI GI	g116527
BLAST score	195
E value	7.0e-15
Match length	67
% identity	46
NCBI Description	PROBABLE CLPP-LIKE PROTEASE (ENDOPEPTIDASE CLP) (ORF 196) >gi_1143166 (U32397) ClpP protease [Nicotiana tabacum] >gi_2924270_emb_CAA77422_ (Z00044) ATP-dependent protease proteolytic subuni [Nicotiana tabacum]

Seq. No.	158078
Seq. ID	LIB3176-088-P1-K1-D8
Method	BLASTX
NCBI GI	g4559395
BLAST score	519
E value	4.0e-53
Match length	104
% identity	100
NCBI Description	(AC006526) putative cyclic nucleotide-regulated ion channel protein [Arabidopsis thaliana]

Seq. No.	158079
Seq. ID	LIB3176-088-P1-K1-E1
Method	BLASTX
NCBI GI	g2833379
BLAST score	604
E value	5.0e-63
Match length	120
% identity	98
NCBI Description	RIBOSE-PHOSPHATE PYROPHOSPHOKINASE 1 (PHOSPHORIBOSYL PYROPHOSPHATE SYNTHETASE 1) (PRS I) >gi_1076397_pir__S51270 ribose-phosphate pyrophosphokinase (EC 2.7.6.1) - Arabidopsis thaliana >gi_633140_emb_CAA58717_ (X83764) phosphoribosyl diphosphate synthetase [Arabidopsis thaliana] >gi_3608149 (AC005314) phosphoribosyl diphosphate synthetase [Arabidopsis thaliana]

Seq. No.	158080
Seq. ID	LIB3176-088-P1-K1-E10
Method	BLASTX
NCBI GI	g1708313
BLAST score	235
E value	3.0e-20
Match length	55
% identity	87
NCBI Description	HEAT SHOCK PROTEIN 81-3 (HSP81-3) >gi_999396_bbs_163637 (S77849) heat-shock Protein=HSP81-3 [Arabidopsis thaliana=thale-cress, Peptide, 699 aa] [Arabidopsis thaliana]

Seq. No.	158081
Seq. ID	LIB3176-088-P1-K1-E12
Method	BLASTX
NCBI GI	g1076396
BLAST score	114
E value	2.0e-30
Match length	76
% identity	95
NCBI Description	regA protein - Arabidopsis thaliana

Seq. No.	158082
Seq. ID	LIB3176-088-P1-K1-E3
Method	BLASTN
NCBI GI	g2980757
BLAST score	199
E value	1.0e-108
Match length	333
% identity	99
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F6I18 (ESSAII project)

Seq. No.	158083
Seq. ID	LIB3176-088-P1-K1-E4
Method	BLASTN
NCBI GI	g2351068
BLAST score	214
E value	1.0e-117

Match length	214
% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MRH10, complete sequence [Arabidopsis thaliana]

Seq. No.	158084
Seq. ID	LIB3176-088-P1-K1-E6
Method	BLASTN
NCBI GI	g3033373
BLAST score	34
E value	5.0e-10
Match length	46
% identity	96
NCBI Description	Arabidopsis thaliana chromosome II BAC F19I3 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	158085
Seq. ID	LIB3176-088-P1-K1-E7
Method	BLASTX
NCBI GI	g4544375
BLAST score	480
E value	2.0e-48
Match length	119
% identity	75
NCBI Description	(AC006920) putative reverse transcriptase [Arabidopsis thaliana]

Seq. No.	158086
Seq. ID	LIB3176-088-P1-K1-E8
Method	BLASTN
NCBI GI	g4757409
BLAST score	67
E value	3.0e-29
Match length	421
% identity	73
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MVC8, complete sequence

Seq. No.	158087
Seq. ID	LIB3176-088-P1-K1-E9
Method	BLASTX
NCBI GI	g507808
BLAST score	552
E value	5.0e-57
Match length	110
% identity	99
NCBI Description	(D13987) phosphoenolpyruvate carboxylase [Brassica napus] >gi_743641_prf__2013218A phosphoenolpyruvate carboxylase [Brassica napus]

Seq. No.	158088
Seq. ID	LIB3176-088-P1-K1-F1
Method	BLASTX
NCBI GI	g1402912
BLAST score	267
E value	7.0e-24
Match length	69

% identity	75
NCBI Description	(X98317) peroxidase [Arabidopsis thaliana]

Seq. No.	158089
Seq. ID	LIB3176-088-P1-K1-F10
Method	BLASTX
NCBI GI	g3688123
BLAST score	235
E value	3.0e-20
Match length	48
% identity	85
NCBI Description	(AJ006293) granule-bound starch synthase [Antirrhinum majus]

Seq. No.	158090
Seq. ID	LIB3176-088-P1-K1-F12
Method	BLASTN
NCBI GI	g786465
BLAST score	143
E value	1.0e-74
Match length	282
% identity	98
NCBI Description	sedoheptulose-1,7-bisphosphatase [Arabidopsis thaliana, C24, Genomic, 2747 nt]

Seq. No.	158091
Seq. ID	LIB3176-088-P1-K1-F2
Method	BLASTX
NCBI GI	g4512658
BLAST score	145
E value	3.0e-09
Match length	63
% identity	41
NCBI Description	(AC006931) hypothetical protein [Arabidopsis thaliana]

Seq. No.	158092
Seq. ID	LIB3176-088-P1-K1-F3
Method	BLASTX
NCBI GI	g1546692
BLAST score	313
E value	7.0e-29
Match length	62
% identity	100
NCBI Description	(X98805) peroxidase ATP19a [Arabidopsis thaliana]

Seq. No.	158093
Seq. ID	LIB3176-088-P1-K1-F6
Method	BLASTN
NCBI GI	g3869074
BLAST score	185
E value	1.0e-100
Match length	297
% identity	99
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MMI9, complete sequence [Arabidopsis thaliana]

Seq. No.	158094

Seq. ID	LIB3176-088-P1-K1-F7
Method	BLASTX
NCBI GI	g4454036
BLAST score	541
E value	1.0e-55
Match length	101
% identity	99
NCBI Description	(AL035394) putative major latex protein [Arabidopsis thaliana]

Seq. No.	158095
Seq. ID	LIB3176-088-P1-K1-F8
Method	BLASTX
NCBI GI	g1363489
BLAST score	386
E value	1.0e-37
Match length	71
% identity	99
NCBI Description	thioglucosidase (EC 3.2.3.1) 3D precursor - Arabidopsis thaliana >gi_984052_emb_CAA61592_ (X89413) thioglucoside glucohydrolase [Arabidopsis thaliana]

Seq. No.	158096
Seq. ID	LIB3176-088-P1-K1-F9
Method	BLASTN
NCBI GI	g4376087
BLAST score	314
E value	1.0e-176
Match length	353
% identity	97
NCBI Description	Arabidopsis thaliana DNA chromosome 4, ESSA I AP2 contig fragment No

Seq. No.	158097
Seq. ID	LIB3176-088-P1-K1-G1
Method	BLASTN
NCBI GI	g3599967
BLAST score	257
E value	1.0e-143
Match length	257
% identity	100
NCBI Description	Arabidopsis thaliana clp protease (CLP) mRNA, partial cds

Seq. No.	158098
Seq. ID	LIB3176-088-P1-K1-G12
Method	BLASTN
NCBI GI	g2980757
BLAST score	151
E value	1.0e-79
Match length	208
% identity	94
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F6I18 (ESSAII project)

Seq. No.	158099
Seq. ID	LIB3176-088-P1-K1-G2
Method	BLASTX

NCBI GI	g1408471
BLAST score	520
E value	4.0e-53
Match length	120
% identity	85
NCBI Description	(U48938) actin depolymerizing factor 1 [Arabidopsis thaliana] >gi_3851707 (AF102173) actin depolymerizing factor 1 [Arabidopsis thaliana]

Seq. No.	158100
Seq. ID	LIB3176-088-P1-K1-G3
Method	BLASTX
NCBI GI	g625977
BLAST score	475
E value	1.0e-49
Match length	107
% identity	95
NCBI Description	p40 protein homolog - Arabidopsis thaliana >gi_402904 (U01955) laminin receptor-like protein [Arabidopsis thaliana]

Seq. No.	158101
Seq. ID	LIB3176-088-P1-K1-G4
Method	BLASTN
NCBI GI	g3193311
BLAST score	36
E value	3.0e-11
Match length	80
% identity	88
NCBI Description	Arabidopsis thaliana BAC F6N15

Seq. No.	158102
Seq. ID	LIB3176-088-P1-K1-G5
Method	BLASTN
NCBI GI	g3449326
BLAST score	44
E value	5.0e-16
Match length	84
% identity	88
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K19M22, complete sequence [Arabidopsis thaliana]

Seq. No.	158103
Seq. ID	LIB3176-088-P1-K1-G7
Method	BLASTN
NCBI GI	g3402695
BLAST score	353
E value	0.0e+00
Match length	371
% identity	99
NCBI Description	Arabidopsis thaliana chromosome II BAC T3K9 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	158104
Seq. ID	LIB3176-088-P1-K1-G8
Method	BLASTX
NCBI GI	g2129578

BLAST score	296
E value	4.0e-27
Match length	57
% identity	100
NCBI Description	dTDP-glucose 4-6-dehydratases homolog - Arabidopsis thaliana >gi_928932_emb_CAA89205_ (Z49239) homolog of dTDP-glucose 4-6-dehydratases [Arabidopsis thaliana] >gi_1585435_prf__2124427B diamide resistance gene [Arabidopsis thaliana]

Seq. No.	158105
Seq. ID	LIB3176-088-P1-K1-G9
Method	BLASTX
NCBI GI	g2129755
BLAST score	300
E value	2.0e-52
Match length	109
% identity	97
NCBI Description	tryptophan synthase (EC 4.2.1.20) alpha chain - Arabidopsis thaliana >gi_619753 (U18993) tryptophan synthase alpha chain [Arabidopsis thaliana] >gi_1585768_prf__2201482A Trp synthase:SUBUNIT=alpha [Arabidopsis thaliana]

Seq. No.	158106
Seq. ID	LIB3176-088-P1-K1-H1
Method	BLASTX
NCBI GI	g417381
BLAST score	543
E value	3.0e-56
Match length	114
% identity	100
NCBI Description	NITRILASE 1 >gi_99738_pir__S22398 nitrilase (EC 3.5.5.1) - Arabidopsis thaliana >gi_16400_emb_CAA45041_ (X63445) nitrilase I [Arabidopsis thaliana]

Seq. No.	158107
Seq. ID	LIB3176-088-P1-K1-H10
Method	BLASTN
NCBI GI	g4589412
BLAST score	107
E value	2.0e-53
Match length	231
% identity	97
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: F6N7, complete sequence

Seq. No.	158108
Seq. ID	LIB3176-088-P1-K1-H11
Method	BLASTX
NCBI GI	g2062161
BLAST score	246
E value	2.0e-21
Match length	47
% identity	51
NCBI Description	(AC001645) jasmonate inducible protein isolog [Arabidopsis thaliana]

Seq. No.	158109
Seq. ID	LIB3176-088-P1-K1-H12
Method	BLASTN
NCBI GI	g2980757
BLAST score	148
E value	6.0e-78
Match length	181
% identity	94
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F6I18 (ESSAII project)

Seq. No.	158110
Seq. ID	LIB3176-088-P1-K1-H2
Method	BLASTX
NCBI GI	g1084350
BLAST score	542
E value	1.0e-55
Match length	108
% identity	93
NCBI Description	glutamate--ammonia ligase (EC 6.3.1.2) - rape >gi_599656_emb_CAA58118.1_ (X82997) glutamate--ammonia ligase [Brassica napus]

Seq. No.	158111
Seq. ID	LIB3176-088-P1-K1-H3
Method	BLASTN
NCBI GI	g3402745
BLAST score	224
E value	1.0e-123
Match length	323
% identity	99
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F18E5 (ESSAII project)

Seq. No.	158112
Seq. ID	LIB3176-088-P1-K1-H5
Method	BLASTN
NCBI GI	g3985958
BLAST score	43
E value	2.0e-15
Match length	104
% identity	91
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MZN1, complete sequence [Arabidopsis thaliana]

Seq. No.	158113
Seq. ID	LIB3176-088-P1-K1-H6
Method	BLASTN
NCBI GI	g4586241
BLAST score	121
E value	7.0e-62
Match length	145
% identity	96
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone T20K18 (ESSA project)

Seq. No.	158114

Seq. ID	LIB3176-088-P1-K1-H7
Method	BLASTX
NCBI GI	g4006934
BLAST score	644
E value	1.0e-67
Match length	126
% identity	98
NCBI Description	(AJ012571) glutathione transferase [Arabidopsis thaliana]

Seq. No.	158115
Seq. ID	LIB3176-088-P1-K1-H8
Method	BLASTX
NCBI GI	g1350680
BLAST score	258
E value	2.0e-22
Match length	50
% identity	100
NCBI Description	60S RIBOSOMAL PROTEIN L1

Seq. No.	158116
Seq. ID	LIB3176-088-P1-K1-H9
Method	BLASTX
NCBI GI	g4539007
BLAST score	267
E value	9.0e-24
Match length	52
% identity	96
NCBI Description	(AL049481) cytochrome c [Arabidopsis thaliana]

Seq. No.	158117
Seq. ID	LIB3176-089-P1-K1-A10
Method	BLASTX
NCBI GI	g1841468
BLAST score	204
E value	6.0e-16
Match length	150
% identity	54
NCBI Description	(Y10990) Tyrosyl-tRNA synthetase [Nicotiana tabacum]

Seq. No.	158118
Seq. ID	LIB3176-089-P1-K1-A2
Method	BLASTX
NCBI GI	g3738291
BLAST score	484
E value	7.0e-49
Match length	133
% identity	76
NCBI Description	(AC005309) unknown protein [Arabidopsis thaliana]

Seq. No.	158119
Seq. ID	LIB3176-089-P1-K1-A3
Method	BLASTX
NCBI GI	g1854386
BLAST score	256
E value	5.0e-22
Match length	98
% identity	49

NCBI Description	(AB001375) similar to soluble NSF attachment protein [Vitis vinifera]
Seq. No.	158120
Seq. ID	LIB3176-089-P1-K1-A4
Method	BLASTX
NCBI GI	g3738257
BLAST score	243
E value	6.0e-21
Match length	58
% identity	84
NCBI Description	(AB018410) cytosolic phosphoglycerate kinase 1 [Populus nigra]
Seq. No.	158121
Seq. ID	LIB3176-089-P1-K1-A5
Method	BLASTX
NCBI GI	g548655
BLAST score	535
E value	9.0e-55
Match length	131
% identity	86
NCBI Description	50S RIBOSOMAL PROTEIN L12-C, CHLOROPLAST PRECURSOR (CL12-C) >gi_541897_pir__C53394 ribosomal protein L12.C, chloroplast - Arabidopsis thaliana >gi_468773_emb_CAA48183_ (X68046) ribosomal protein L12 [Arabidopsis thaliana]
Seq. No.	158122
Seq. ID	LIB3176-089-P1-K1-A6
Method	BLASTX
NCBI GI	g3687249
BLAST score	392
E value	4.0e-38
Match length	102
% identity	77
NCBI Description	(AC005169) putative copia-like transposable element [Arabidopsis thaliana]
Seq. No.	158123
Seq. ID	LIB3176-089-P1-K1-A7
Method	BLASTX
NCBI GI	g587566
BLAST score	166
E value	1.0e-11
Match length	56
% identity	59
NCBI Description	(X80237) mitochondrial processing peptidase [Solanum tuberosum]
Seq. No.	158124
Seq. ID	LIB3176-089-P1-K1-A9
Method	BLASTN
NCBI GI	g2656024
BLAST score	100
E value	7.0e-49
Match length	356
% identity	86

NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K15E6

Seq. No.	158125
Seq. ID	LIB3176-089-P1-K1-B1
Method	BLASTX
NCBI GI	g2677828
BLAST score	447
E value	2.0e-44
Match length	121
% identity	67
NCBI Description	(U93166) cysteine protease [Prunus armeniaca]

Seq. No.	158126
Seq. ID	LIB3176-089-P1-K1-B10
Method	BLASTX
NCBI GI	g3953473
BLAST score	648
E value	5.0e-68
Match length	139
% identity	96
NCBI Description	(AC002328) F22O2.18 [Arabidopsis thaliana]

Seq. No.	158127
Seq. ID	LIB3176-089-P1-K1-B12
Method	BLASTN
NCBI GI	g2924733
BLAST score	167
E value	5.0e-89
Match length	278
% identity	96
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MUF9, complete sequence [Arabidopsis thaliana]

Seq. No.	158128
Seq. ID	LIB3176-089-P1-K1-B2
Method	BLASTX
NCBI GI	g4835227
BLAST score	822
E value	2.0e-88
Match length	150
% identity	100
NCBI Description	(AL049862) glycosyltransferase-like protein [Arabidopsis thaliana]

Seq. No.	158129
Seq. ID	LIB3176-089-P1-K1-B5
Method	BLASTX
NCBI GI	g1173283
BLAST score	146
E value	3.0e-09
Match length	31
% identity	87
NCBI Description	CHLOROPLAST 30S RIBOSOMAL PROTEIN S8 >gi_1262682_dbj_BAA04399.1_ (D17510) ribosomal protein S8 [Pinus thunbergii]

Seq. No.	158130
Seq. ID	LIB3176-089-P1-K1-B7
Method	BLASTX
NCBI GI	g2244896
BLAST score	796
E value	2.0e-85
Match length	152
% identity	99
NCBI Description	(Z97338) similar to HSR201 protein N.tabacum [Arabidopsis thaliana]

Seq. No.	158131
Seq. ID	LIB3176-089-P1-K1-B9
Method	BLASTX
NCBI GI	g4755193
BLAST score	546
E value	5.0e-57
Match length	152
% identity	84
NCBI Description	(AC007018) putative ribosomal protein S17 [Arabidopsis thaliana]

Seq. No.	158132
Seq. ID	LIB3176-089-P1-K1-C1
Method	BLASTN
NCBI GI	g4191771
BLAST score	131
E value	7.0e-68
Match length	131
% identity	100
NCBI Description	Arabidopsis thaliana chromosome II BAC F3P11 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	158133
Seq. ID	LIB3176-089-P1-K1-C11
Method	BLASTN
NCBI GI	g3135250
BLAST score	422
E value	0.0e+00
Match length	430
% identity	100
NCBI Description	Arabidopsis thaliana chromosome II BAC F27F23 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	158134
Seq. ID	LIB3176-089-P1-K1-C12
Method	BLASTX
NCBI GI	g3360289
BLAST score	154
E value	4.0e-10
Match length	43
% identity	60
NCBI Description	(AF023164) leucine-rich repeat transmembrane protein kinase 1 [Zea mays]

Seq. No.	158135
Seq. ID	LIB3176-089-P1-K1-C3

Method	BLASTX
NCBI GI	g2116558
BLAST score	193
E value	9.0e-15
Match length	76
% identity	58
NCBI Description	(AB003549) F1 ATPase [Pisum sativum]

Seq. No.	158136
Seq. ID	LIB3176-089-P1-K1-C4
Method	BLASTN
NCBI GI	g4584841
BLAST score	188
E value	1.0e-101
Match length	319
% identity	93
NCBI Description	Genomic sequence for Arabidopsis thaliana BAC T23E23, complete sequence

Seq. No.	158137
Seq. ID	LIB3176-089-P1-K1-C6
Method	BLASTX
NCBI GI	g4218120
BLAST score	602
E value	1.0e-62
Match length	149
% identity	77
NCBI Description	(AL035353) Proline-rich APG-like protein [Arabidopsis thaliana]

Seq. No.	158138
Seq. ID	LIB3176-089-P1-K1-C8
Method	BLASTX
NCBI GI	g4127456
BLAST score	313
E value	3.0e-29
Match length	71
% identity	96
NCBI Description	(AJ010818) Cpn21 protein [Arabidopsis thaliana]

Seq. No.	158139
Seq. ID	LIB3176-089-P1-K1-D1
Method	BLASTX
NCBI GI	g4741960
BLAST score	558
E value	2.0e-57
Match length	126
% identity	85
NCBI Description	(AF134130) Lhcb6 protein [Arabidopsis thaliana]

Seq. No.	158140
Seq. ID	LIB3176-089-P1-K1-D10
Method	BLASTX
NCBI GI	g3820648
BLAST score	667
E value	3.0e-70
Match length	142

% identity	91
NCBI Description	(Y12636) allene oxide synthase [Arabidopsis thaliana]

Seq. No.	158141
Seq. ID	LIB3176-089-P1-K1-D11
Method	BLASTX
NCBI GI	g99735
BLAST score	294
E value	4.0e-27
Match length	58
% identity	97
NCBI Description	L-ascorbate peroxidase (EC 1.11.1.11) precursor - Arabidopsis thaliana (fragment)

Seq. No.	158142
Seq. ID	LIB3176-089-P1-K1-D12
Method	BLASTN
NCBI GI	g4455348
BLAST score	190
E value	1.0e-102
Match length	215
% identity	92
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone T13J8 (ESSAII project)

Seq. No.	158143
Seq. ID	LIB3176-089-P1-K1-D2
Method	BLASTX
NCBI GI	g2062158
BLAST score	313
E value	3.0e-29
Match length	76
% identity	42
NCBI Description	(AC001645) jasmonate inducible protein isolog [Arabidopsis thaliana]

Seq. No.	158144
Seq. ID	LIB3176-089-P1-K1-D4
Method	BLASTX
NCBI GI	g4102582
BLAST score	177
E value	2.0e-13
Match length	66
% identity	59
NCBI Description	(AF013115) CAO [Arabidopsis thaliana]

Seq. No.	158145
Seq. ID	LIB3176-089-P1-K1-D6
Method	BLASTX
NCBI GI	g4336756
BLAST score	529
E value	3.0e-54
Match length	102
% identity	98
NCBI Description	(AF104453) catalase [Brassica juncea]

Seq. No.	158146

Seq. ID	LIB3176-089-P1-K1-D7
Method	BLASTX
NCBI GI	g3540183
BLAST score	466
E value	1.0e-46
Match length	146
% identity	62
NCBI Description	(AC004122) Highly Similar to branched-chain amino acid aminotransferase [Arabidopsis thaliana]

Seq. No.	158147
Seq. ID	LIB3176-089-P1-K1-D9
Method	BLASTX
NCBI GI	g2495365
BLAST score	778
E value	3.0e-83
Match length	152
% identity	99
NCBI Description	HEAT SHOCK PROTEIN 81-2 (HSP81-2) >gi_445127_prf__1908431B heat shock protein HSP81-2 [Arabidopsis thaliana]

Seq. No.	158148
Seq. ID	LIB3176-089-P1-K1-E1
Method	BLASTX
NCBI GI	g3421096
BLAST score	692
E value	4.0e-73
Match length	138
% identity	97
NCBI Description	(AF043528) 20S proteasome subunit PAG1 [Arabidopsis thaliana] >gi_3885332 (AC005623) proteasome component [Arabidopsis thaliana]

Seq. No.	158149
Seq. ID	LIB3176-089-P1-K1-E10
Method	BLASTX
NCBI GI	g99688
BLAST score	166
E value	5.0e-12
Match length	69
% identity	59
NCBI Description	translation elongation factor eEF-1 alpha chain (gene A4) - Arabidopsis thaliana >gi_295789_emb_CAA34456_ (X16432) elongation factor 1-alpha [Arabidopsis thaliana]

Seq. No.	158150
Seq. ID	LIB3176-089-P1-K1-E11
Method	BLASTX
NCBI GI	g2239083
BLAST score	381
E value	1.0e-36
Match length	146
% identity	56
NCBI Description	(Z84383) anthranilate N-hydroxycinnamoyl/benzoyltransferase [Dianthus caryophyllus] >gi_2239087_emb_CAB06429_ (Z84385) anthranilate N-hydroxycinnamoyl/benzoyltransferase [Dianthus caryophyllus]

Seq. No.	158151
Seq. ID	LIB3176-089-P1-K1-E3
Method	BLASTX
NCBI GI	g1170660
BLAST score	580
E value	4.0e-60
Match length	143
% identity	81
NCBI Description	MEVALONATE KINASE (MK) >gi_541880_pir__S42088 mevalonate kinase (EC 2.7.1.36) - Arabidopsis thaliana >gi_456614_emb_CAA54820_ (X77793) mevalonate kinase [Arabidopsis thaliana]

Seq. No.	158152
Seq. ID	LIB3176-089-P1-K1-E5
Method	BLASTX
NCBI GI	g2764941
BLAST score	607
E value	3.0e-63
Match length	106
% identity	100
NCBI Description	(X98255) transcriptionally stimulated by gibberellins; expressed in meristematic region, and style [Arabidopsis thaliana]

Seq. No.	158153
Seq. ID	LIB3176-089-P1-K1-E6
Method	BLASTN
NCBI GI	g2244829
BLAST score	186
E value	1.0e-100
Match length	198
% identity	98
NCBI Description	Arabidopsis thaliana DNA chromosome 4, ESSA I contig fragment No

Seq. No.	158154
Seq. ID	LIB3176-089-P1-K1-E7
Method	BLASTN
NCBI GI	g4309683
BLAST score	69
E value	6.0e-31
Match length	85
% identity	95
NCBI Description	Arabidopsis thaliana chromosome 1 BAC T31J12 sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	158155
Seq. ID	LIB3176-089-P1-K1-E8
Method	BLASTN
NCBI GI	g2924733
BLAST score	197
E value	1.0e-107
Match length	243
% identity	98
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:

MUF9, complete sequence [Arabidopsis thaliana]

Seq. No.	158156
Seq. ID	LIB3176-089-P1-K1-E9
Method	BLASTX
NCBI GI	g4006883
BLAST score	595
E value	8.0e-62
Match length	140
% identity	84
NCBI Description	(Z99707) cysteine proteinase [Arabidopsis thaliana]

Seq. No.	158157
Seq. ID	LIB3176-089-P1-K1-F1
Method	BLASTX
NCBI GI	g166410
BLAST score	320
E value	1.0e-29
Match length	103
% identity	59
NCBI Description	(L07291) Alfin-1 [Medicago sativa]

Seq. No.	158158
Seq. ID	LIB3176-089-P1-K1-F10
Method	BLASTX
NCBI GI	g2979561
BLAST score	365
E value	8.0e-35
Match length	81
% identity	85
NCBI Description	(AC003680) putative ribosomal protein S27 [Arabidopsis thaliana] >gi_3386624 (AC004665) putative ribosomal protein S27 [Arabidopsis thaliana]

Seq. No.	158159
Seq. ID	LIB3176-089-P1-K1-F11
Method	BLASTX
NCBI GI	g4104931
BLAST score	618
E value	2.0e-78
Match length	150
% identity	98
NCBI Description	(AF042196) auxin response factor 8 [Arabidopsis thaliana]

Seq. No.	158160
Seq. ID	LIB3176-089-P1-K1-F12
Method	BLASTX
NCBI GI	g2369714
BLAST score	497
E value	2.0e-50
Match length	122
% identity	79
NCBI Description	(Z97178) elongation factor 2 [Beta vulgaris]

Seq. No.	158161
Seq. ID	LIB3176-089-P1-K1-F2
Method	BLASTN

NCBI GI	g3128137
BLAST score	65
E value	4.0e-28
Match length	128
% identity	96
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K9I9, complete sequence [Arabidopsis thaliana]

Seq. No.	158162
Seq. ID	LIB3176-089-P1-K1-F3
Method	BLASTX
NCBI GI	g4337175
BLAST score	665
E value	5.0e-70
Match length	142
% identity	92
NCBI Description	(AC006416) ESTs gb_T20589, gb_T04648, gb_AA597906, gb_T04111, gb_R84180, gb_R65428, gb_T44439, gb_T76570, gb_R90004, gb_T45020, gb_T42457, gb_T20921, gb_AA042762 and gb_AA720210 come from this gene. [Arabidopsis thaliana]

Seq. No.	158163
Seq. ID	LIB3176-089-P1-K1-F4
Method	BLASTX
NCBI GI	g3367568
BLAST score	182
E value	5.0e-14
Match length	56
% identity	61
NCBI Description	(AL031135) protein kinase - like protein [Arabidopsis thaliana]

Seq. No.	158164
Seq. ID	LIB3176-089-P1-K1-F5
Method	BLASTX
NCBI GI	g544134
BLAST score	140
E value	7.0e-41
Match length	106
% identity	85
NCBI Description	DNA-DAMAGE-REPAIR/TOLERATION PROTEIN DRT100 PRECURSOR >gi_99720_pir__S22863 hypothetical protein - Arabidopsis thaliana >gi_421844_pir__A46260 RecA functional analog DRT100 - Arabidopsis thaliana (fragment)

Seq. No.	158165
Seq. ID	LIB3176-089-P1-K1-F6
Method	BLASTX
NCBI GI	g932
BLAST score	164
E value	1.0e-11
Match length	84
% identity	43
NCBI Description	(X53744) 68kDA subunit of signal recognition particle [Canis familiaris]

Seq. No.	158166

Seq. ID	LIB3176-089-P1-K1-F7
Method	BLASTX
NCBI GI	g3212869
BLAST score	474
E value	8.0e-48
Match length	102
% identity	89
NCBI Description	(AC004005) unknown protein [Arabidopsis thaliana]

Seq. No.	158167
Seq. ID	LIB3176-089-P1-K1-F8
Method	BLASTN
NCBI GI	g3702734
BLAST score	186
E value	1.0e-100
Match length	202
% identity	98
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MNB8, complete sequence [Arabidopsis thaliana]

Seq. No.	158168
Seq. ID	LIB3176-089-P1-K1-F9
Method	BLASTX
NCBI GI	g2119846
BLAST score	492
E value	4.0e-50
Match length	93
% identity	99
NCBI Description	chlorophyll a/b-binding protein type I precursor Lhb1B2 - Arabidopsis thaliana >gi_16364_emb_CAA45790_ (X64460) photosystem II type I chlorophyll a /b binding protein [Arabidopsis thaliana] >gi_3128230 (AC004077) photosystem II type I chlorophyll a/b binding protein [Arabidopsis thaliana] >gi_3337371 (AC004481) photosystem II type I chlorophyll a/b binding protein [Arabidopsis thaliana]

Seq. No.	158169
Seq. ID	LIB3176-089-P1-K1-G1
Method	BLASTX
NCBI GI	g4102839
BLAST score	221
E value	6.0e-18
Match length	116
% identity	40
NCBI Description	(AF016713) LeOPT1 [Lycopersicon esculentum]

Seq. No.	158170
Seq. ID	LIB3176-089-P1-K1-G10
Method	BLASTX
NCBI GI	g4582787
BLAST score	462
E value	3.0e-46
Match length	107
% identity	81
NCBI Description	(AJ012281) adenosine kinase [Zea mays]

Seq. No. 158171

Seq. ID	LIB3176-089-P1-K1-G11
Method	BLASTX
NCBI GI	g3273743
BLAST score	620
E value	1.0e-64
Match length	118
% identity	100
NCBI Description	(AF057357) lipid transfer protein 2 precursor [Arabidopsis thaliana] >gi_3786019 (AC005499) unknown protein [Arabidopsis thaliana]

Seq. No.	158172
Seq. ID	LIB3176-089-P1-K1-G12
Method	BLASTN
NCBI GI	g4589440
BLAST score	260
E value	1.0e-144
Match length	327
% identity	94
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MSD21, complete sequence

Seq. No.	158173
Seq. ID	LIB3176-089-P1-K1-G2
Method	BLASTX
NCBI GI	g2129944
BLAST score	341
E value	3.0e-32
Match length	77
% identity	81
NCBI Description	RNA-binding protein RZ-1 - wood tobacco >gi_1395193_dbj_BAA12064_ (D83696) RNA-binding protein RZ-1 [Nicotiana sylvestris] >gi_1435062_dbj_BAA06012_ (D28861) RNA binding protein, RZ-1 [Nicotiana sylvestris]

Seq. No.	158174
Seq. ID	LIB3176-089-P1-K1-G3
Method	BLASTX
NCBI GI	g4678261
BLAST score	62
E value	1.0e-56
Match length	137
% identity	91
NCBI Description	(AL049657) putative proteasome regulatory subunit [Arabidopsis thaliana]

Seq. No.	158175
Seq. ID	LIB3176-089-P1-K1-G4
Method	BLASTX
NCBI GI	g2827704
BLAST score	469
E value	4.0e-47
Match length	94
% identity	95
NCBI Description	(AL021684) LRR-like protein [Arabidopsis thaliana]

Seq. No. 158176

Seq. ID	LIB3176-089-P1-K1-G5
Method	BLASTX
NCBI GI	g4741948
BLAST score	708
E value	4.0e-75
Match length	134
% identity	99
NCBI Description	(AF134124) Lhcb2 protein [Arabidopsis thaliana]

Seq. No.	158177
Seq. ID	LIB3176-089-P1-K1-G6
Method	BLASTX
NCBI GI	g547867
BLAST score	539
E value	3.0e-55
Match length	132
% identity	82
NCBI Description	LIPOXYGENASE 1 >gi_541878_pir__JQ2267 lipoxygenase (EC 1.13.11.12) AtLox1 - Arabidopsis thaliana >gi_289203 (L04637) lipoxygenase [Arabidopsis thaliana] >gi_436920 (U01843) lipoxygenase 1 [Arabidopsis thaliana]

Seq. No.	158178
Seq. ID	LIB3176-089-P1-K1-G7
Method	BLASTX
NCBI GI	g1709786
BLAST score	185
E value	2.0e-14
Match length	68
% identity	63
NCBI Description	PYRROLINE-5-CARBOXYLATE REDUCTASE (P5CR) (P5C REDUCTASE) >gi_541894_pir__JQ2334 pyrroline-5-carboxylate reductase (EC 1.5.1.2) - Arabidopsis thaliana >gi_166815 (M76538) pyrroline carboxylate reductase [Arabidopsis thaliana] >gi_1632776_emb_CAA70148_ (Y08951) T5r protein [Arabidopsis thaliana]

Seq. No.	158179
Seq. ID	LIB3176-089-P1-K1-G8
Method	BLASTX
NCBI GI	g120675
BLAST score	454
E value	3.0e-45
Match length	106
% identity	82
NCBI Description	GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE, CYTOSOLIC >gi_66011_pir__DEIS3C glyceraldehyde-3-phosphate dehydrogenase (EC 1.2.1.12), cytosolic - white mustard >gi_21143_emb_CAA27844_ (X04301) GAPDH (aa 1-338) [Sinapis alba]

Seq. No.	158180
Seq. ID	LIB3176-089-P1-K1-G9
Method	BLASTN
NCBI GI	g3128137
BLAST score	66
E value	1.0e-28

Match length	102
% identity	91
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K9I9, complete sequence [Arabidopsis thaliana]

Seq. No.	158181
Seq. ID	LIB3176-089-P1-K1-H10
Method	BLASTX
NCBI GI	g2735841
BLAST score	143
E value	8.0e-09
Match length	74
% identity	47
NCBI Description	(AF010283) No definition line found [Sorghum bicolor]

Seq. No.	158182
Seq. ID	LIB3176-089-P1-K1-H11
Method	BLASTX
NCBI GI	g4581146
BLAST score	524
E value	1.0e-53
Match length	113
% identity	96
NCBI Description	(AC006919) putative fructose-bisphosphate aldolase, cytoplasmic [Arabidopsis thaliana]

Seq. No.	158183
Seq. ID	LIB3176-089-P1-K1-H12
Method	BLASTN
NCBI GI	g4572664
BLAST score	438
E value	0.0e+00
Match length	465
% identity	98
NCBI Description	Arabidopsis thaliana chromosome II BAC F25P17 genomic sequence, complete sequence

Seq. No.	158184
Seq. ID	LIB3176-089-P1-K1-H2
Method	BLASTX
NCBI GI	g115767
BLAST score	732
E value	7.0e-78
Match length	139
% identity	100
NCBI Description	CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR (CAB-165/180) (LHCP) >gi_81603_pir__A29280 chlorophyll a/b-binding protein ab165 - Arabidopsis thaliana >gi_16368_emb_CAA27540_ (X03907) chlorophyll a/b binding protein (LHCP AB 65) [Arabidopsis thaliana] >gi_16372_emb_CAA27541_ (X03908) chlorophyll a/b binding protein (LHCP AB 180) [Arabidopsis thaliana]

Seq. No.	158185
Seq. ID	LIB3176-089-P1-K1-H3
Method	BLASTN
NCBI GI	g2494106

BLAST score	100
E value	3.0e-49
Match length	148
% identity	92
NCBI Description	Arabidopsis thaliana chromosome 1 YAC YUP8H12R sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	158186
Seq. ID	LIB3176-089-P1-K1-H4
Method	BLASTX
NCBI GI	g3688178
BLAST score	514
E value	2.0e-52
Match length	105
% identity	98
NCBI Description	(AL031804) putative protein [Arabidopsis thaliana]

Seq. No.	158187
Seq. ID	LIB3176-089-P1-K1-H6
Method	BLASTX
NCBI GI	g4490736
BLAST score	374
E value	3.0e-36
Match length	96
% identity	58
NCBI Description	(AL035708) putative protein [Arabidopsis thaliana]

Seq. No.	158188
Seq. ID	LIB3176-089-P1-K1-H7
Method	BLASTN
NCBI GI	g2342673
BLAST score	313
E value	1.0e-176
Match length	420
% identity	98
NCBI Description	Sequence of BAC F7G19 from Arabidopsis thaliana chromosome 1, complete sequence [Arabidopsis thaliana]

Seq. No.	158189
Seq. ID	LIB3176-089-P1-K1-H8
Method	BLASTN
NCBI GI	g3600062
BLAST score	85
E value	3.0e-40
Match length	180
% identity	13
NCBI Description	Arabidopsis thaliana BAC T25C13

Seq. No.	158190
Seq. ID	LIB3176-090-P1-K1-A1
Method	BLASTN
NCBI GI	g4049332
BLAST score	75
E value	4.0e-34
Match length	107
% identity	93
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F8B4

(ESSAII project)

Seq. No.	158191
Seq. ID	LIB3176-090-P1-K1-A10
Method	BLASTN
NCBI GI	g4490324
BLAST score	238
E value	1.0e-131
Match length	263
% identity	97
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone T9A14 (ESSA project)

Seq. No.	158192
Seq. ID	LIB3176-090-P1-K1-A11
Method	BLASTN
NCBI GI	g2894557
BLAST score	129
E value	2.0e-66
Match length	232
% identity	98
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone T8O5 (ESSAII project)

Seq. No.	158193
Seq. ID	LIB3176-090-P1-K1-A12
Method	BLASTN
NCBI GI	g2894557
BLAST score	34
E value	3.0e-10
Match length	63
% identity	95
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone T8O5 (ESSAII project)

Seq. No.	158194
Seq. ID	LIB3176-090-P1-K1-A2
Method	BLASTN
NCBI GI	g166695
BLAST score	130
E value	4.0e-67
Match length	154
% identity	96
NCBI Description	Arabidopsis thaliana recombination and DNA-damage resistance protein (DRT112) mRNA, complete cds

Seq. No.	158195
Seq. ID	LIB3176-090-P1-K1-A3
Method	BLASTN
NCBI GI	g2668491
BLAST score	39
E value	9.0e-13
Match length	128
% identity	88
NCBI Description	Arabidopsis thaliana mRNA for metal-transporting P-type ATPase, complete cds

Seq. No.	158196
Seq. ID	LIB3176-090-P1-K1-A4
Method	BLASTX
NCBI GI	g4127456
BLAST score	265
E value	2.0e-23
Match length	83
% identity	39
NCBI Description	(AJ010818) Cpn21 protein [Arabidopsis thaliana]

Seq. No.	158197
Seq. ID	LIB3176-090-P1-K1-A7
Method	BLASTN
NCBI GI	g387908
BLAST score	65
E value	4.0e-28
Match length	196
% identity	83
NCBI Description	Brassica rapa S-phase-specific (BIS289) mRNA, complete cds. >gi_397400_emb_Z25769_BRSPSG B.rapa mRNA for S phase specific gene

Seq. No.	158198
Seq. ID	LIB3176-090-P1-K1-A8
Method	BLASTX
NCBI GI	g2245118
BLAST score	388
E value	1.0e-37
Match length	124
% identity	67
NCBI Description	(Z97343) hypothetical protein [Arabidopsis thaliana]

Seq. No.	158199
Seq. ID	LIB3176-090-P1-K1-A9
Method	BLASTN
NCBI GI	g2827538
BLAST score	277
E value	1.0e-154
Match length	285
% identity	88
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone T12H17 (ESSAII project)

Seq. No.	158200
Seq. ID	LIB3176-090-P1-K1-B1
Method	BLASTX
NCBI GI	g1197461
BLAST score	330
E value	2.0e-31
Match length	65
% identity	97
NCBI Description	(X78819) casein kinase I [Arabidopsis thaliana]

Seq. No.	158201
Seq. ID	LIB3176-090-P1-K1-B10
Method	BLASTN
NCBI GI	g4519188

BLAST score	180
E value	6.0e-97
Match length	212
% identity	96
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K21L19, complete sequence

Seq. No.	158202
Seq. ID	LIB3176-090-P1-K1-B11
Method	BLASTX
NCBI GI	g3128228
BLAST score	214
E value	9.0e-18
Match length	55
% identity	71
NCBI Description	(AC004077) putative ribosomal protein L18A [Arabidopsis thaliana] >gi_3337376 (AC004481) putative ribosomal protein L18A [Arabidopsis thaliana]

Seq. No.	158203
Seq. ID	LIB3176-090-P1-K1-B12
Method	BLASTN
NCBI GI	g2062153
BLAST score	58
E value	9.0e-25
Match length	58
% identity	69
NCBI Description	Arabidopsis thaliana chromosome III BAC T02O04 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	158204
Seq. ID	LIB3176-090-P1-K1-B2
Method	BLASTX
NCBI GI	g3738329
BLAST score	381
E value	9.0e-37
Match length	84
% identity	92
NCBI Description	(AC005170) unknown protein [Arabidopsis thaliana]

Seq. No.	158205
Seq. ID	LIB3176-090-P1-K1-B3
Method	BLASTX
NCBI GI	g1621268
BLAST score	444
E value	4.0e-44
Match length	120
% identity	67
NCBI Description	(Z81012) unknown [Ricinus communis]

Seq. No.	158206
Seq. ID	LIB3176-090-P1-K1-B4
Method	BLASTX
NCBI GI	g4186184
BLAST score	179
E value	4.0e-13
Match length	93

% identity	41
NCBI Description	(AF111168) unknown [Homo sapiens]

Seq. No.	158207
Seq. ID	LIB3176-090-P1-K1-B6
Method	BLASTX
NCBI GI	g4741952
BLAST score	427
E value	2.0e-42
Match length	93
% identity	87
NCBI Description	(AF134126) Lhcb3 protein [Arabidopsis thaliana]

Seq. No.	158208
Seq. ID	LIB3176-090-P1-K1-B7
Method	BLASTX
NCBI GI	g3413714
BLAST score	72
E value	4.1e-01
Match length	54
% identity	13
NCBI Description	(AC004747) putative myrosinase-binding protein [Arabidopsis thaliana]

Seq. No.	158209
Seq. ID	LIB3176-090-P1-K1-C10
Method	BLASTX
NCBI GI	g2827143
BLAST score	154
E value	1.0e-10
Match length	33
% identity	88
NCBI Description	(AF027174) cellulose synthase catalytic subunit [Arabidopsis thaliana]

Seq. No.	158210
Seq. ID	LIB3176-090-P1-K1-C11
Method	BLASTX
NCBI GI	g1361991
BLAST score	340
E value	2.0e-47
Match length	135
% identity	75
NCBI Description	homeotic protein ATK1 - Arabidopsis thaliana >gi_984046_emb_CAA57122_ (X81354) ATK1 [Arabidopsis thaliana] >gi_984048_emb_CAA57121_ (X81353) ATK1 [Arabidopsis thaliana]

Seq. No.	158211
Seq. ID	LIB3176-090-P1-K1-C12
Method	BLASTX
NCBI GI	g2865623
BLAST score	521
E value	4.0e-53
Match length	116
% identity	88
NCBI Description	(AF045286)

GDP-4-keto-6-deoxy-D-mannose-3,5-epimerase-4-reductase [Arabidopsis thaliana]

Seq. No.	158212
Seq. ID	LIB3176-090-P1-K1-C3
Method	BLASTX
NCBI GI	g3386615
BLAST score	596
E value	6.0e-62
Match length	112
% identity	98
NCBI Description	(AC004665) putative phosphomannomutase [Arabidopsis thaliana]

Seq. No.	158213
Seq. ID	LIB3176-090-P1-K1-C6
Method	BLASTX
NCBI GI	g2865623
BLAST score	262
E value	7.0e-23
Match length	88
% identity	65
NCBI Description	(AF045286) GDP-4-keto-6-deoxy-D-mannose-3,5-epimerase-4-reductase [Arabidopsis thaliana]

Seq. No.	158214
Seq. ID	LIB3176-090-P1-K1-C8
Method	BLASTN
NCBI GI	g4309683
BLAST score	138
E value	4.0e-72
Match length	138
% identity	100
NCBI Description	Arabidopsis thaliana chromosome 1 BAC T31J12 sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	158215
Seq. ID	LIB3176-090-P1-K1-C9
Method	BLASTN
NCBI GI	g4678258
BLAST score	169
E value	2.0e-90
Match length	226
% identity	100
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F6I7 (ESSA project)

Seq. No.	158216
Seq. ID	LIB3176-090-P1-K1-D1
Method	BLASTX
NCBI GI	g3914740
BLAST score	484
E value	3.0e-52
Match length	140
% identity	77
NCBI Description	60S RIBOSOMAL PROTEIN L26 >gi_2160300_dbj_BAA18941_

(D78495) ribosomal protein [Brassica rapa]

Seq. No.	158217
Seq. ID	LIB3176-090-P1-K1-D12
Method	BLASTX
NCBI GI	g1363489
BLAST score	561
E value	7.0e-58
Match length	109
% identity	94
NCBI Description	thioglucosidase (EC 3.2.3.1) 3D precursor - Arabidopsis thaliana >gi_984052_emb_CAA61592_ (X89413) thioglucoside glucohydrolase [Arabidopsis thaliana]

Seq. No.	158218
Seq. ID	LIB3176-090-P1-K1-D2
Method	BLASTN
NCBI GI	g2281081
BLAST score	47
E value	1.0e-17
Match length	102
% identity	87
NCBI Description	Arabidopsis thaliana chromosome II BAC F18O19 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	158219
Seq. ID	LIB3176-090-P1-K1-D3
Method	BLASTX
NCBI GI	g2970036
BLAST score	179
E value	1.0e-13
Match length	33
% identity	100
NCBI Description	(D88537) delta 9 desaturase [Arabidopsis thaliana]

Seq. No.	158220
Seq. ID	LIB3176-090-P1-K1-D4
Method	BLASTN
NCBI GI	g1143391
BLAST score	146
E value	1.0e-76
Match length	179
% identity	94
NCBI Description	A.thaliana mRNA for uridine diphosphate glucose epimerase

Seq. No.	158221
Seq. ID	LIB3176-090-P1-K1-D5
Method	BLASTX
NCBI GI	g1773330
BLAST score	461
E value	3.0e-46
Match length	104
% identity	86
NCBI Description	(U80071) glycolate oxidase [Mesembryanthemum crystallinum]

Seq. No.	158222
Seq. ID	LIB3176-090-P1-K1-D7

Method	BLASTX
NCBI GI	g115767
BLAST score	712
E value	2.0e-75
Match length	138
% identity	99
NCBI Description	CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR (CAB-165/180) (LHCP) >gi_81603_pir__A29280 chlorophyll a/b-binding protein ab165 - Arabidopsis thaliana >gi_16368_emb_CAA27540_ (X03907) chlorophyll a/b binding protein (LHCP AB 65) [Arabidopsis thaliana] >gi_16372_emb_CAA27541_ (X03908) chlorophyll a/b binding protein (LHCP AB 180) [Arabidopsis thaliana]

Seq. No.	158223
Seq. ID	LIB3176-090-P1-K1-D8
Method	BLASTX
NCBI GI	g4688596
BLAST score	330
E value	2.0e-31
Match length	66
% identity	92
NCBI Description	(AJ005682) inositol 1,4,5-trisphosphate 5-phosphatase [Arabidopsis thaliana]

Seq. No.	158224
Seq. ID	LIB3176-090-P1-K1-D9
Method	BLASTN
NCBI GI	g4512656
BLAST score	164
E value	4.0e-87
Match length	355
% identity	88
NCBI Description	Arabidopsis thaliana chromosome II BAC F7D19 genomic sequence, complete sequence

Seq. No.	158225
Seq. ID	LIB3176-090-P1-K1-E1
Method	BLASTN
NCBI GI	g166810
BLAST score	333
E value	0.0e+00
Match length	393
% identity	96
NCBI Description	Arabidopsis thaliana Columbia protein kinase mRNA, complete cds

Seq. No.	158226
Seq. ID	LIB3176-090-P1-K1-E11
Method	BLASTN
NCBI GI	g3660468
BLAST score	153
E value	1.0e-80
Match length	241
% identity	91
NCBI Description	Arabidopsis thaliana mRNA for Succinyl-CoA-ligase beta subunit

Seq. No.	158227
Seq. ID	LIB3176-090-P1-K1-E12
Method	BLASTN
NCBI GI	g2981615
BLAST score	74
E value	1.0e-33
Match length	82
% identity	98
NCBI Description	Arabidopsis thaliana mRNA for 3-ketoacyl-CoA thiolase, complete cds

Seq. No.	158228
Seq. ID	LIB3176-090-P1-K1-E2
Method	BLASTX
NCBI GI	g3402686
BLAST score	372
E value	2.0e-45
Match length	117
% identity	86
NCBI Description	(AC004697) putative serine/threonine protein kinase [Arabidopsis thaliana]

Seq. No.	158229
Seq. ID	LIB3176-090-P1-K1-E4
Method	BLASTX
NCBI GI	g399013
BLAST score	375
E value	2.0e-36
Match length	79
% identity	92
NCBI Description	ADP,ATP CARRIER PROTEIN 1 PRECURSOR (ADP/ATP TRANSLOCASE 1) (ADENINE NUCLEOTIDE TRANSLOCATOR 1) (ANT 1) >gi_99658_pir__S21313 ADP,ATP carrier protein - Arabidopsis thaliana (fragment) >gi_16175_emb_CAA46518_ (X65549) adenylate translocator [Arabidopsis thaliana] >gi_445607_prf__1909354A adenylate translocator [Arabidopsis thaliana]

Seq. No.	158230
Seq. ID	LIB3176-090-P1-K1-E5
Method	BLASTX
NCBI GI	g1213594
BLAST score	388
E value	2.0e-59
Match length	127
% identity	96
NCBI Description	(X93080) responsible for fatty acid elongation from C28 to C30 [Arabidopsis thaliana] >gi_1655786 (U40849) CER2 gene product [Arabidopsis thaliana] >gi_4220539_emb_CAA23012_ (AL035356) CER2 [Arabidopsis thaliana]

Seq. No.	158231
Seq. ID	LIB3176-090-P1-K1-E6
Method	BLASTX
NCBI GI	g3395436
BLAST score	446

E value	2.0e-44
Match length	107
% identity	87
NCBI Description	(AC004683) unknown protein [Arabidopsis thaliana]

Seq. No.	158232
Seq. ID	LIB3176-090-P1-K1-E7
Method	BLASTN
NCBI GI	g1565224
BLAST score	52
E value	9.0e-21
Match length	72
% identity	93
NCBI Description	A.thaliana mRNA for salt-tolerance protein

Seq. No.	158233
Seq. ID	LIB3176-090-P1-K1-E8
Method	BLASTN
NCBI GI	g3047100
BLAST score	90
E value	4.0e-43
Match length	106
% identity	97
NCBI Description	Arabidopsis thaliana BAC F6N23

Seq. No.	158234
Seq. ID	LIB3176-090-P1-K1-E9
Method	BLASTN
NCBI GI	g3869069
BLAST score	35
E value	4.0e-11
Match length	43
% identity	98
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MEB5, complete sequence [Arabidopsis thaliana]

Seq. No.	158235
Seq. ID	LIB3176-090-P1-K1-F10
Method	BLASTX
NCBI GI	g3776005
BLAST score	545
E value	4.0e-56
Match length	121
% identity	88
NCBI Description	(AJ010466) RNA helicase [Arabidopsis thaliana]

Seq. No.	158236
Seq. ID	LIB3176-090-P1-K1-F12
Method	BLASTX
NCBI GI	g4567207
BLAST score	619
E value	9.0e-65
Match length	116
% identity	98
NCBI Description	(AC007168) unknown protein [Arabidopsis thaliana]

Seq. No.	158237

Seq. ID	LIB3176-090-P1-K1-F3
Method	BLASTN
NCBI GI	g4206762
BLAST score	212
E value	1.0e-116
Match length	240
% identity	97
NCBI Description	Arabidopsis thaliana cell wall-plasma membrane linker protein homolog (CWLP) mRNA, complete cds

Seq. No.	158238
Seq. ID	LIB3176-090-P1-K1-F4
Method	BLASTX
NCBI GI	g417103
BLAST score	679
E value	1.0e-71
Match length	136
% identity	100
NCBI Description	HISTONE H3.2, MINOR >gi_282871_pir__S24346 histone H3.3-like protein - Arabidopsis thaliana >gi_16324_emb_CAA42957_ (X60429) histone H3.3 like protein [Arabidopsis thaliana] >gi_404825_emb_CAA42958_ (X60429) histone H3.3 like protein [Arabidopsis thaliana] >gi_488563 (U09458) histone H3.2 [Medicago sativa] >gi_488567 (U09460) histone H3.2 [Medicago sativa] >gi_488569 (U09461) histone H3.2 [Medicago sativa] >gi_488575 (U09464) histone H3.2 [Medicago sativa] >gi_488577 (U09465) histone H3.2 [Medicago sativa] >gi_510911_emb_CAA56153_ (X79714) histone H3 [Lolium temulentum] >gi_1435157_emb_CAA58445_ (X83422) histone H3 variant H3.3 [Lycopersicon esculentum] >gi_2558944 (AF024716) histone 3 [Gossypium hirsutum] >gi_3273350_dbj_BAA31218_ (AB015760) histone H3 [Nicotiana tabacum] >gi_3885890 (AF093633) histone H3 [Oryza sativa] >gi_4038469_gb_AAC97380_ (AF109910) histone H3 [Porteresia coarctata] >gi_4490754_emb_CAB38916.1_ (AL035708) histone H3.3 [Arabidopsis thaliana] >gi_4490755_emb_CAB38917.1_ (AL035708) Histon H3 [Arabidopsis thaliana]

Seq. No.	158239
Seq. ID	LIB3176-090-P1-K1-F5
Method	BLASTX
NCBI GI	g1168258
BLAST score	264
E value	3.0e-23
Match length	76
% identity	67
NCBI Description	ASPARTATE AMINOTRANSFERASE, CHLOROPLAST PRECURSOR (TRANSAMINASE A) >gi_693692 (U15034) aspartate aminotransferase [Arabidopsis thaliana]

Seq. No.	158240
Seq. ID	LIB3176-090-P1-K1-F6
Method	BLASTX
NCBI GI	g115783
BLAST score	594
E value	1.0e-61
Match length	114

% identity	98
NCBI Description	CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR (CAB-140) (LHCP) >gi_16376_emb_CAA27543_ (X03909) chlorophyll a/b binding protein (LHCP AB 140) [Arabidopsis thaliana]
Seq. No.	158241
Seq. ID	LIB3176-090-P1-K1-F8
Method	BLASTN
NCBI GI	g3402695
BLAST score	268
E value	1.0e-149
Match length	272
% identity	100
NCBI Description	Arabidopsis thaliana chromosome II BAC T3K9 genomic sequence, complete sequence [Arabidopsis thaliana]
Seq. No.	158242
Seq. ID	LIB3176-090-P1-K1-F9
Method	BLASTX
NCBI GI	g2529665
BLAST score	394
E value	9.0e-66
Match length	149
% identity	89
NCBI Description	(AC002535) putative ribosomal protein L7A [Arabidopsis thaliana]
Seq. No.	158243
Seq. ID	LIB3176-090-P1-K1-G1
Method	BLASTX
NCBI GI	g2446981
BLAST score	583
E value	3.0e-62
Match length	127
% identity	93
NCBI Description	(AB005560) AtGDI2 [Arabidopsis thaliana] >gi_2569936_emb_CAA04727_ (AJ001397) GDI2 [Arabidopsis thaliana]
Seq. No.	158244
Seq. ID	LIB3176-090-P1-K1-G10
Method	BLASTX
NCBI GI	g4263818
BLAST score	289
E value	6.0e-26
Match length	80
% identity	68
NCBI Description	(AC006067) unknown protein [Arabidopsis thaliana]
Seq. No.	158245
Seq. ID	LIB3176-090-P1-K1-G11
Method	BLASTX
NCBI GI	g2924779
BLAST score	658
E value	3.0e-69
Match length	130

% identity	100
NCBI Description	(AC002334) putative 3-ketoacyl-CoA thiolase [Arabidopsis thaliana] >gi_2981616_dbj_BAA25248_ (AB008854) 3-ketoacyl-CoA thiolase [Arabidopsis thaliana] >gi_2981618_dbj_BAA25249_ (AB008855) 3-ketoacyl-CoA thiolase [Arabidopsis thaliana]
Seq. No.	158246
Seq. ID	LIB3176-090-P1-K1-G12
Method	BLASTX
NCBI GI	g2388710
BLAST score	474
E value	1.0e-47
Match length	122
% identity	71
NCBI Description	(AF017150) betaine aldehyde dehydrogenase [Amaranthus hypochondriacus]
Seq. No.	158247
Seq. ID	LIB3176-090-P1-K1-G3
Method	BLASTX
NCBI GI	g1695719
BLAST score	61
E value	7.7e+00
Match length	41
% identity	59
NCBI Description	(D89342) luminal binding protein [Arabidopsis thaliana]
Seq. No.	158248
Seq. ID	LIB3176-090-P1-K1-G4
Method	BLASTN
NCBI GI	g3790582
BLAST score	125
E value	4.0e-64
Match length	197
% identity	97
NCBI Description	Arabidopsis thaliana RING-H2 finger protein RHC1a mRNA, complete cds
Seq. No.	158249
Seq. ID	LIB3176-090-P1-K1-G5
Method	BLASTN
NCBI GI	g4220627
BLAST score	83
E value	9.0e-39
Match length	147
% identity	5
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K20J1, complete sequence [Arabidopsis thaliana]
Seq. No.	158250
Seq. ID	LIB3176-090-P1-K1-G6
Method	BLASTN
NCBI GI	g3869065
BLAST score	75
E value	9.0e-35
Match length	75

% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K24M7, complete sequence [Arabidopsis thaliana]

Seq. No.	158251
Seq. ID	LIB3176-090-P1-K1-G7
Method	BLASTX
NCBI GI	g4587542
BLAST score	655
E value	6.0e-69
Match length	125
% identity	100
NCBI Description	(AC006577) Belongs to the PF_00657 Lipase/Acylhydrolase with GDSL-motif family. ESTs gb_T45815, gb_T45130 and gb_Z38046 come from this gene. [Arabidopsis thaliana]

Seq. No.	158252
Seq. ID	LIB3176-090-P1-K1-G8
Method	BLASTX
NCBI GI	g3044212
BLAST score	577
E value	6.0e-60
Match length	107
% identity	99
NCBI Description	(AF057043) acyl-CoA oxidase [Arabidopsis thaliana]

Seq. No.	158253
Seq. ID	LIB3176-090-P1-K1-G9
Method	BLASTX
NCBI GI	g1419388
BLAST score	345
E value	2.0e-32
Match length	79
% identity	82
NCBI Description	(X98925) stromal ascorbate peroxidase [Arabidopsis thaliana]

Seq. No.	158254
Seq. ID	LIB3176-090-P1-K1-H1
Method	BLASTN
NCBI GI	g2656026
BLAST score	76
E value	5.0e-35
Match length	116
% identity	91
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MDF20

Seq. No.	158255
Seq. ID	LIB3176-090-P1-K1-H10
Method	BLASTN
NCBI GI	g2281648
BLAST score	157
E value	6.0e-83
Match length	173
% identity	98
NCBI Description	Arabidopsis thaliana AP2 domain containing protein RAP2.12

mRNA, partial cds

Seq. No.	158256
Seq. ID	LIB3176-090-P1-K1-H11
Method	BLASTN
NCBI GI	g3980374
BLAST score	149
E value	2.0e-78
Match length	206
% identity	98
NCBI Description	Arabidopsis thaliana chromosome II BAC F16P2 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	158257
Seq. ID	LIB3176-090-P1-K1-H12
Method	BLASTX
NCBI GI	g1103322
BLAST score	397
E value	1.0e-38
Match length	140
% identity	61
NCBI Description	(X78820) casein kinase I [Arabidopsis thaliana]

Seq. No.	158258
Seq. ID	LIB3176-090-P1-K1-H2
Method	BLASTX
NCBI GI	g3157937
BLAST score	229
E value	2.0e-19
Match length	47
% identity	100
NCBI Description	(AC002131) Identical to aspartic proteinase cDNA gb_U51036 from A. thaliana. ESTs gb_N96313, gb_T21893, gb_R30158, gb_T21482, gb_T43650, gb_R64749, gb_R65157, gb_T88269, gb_T44552, gb_T22542, gb_T76533, gb_T44350, gb_Z34591, gb_AA728734, gb

Seq. No.	158259
Seq. ID	LIB3176-090-P1-K1-H3
Method	BLASTN
NCBI GI	g3928074
BLAST score	191
E value	1.0e-103
Match length	227
% identity	96
NCBI Description	Arabidopsis thaliana chromosome II BAC T7F6 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	158260
Seq. ID	LIB3176-090-P1-K1-H4
Method	BLASTX
NCBI GI	g4741948
BLAST score	401
E value	5.0e-39
Match length	137
% identity	49
NCBI Description	(AF134124) Lhcb2 protein [Arabidopsis thaliana]

Seq. No.	158261
Seq. ID	LIB3176-090-P1-K1-H5
Method	BLASTX
NCBI GI	g3738092
BLAST score	394
E value	3.0e-38
Match length	76
% identity	100
NCBI Description	(AC005617) similar to glyoxysomal malate dehydrogenase [Arabidopsis thaliana]

Seq. No.	158262
Seq. ID	LIB3176-090-P1-K1-H6
Method	BLASTX
NCBI GI	g2245108
BLAST score	207
E value	7.0e-17
Match length	72
% identity	64
NCBI Description	(Z97343) EREBP-4 homolog [Arabidopsis thaliana]

Seq. No.	158263
Seq. ID	LIB3176-090-P1-K1-H8
Method	BLASTX
NCBI GI	g2129636
BLAST score	356
E value	2.0e-35
Match length	89
% identity	87
NCBI Description	lipase - Arabidopsis thaliana >gi_1145627 (U38916) lipase [Arabidopsis thaliana]

Seq. No.	158264
Seq. ID	LIB3176-091-P1-K1-A1
Method	BLASTX
NCBI GI	g1350680
BLAST score	325
E value	2.0e-30
Match length	74
% identity	85
NCBI Description	60S RIBOSOMAL PROTEIN L1

Seq. No.	158265
Seq. ID	LIB3176-091-P1-K1-A10
Method	BLASTN
NCBI GI	g4220637
BLAST score	394
E value	0.0e+00
Match length	402
% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MIE1, complete sequence [Arabidopsis thaliana]

Seq. No.	158266
Seq. ID	LIB3176-091-P1-K1-A11
Method	BLASTN

NCBI GI	g2791999
BLAST score	262
E value	1.0e-146
Match length	280
% identity	99
NCBI Description	Arabidopsis thaliana mRNA for ribosomal protein L4

Seq. No.	158267
Seq. ID	LIB3176-091-P1-K1-A12
Method	BLASTN
NCBI GI	g4589442
BLAST score	103
E value	5.0e-51
Match length	213
% identity	98
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MVP2, complete sequence

Seq. No.	158268
Seq. ID	LIB3176-091-P1-K1-A2
Method	BLASTN
NCBI GI	g4263694
BLAST score	318
E value	1.0e-179
Match length	385
% identity	99
NCBI Description	Arabidopsis thaliana chromosome II BAC F22D22 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	158269
Seq. ID	LIB3176-091-P1-K1-A7
Method	BLASTX
NCBI GI	g730526
BLAST score	431
E value	8.0e-43
Match length	81
% identity	98
NCBI Description	60S RIBOSOMAL PROTEIN L13 (BBC1 PROTEIN HOMOLOG) >gi_480787_pir__S37271 ribosomal protein L13 - Arabidopsis thaliana >gi_404166_emb_CAA53005_ (X75162) BBC1 protein [Arabidopsis thaliana]

Seq. No.	158270
Seq. ID	LIB3176-091-P1-K1-A8
Method	BLASTN
NCBI GI	g16210
BLAST score	173
E value	8.0e-93
Match length	185
% identity	98
NCBI Description	Arabidopsis thaliana calnexin homolog

Seq. No.	158271
Seq. ID	LIB3176-091-P1-K1-B1
Method	BLASTN
NCBI GI	g2244788
BLAST score	70

E value	1.0e-31
Match length	110
% identity	99
NCBI Description	Arabidopsis thaliana DNA chromosome 4, ESSA I contig fragment No

Seq. No.	158272
Seq. ID	LIB3176-091-P1-K1-B10
Method	BLASTX
NCBI GI	g3193323
BLAST score	278
E value	4.0e-25
Match length	58
% identity	93
NCBI Description	(AF069299) similar to ribosomal protein S13 (Pfam; S15.hmm, score: 78.35); identical to Arabidopsis 40S ribosomal protein S13 (fragment) (SW: P49203A) except the first 32 amino acids are different [Arabidopsis thaliana]

Seq. No.	158273
Seq. ID	LIB3176-091-P1-K1-B11
Method	BLASTN
NCBI GI	g2664199
BLAST score	34
E value	1.0e-09
Match length	34
% identity	100
NCBI Description	Arabidopsis thaliana GTL2 gene

Seq. No.	158274
Seq. ID	LIB3176-091-P1-K1-B12
Method	BLASTN
NCBI GI	g3128138
BLAST score	162
E value	4.0e-86
Match length	246
% identity	92
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MFO20, complete sequence [Arabidopsis thaliana]

Seq. No.	158275
Seq. ID	LIB3176-091-P1-K1-B3
Method	BLASTX
NCBI GI	g2271485
BLAST score	448
E value	6.0e-45
Match length	89
% identity	97
NCBI Description	(AF009647) arginine decarboxylase [Arabidopsis thaliana] >gi_3096940_emb_CAA18850.1_ (AL023094) arginine decarboxylase SPE2 [Arabidopsis thaliana]

Seq. No.	158276
Seq. ID	LIB3176-091-P1-K1-B4
Method	BLASTX
NCBI GI	g3024022
BLAST score	663

E value	9.0e-70
Match length	149
% identity	84
NCBI Description	INITIATION FACTOR 5A-5 (EIF-5A) (EIF-4D) >gi_2225885_dbj_BAA20879_ (AB004826) eukaryotic initiation factor 5A5 [Solanum tuberosum]

Seq. No.	158277
Seq. ID	LIB3176-091-P1-K1-B5
Method	BLASTN
NCBI GI	g4056476
BLAST score	36
E value	3.0e-11
Match length	82
% identity	85
NCBI Description	Arabidopsis thaliana chromosome II BAC F3G5 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	158278
Seq. ID	LIB3176-091-P1-K1-C10
Method	BLASTX
NCBI GI	g3859606
BLAST score	142
E value	2.0e-09
Match length	51
% identity	65
NCBI Description	(AF104919) contains similarity to cysteine proteases (Pfam: PF00112, E=1.3e-79, N=1) [Arabidopsis thaliana]

Seq. No.	158279
Seq. ID	LIB3176-091-P1-K1-C11
Method	BLASTX
NCBI GI	g3822223
BLAST score	545
E value	4.0e-56
Match length	122
% identity	80
NCBI Description	(AF077955) branched-chain alpha keto-acid dehydrogenase E1 alpha subunit [Arabidopsis thaliana]

Seq. No.	158280
Seq. ID	LIB3176-091-P1-K1-C2
Method	BLASTX
NCBI GI	g4538930
BLAST score	329
E value	9.0e-31
Match length	66
% identity	100
NCBI Description	(AL049483) putative peroxidase [Arabidopsis thaliana]

Seq. No.	158281
Seq. ID	LIB3176-091-P1-K1-C3
Method	BLASTX
NCBI GI	g4454014
BLAST score	258
E value	2.0e-22
Match length	89

% identity	53
NCBI Description	(AL035396) putative protein [Arabidopsis thaliana]

Seq. No.	158282
Seq. ID	LIB3176-091-P1-K1-C5
Method	BLASTN
NCBI GI	g166645
BLAST score	64
E value	5.0e-28
Match length	111
% identity	89
NCBI Description	Arabidopsis thaliana light-harvesting chlorophyll a/b-binding protein (Cab4) mRNA, complete cds

Seq. No.	158283
Seq. ID	LIB3176-091-P1-K1-C7
Method	BLASTN
NCBI GI	g4757405
BLAST score	293
E value	1.0e-164
Match length	301
% identity	99
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MOJ10, complete sequence

Seq. No.	158284
Seq. ID	LIB3176-091-P1-K1-C8
Method	BLASTX
NCBI GI	g399013
BLAST score	318
E value	1.0e-29
Match length	67
% identity	94
NCBI Description	ADP,ATP CARRIER PROTEIN 1 PRECURSOR (ADP/ATP TRANSLOCASE 1) (ADENINE NUCLEOTIDE TRANSLOCATOR 1) (ANT 1) >gi_99658_pir__S21313 ADP,ATP carrier protein - Arabidopsis thaliana (fragment) >gi_16175_emb_CAA46518_ (X65549) adenylate translocator [Arabidopsis thaliana] >gi_445607_prf__1909354A adenylate translocator [Arabidopsis thaliana]

Seq. No.	158285
Seq. ID	LIB3176-091-P1-K1-C9
Method	BLASTN
NCBI GI	g3985931
BLAST score	357
E value	0.0e+00
Match length	377
% identity	99
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K21H1, complete sequence [Arabidopsis thaliana]

Seq. No.	158286
Seq. ID	LIB3176-091-P1-K1-D1
Method	BLASTX
NCBI GI	g1169201
BLAST score	499

E value	2.0e-50
Match length	140
% identity	76
NCBI Description	DNA-DAMAGE-REPAIR/TOLERATION PROTEIN DRT112 PRECURSOR >gi_421830_pir__S33707 DRT112 protein - Arabidopsis thaliana >gi_166696 (M98456) DRT112 [Arabidopsis thaliana]

Seq. No.	158287
Seq. ID	LIB3176-091-P1-K1-D10
Method	BLASTN
NCBI GI	g4220644
BLAST score	231
E value	1.0e-127
Match length	242
% identity	99
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MXL8, complete sequence [Arabidopsis thaliana]

Seq. No.	158288
Seq. ID	LIB3176-091-P1-K1-D11
Method	BLASTX
NCBI GI	g4049354
BLAST score	402
E value	1.0e-39
Match length	77
% identity	97
NCBI Description	(AL034567) glycine hydroxymethyltransferase (EC 2.1.2.1)-like protein [Arabidopsis thaliana]

Seq. No.	158289
Seq. ID	LIB3176-091-P1-K1-D12
Method	BLASTX
NCBI GI	g3281858
BLAST score	287
E value	2.0e-26
Match length	59
% identity	95
NCBI Description	(AL031004) ribosomal protein S6 - like [Arabidopsis thaliana]

Seq. No.	158290
Seq. ID	LIB3176-091-P1-K1-D2
Method	BLASTX
NCBI GI	g3551052
BLAST score	551
E value	1.0e-56
Match length	107
% identity	100
NCBI Description	(AB011545) GF14 mu [Arabidopsis thaliana] >gi_4559343_gb_AAD23005.1_AC007087_24 (AC007087) DNA regulatory protein GF14 mu [Arabidopsis thaliana]

Seq. No.	158291
Seq. ID	LIB3176-091-P1-K1-D3
Method	BLASTX
NCBI GI	g1914683
BLAST score	366

E value	6.0e-35
Match length	147
% identity	55
NCBI Description	(Y12013) RAD23, isoform I [Daucus carota]

Seq. No.	158292
Seq. ID	LIB3176-091-P1-K1-D4
Method	BLASTN
NCBI GI	g4512656
BLAST score	43
E value	4.0e-15
Match length	54
% identity	94
NCBI Description	Arabidopsis thaliana chromosome II BAC F7D19 genomic sequence, complete sequence

Seq. No.	158293
Seq. ID	LIB3176-091-P1-K1-D8
Method	BLASTN
NCBI GI	g3985931
BLAST score	223
E value	1.0e-122
Match length	374
% identity	95
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K21H1, complete sequence [Arabidopsis thaliana]

Seq. No.	158294
Seq. ID	LIB3176-091-P1-K1-E1
Method	BLASTN
NCBI GI	g4559375
BLAST score	180
E value	1.0e-96
Match length	315
% identity	97
NCBI Description	Arabidopsis thaliana chromosome II BAC F11C10 genomic sequence, complete sequence

Seq. No.	158295
Seq. ID	LIB3176-091-P1-K1-E11
Method	BLASTN
NCBI GI	g4581103
BLAST score	313
E value	1.0e-176
Match length	313
% identity	100
NCBI Description	Arabidopsis thaliana chromosome II BAC T24I21 genomic sequence, complete sequence

Seq. No.	158296
Seq. ID	LIB3176-091-P1-K1-E12
Method	BLASTN
NCBI GI	g2459406
BLAST score	158
E value	1.0e-83
Match length	375
% identity	99

NCBI Description	Arabidopsis thaliana chromosome II BAC F4P9 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	158297
Seq. ID	LIB3176-091-P1-K1-E2
Method	BLASTX
NCBI GI	g2781394
BLAST score	629
E value	8.0e-66
Match length	134
% identity	90
NCBI Description	(U70424) O-methyltransferase 1 [Arabidopsis thaliana]

Seq. No.	158298
Seq. ID	LIB3176-091-P1-K1-E3
Method	BLASTX
NCBI GI	g4454036
BLAST score	453
E value	2.0e-45
Match length	85
% identity	98
NCBI Description	(AL035394) putative major latex protein [Arabidopsis thaliana]

Seq. No.	158299
Seq. ID	LIB3176-091-P1-K1-E4
Method	BLASTX
NCBI GI	g2655420
BLAST score	139
E value	5.0e-09
Match length	32
% identity	81
NCBI Description	(AF035414) heat shock cognate protein HSC70 [Brassica napus]

Seq. No.	158300
Seq. ID	LIB3176-091-P1-K1-E5
Method	BLASTN
NCBI GI	g2924652
BLAST score	269
E value	1.0e-150
Match length	273
% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K9L2, complete sequence [Arabidopsis thaliana]

Seq. No.	158301
Seq. ID	LIB3176-091-P1-K1-E6
Method	BLASTN
NCBI GI	g3063438
BLAST score	245
E value	1.0e-135
Match length	249
% identity	91
NCBI Description	Complete sequence of Arabidopsis F22013, complete sequence [Arabidopsis thaliana]

Seq. No.	158302
Seq. ID	LIB3176-091-P1-K1-E7
Method	BLASTX
NCBI GI	g114335
BLAST score	182
E value	6.0e-14
Match length	44
% identity	89
NCBI Description	PLASMA MEMBRANE ATPASE 2 (PROTON PUMP) >gi_67973_pir__PXMUP2 H+-transporting ATPase (EC 3.6.1.35) type 2, plasma membrane - Arabidopsis thaliana >gi_166629 (J05570) H+-ATPase [Arabidopsis thaliana]

Seq. No.	158303
Seq. ID	LIB3176-091-P1-K1-E9
Method	BLASTN
NCBI GI	g2828188
BLAST score	117
E value	2.0e-59
Match length	161
% identity	99
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K3K3, complete sequence [Arabidopsis thaliana]

Seq. No.	158304
Seq. ID	LIB3176-091-P1-K1-F1
Method	BLASTX
NCBI GI	g2498397
BLAST score	269
E value	1.0e-23
Match length	79
% identity	61
NCBI Description	FERREDOXIN-THIOREDOXIN REDUCTASE, VARIABLE CHAIN (FTR-V) (FERREDOXIN-THIOREDOXIN REDUCTASE SUBUNIT A) (FTR-A)

Seq. No.	158305
Seq. ID	LIB3176-091-P1-K1-F11
Method	BLASTN
NCBI GI	g4220627
BLAST score	132
E value	5.0e-68
Match length	394
% identity	4
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K20J1, complete sequence [Arabidopsis thaliana]

Seq. No.	158306
Seq. ID	LIB3176-091-P1-K1-F12
Method	BLASTX
NCBI GI	g1172977
BLAST score	595
E value	4.0e-70
Match length	145
% identity	99
NCBI Description	60S RIBOSOMAL PROTEIN L18 >gi_606970 (U15741) cytoplasmic ribosomal protein L18 [Arabidopsis thaliana]

Seq. No.	158307
Seq. ID	LIB3176-091-P1-K1-F3
Method	BLASTN
NCBI GI	g2351073
BLAST score	284
E value	1.0e-159
Match length	292
% identity	99
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MYJ24, complete sequence [Arabidopsis thaliana]

Seq. No.	158308
Seq. ID	LIB3176-091-P1-K1-F4
Method	BLASTX
NCBI GI	g2306917
BLAST score	430
E value	8.0e-43
Match length	80
% identity	100
NCBI Description	(AF003728) plasma membrane intrinsic protein [Arabidopsis thaliana]

Seq. No.	158309
Seq. ID	LIB3176-091-P1-K1-F5
Method	BLASTX
NCBI GI	g4490732
BLAST score	502
E value	3.0e-51
Match length	97
% identity	98
NCBI Description	(AL035709) phosphoenolpyruvate carboxykinase (ATP)-like protein [Arabidopsis thaliana]

Seq. No.	158310
Seq. ID	LIB3176-091-P1-K1-F6
Method	BLASTN
NCBI GI	g4544461
BLAST score	146
E value	2.0e-76
Match length	194
% identity	94
NCBI Description	Arabidopsis thaliana chromosome II BAC F23E6 genomic sequence, complete sequence

Seq. No.	158311
Seq. ID	LIB3176-091-P1-K1-F7
Method	BLASTX
NCBI GI	g629692
BLAST score	364
E value	3.0e-35
Match length	76
% identity	87
NCBI Description	hypothetical protein - common tobacco >gi_506471_emb_CAA56189_ (X79794) unnamed protein product [Nicotiana tabacum]

Seq. No.	158312

Seq. ID	LIB3176-091-P1-K1-F8
Method	BLASTX
NCBI GI	g399013
BLAST score	289
E value	3.0e-26
Match length	55
% identity	100
NCBI Description	ADP,ATP CARRIER PROTEIN 1 PRECURSOR (ADP/ATP TRANSLOCASE 1) (ADENINE NUCLEOTIDE TRANSLOCATOR 1) (ANT 1) >gi_99658_pir__S21313 ADP,ATP carrier protein - Arabidopsis thaliana (fragment) >gi_16175_emb_CAA46518_ (X65549) adenylate translocator [Arabidopsis thaliana] >gi_445607_prf__1909354A adenylate translocator [Arabidopsis thaliana]

Seq. No.	158313
Seq. ID	LIB3176-091-P1-K1-G1
Method	BLASTX
NCBI GI	g2130028
BLAST score	235
E value	3.0e-20
Match length	53
% identity	79
NCBI Description	B12D protein - barley >gi_471319_emb_CAA54065.1_ (X76604) HvB12D [Hordeum vulgare] >gi_3445292_emb_CAA70936_ (Y09805) B12Dg1 [Hordeum vulgare]

Seq. No.	158314
Seq. ID	LIB3176-091-P1-K1-G10
Method	BLASTN
NCBI GI	g681901
BLAST score	42
E value	2.0e-15
Match length	54
% identity	94
NCBI Description	Arabidopsis thaliana gene for chloroplast RNA-binding protein cp29, complete cds (exon1, exon2, exon3, exon4)

Seq. No.	158315
Seq. ID	LIB3176-091-P1-K1-G11
Method	BLASTX
NCBI GI	g1145697
BLAST score	504
E value	3.0e-51
Match length	106
% identity	96
NCBI Description	(U39485) delta tonoplast integral protein [Arabidopsis thaliana]

Seq. No.	158316
Seq. ID	LIB3176-091-P1-K1-G12
Method	BLASTN
NCBI GI	g405130
BLAST score	346
E value	0.0e+00
Match length	350
% identity	100

NCBI Description	Arabidopsis thaliana nuclear-encoded chloroplast stromal cyclophilin (ROC4) mRNA, complete cds
Seq. No.	158317
Seq. ID	LIB3176-091-P1-K1-G2
Method	BLASTX
NCBI GI	g116229
BLAST score	283
E value	3.0e-25
Match length	73
% identity	82
NCBI Description	MITOCHONDRIAL CHAPERONIN HSP60 PRECURSOR >gi_99676_pir__S20876 chaperonin hsp60 precursor - Arabidopsis thaliana >gi_16221_emb_CAA77646_ (Z11547) chaperonin hsp60 [Arabidopsis thaliana]
Seq. No.	158318
Seq. ID	LIB3176-091-P1-K1-G3
Method	BLASTN
NCBI GI	g2264318
BLAST score	213
E value	1.0e-116
Match length	420
% identity	98
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MUP24, complete sequence [Arabidopsis thaliana]
Seq. No.	158319
Seq. ID	LIB3176-091-P1-K1-G4
Method	BLASTN
NCBI GI	g2244829
BLAST score	49
E value	6.0e-19
Match length	89
% identity	98
NCBI Description	Arabidopsis thaliana DNA chromosome 4, ESSA I contig fragment No
Seq. No.	158320
Seq. ID	LIB3176-091-P1-K1-G5
Method	BLASTX
NCBI GI	g4678353
BLAST score	471
E value	1.0e-47
Match length	94
% identity	96
NCBI Description	(AL049659) cysteine endopeptidase precursor-like protein [Arabidopsis thaliana]
Seq. No.	158321
Seq. ID	LIB3176-091-P1-K1-G7
Method	BLASTX
NCBI GI	g3123271
BLAST score	489
E value	2.0e-49
Match length	115
% identity	83

NCBI Description	40S RIBOSOMAL PROTEIN S6 >gi_2224751_emb_CAA74381_ (Y14052) ribosomal protein S6 [Arabidopsis thaliana]
Seq. No.	158322
Seq. ID	LIB3176-091-P1-K1-G8
Method	BLASTN
NCBI GI	g4538972
BLAST score	194
E value	1.0e-105
Match length	454
% identity	100
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F28M11 (ESSA project)
Seq. No.	158323
Seq. ID	LIB3176-091-P1-K1-G9
Method	BLASTN
NCBI GI	g2462780
BLAST score	296
E value	1.0e-166
Match length	304
% identity	99
NCBI Description	Arabidopsis thaliana carbamoyl phosphate synthetase small subunit mRNA (carA), complete cds
Seq. No.	158324
Seq. ID	LIB3176-091-P1-K1-H1
Method	BLASTX
NCBI GI	g3660469
BLAST score	680
E value	9.0e-72
Match length	146
% identity	95
NCBI Description	(AJ001808) succinyl-CoA-ligase beta subunit [Arabidopsis thaliana] >gi_4512693_gb_AAD21746.1_ (AC006569) succinyl-CoA ligase beta subunit [Arabidopsis thaliana]
Seq. No.	158325
Seq. ID	LIB3176-091-P1-K1-H10
Method	BLASTX
NCBI GI	g2854070
BLAST score	603
E value	9.0e-63
Match length	126
% identity	94
NCBI Description	(AF044914) putative histone deacetylase [Arabidopsis thaliana]
Seq. No.	158326
Seq. ID	LIB3176-091-P1-K1-H11
Method	BLASTX
NCBI GI	g3123279
BLAST score	367
E value	4.0e-35
Match length	110
% identity	67
NCBI Description	40S RIBOSOMAL PROTEIN S26 >gi_2651298 (AC002336) putative

ribosomal protein S26 [Arabidopsis thaliana]

Seq. No.	158327
Seq. ID	LIB3176-091-P1-K1-H12
Method	BLASTX
NCBI GI	g1621268
BLAST score	469
E value	5.0e-47
Match length	139
% identity	64
NCBI Description	(Z81012) unknown [Ricinus communis]

Seq. No.	158328
Seq. ID	LIB3176-091-P1-K1-H2
Method	BLASTN
NCBI GI	g4159706
BLAST score	188
E value	1.0e-101
Match length	196
% identity	99
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MGL6, complete sequence

Seq. No.	158329
Seq. ID	LIB3176-091-P1-K1-H3
Method	BLASTN
NCBI GI	g3869068
BLAST score	34
E value	2.0e-09
Match length	126
% identity	92
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MDC16, complete sequence [Arabidopsis thaliana]

Seq. No.	158330
Seq. ID	LIB3176-091-P1-K1-H8
Method	BLASTN
NCBI GI	g3869068
BLAST score	96
E value	2.0e-46
Match length	435
% identity	98
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MDC16, complete sequence [Arabidopsis thaliana]

Seq. No.	158331
Seq. ID	LIB3176-091-P1-K1-H9
Method	BLASTX
NCBI GI	g2664200
BLAST score	401
E value	5.0e-39
Match length	147
% identity	60
NCBI Description	(AJ003216) GTL2 [Arabidopsis thaliana]

Seq. No.	158332
Seq. ID	LIB3176-092-P1-K1-A1

Method	BLASTX
NCBI GI	g480450
BLAST score	167
E value	1.0e-11
Match length	86
% identity	52
NCBI Description	ketol-acid reductoisomerase (EC 1.1.1.86) - Arabidopsis thaliana >gi_402552_emb_CAA49506_ (X69880) ketol-acid reductoisomerase [Arabidopsis thaliana]

Seq. No.	158333
Seq. ID	LIB3176-092-P1-K1-A10
Method	BLASTX
NCBI GI	g1931639
BLAST score	222
E value	3.0e-18
Match length	87
% identity	48
NCBI Description	(U95973) lysophospholipase isolog [Arabidopsis thaliana]

Seq. No.	158334
Seq. ID	LIB3176-092-P1-K1-A11
Method	BLASTN
NCBI GI	g3128142
BLAST score	178
E value	8.0e-96
Match length	182
% identity	99
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MQN23, complete sequence [Arabidopsis thaliana]

Seq. No.	158335
Seq. ID	LIB3176-092-P1-K1-A12
Method	BLASTX
NCBI GI	g2501188
BLAST score	374
E value	3.0e-36
Match length	86
% identity	88
NCBI Description	THIAZOLE BIOSYNTHETIC ENZYME >gi_2129750_pir__S71191 TH14 protein homolog - Arabidopsis thaliana >gi_1113783 (U17589) Thi1 protein [Arabidopsis thaliana]

Seq. No.	158336
Seq. ID	LIB3176-092-P1-K1-A5
Method	BLASTN
NCBI GI	g2143226
BLAST score	54
E value	3.0e-22
Match length	74
% identity	93
NCBI Description	Brassica napus mRNA for glyoxysomal isocitrate lyase

Seq. No.	158337
Seq. ID	LIB3176-092-P1-K1-A7
Method	BLASTN
NCBI GI	g3406034

BLAST score	57
E value	2.0e-23
Match length	73
% identity	95
NCBI Description	BAC F18A17 from chromosome V containing TINY at 60.5 cM, complete sequence [Arabidopsis thaliana]

Seq. No.	158338
Seq. ID	LIB3176-092-P1-K1-A8
Method	BLASTN
NCBI GI	g4309719
BLAST score	67
E value	3.0e-29
Match length	67
% identity	100
NCBI Description	Arabidopsis thaliana chromosome II BAC T30D6 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	158339
Seq. ID	LIB3176-092-P1-K1-B1
Method	BLASTX
NCBI GI	g2052379
BLAST score	684
E value	2.0e-72
Match length	126
% identity	99
NCBI Description	(U66343) calreticulin [Arabidopsis thaliana]

Seq. No.	158340
Seq. ID	LIB3176-092-P1-K1-B11
Method	BLASTN
NCBI GI	g3785968
BLAST score	89
E value	1.0e-42
Match length	160
% identity	97
NCBI Description	Arabidopsis thaliana chromosome II BAC F2I9 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	158341
Seq. ID	LIB3176-092-P1-K1-B12
Method	BLASTX
NCBI GI	g4539327
BLAST score	462
E value	3.0e-46
Match length	149
% identity	65
NCBI Description	(AL035679) putative proton pump [Arabidopsis thaliana]

Seq. No.	158342
Seq. ID	LIB3176-092-P1-K1-B2
Method	BLASTX
NCBI GI	g135406
BLAST score	619
E value	1.0e-64
Match length	135
% identity	88

NCBI Description	TUBULIN ALPHA-3/ALPHA-5 CHAIN >gi_99768_pir__A32712 tubulin alpha-5 chain - Arabidopsis thaliana >gi_166912 (M17189) alpha-tubulin [Arabidopsis thaliana] >gi_166918 (M84698) alpha-5 tubulin [Arabidopsis thaliana]
Seq. No.	158343
Seq. ID	LIB3176-092-P1-K1-B4
Method	BLASTX
NCBI GI	g3805846
BLAST score	372
E value	4.0e-36
Match length	82
% identity	91
NCBI Description	(AL031986) DNA-directed RNA polymerase (EC 2.7.7.6) II largest chain [Arabidopsis thaliana]
Seq. No.	158344
Seq. ID	LIB3176-092-P1-K1-B5
Method	BLASTN
NCBI GI	g4309683
BLAST score	147
E value	5.0e-77
Match length	213
% identity	99
NCBI Description	Arabidopsis thaliana chromosome 1 BAC T31J12 sequence, complete sequence [Arabidopsis thaliana]
Seq. No.	158345
Seq. ID	LIB3176-092-P1-K1-B6
Method	BLASTN
NCBI GI	g2288979
BLAST score	170
E value	6.0e-91
Match length	174
% identity	99
NCBI Description	Arabidopsis thaliana chromosome II BAC T01O24 genomic sequence, complete sequence [Arabidopsis thaliana]
Seq. No.	158346
Seq. ID	LIB3176-092-P1-K1-B7
Method	BLASTN
NCBI GI	g3449327
BLAST score	118
E value	4.0e-60
Match length	122
% identity	99
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MCA23, complete sequence [Arabidopsis thaliana]
Seq. No.	158347
Seq. ID	LIB3176-092-P1-K1-B9
Method	BLASTX
NCBI GI	g4218120
BLAST score	286
E value	1.0e-27
Match length	95
% identity	72

NCBI Description	(AL035353) Proline-rich APG-like protein [Arabidopsis thaliana]
Seq. No.	158348
Seq. ID	LIB3176-092-P1-K1-C1
Method	BLASTN
NCBI GI	g298035
BLAST score	95
E value	2.0e-46
Match length	125
% identity	95
NCBI Description	A.thaliana Lhcb4 gene
Seq. No.	158349
Seq. ID	LIB3176-092-P1-K1-C10
Method	BLASTX
NCBI GI	g2760086
BLAST score	732
E value	7.0e-78
Match length	149
% identity	28
NCBI Description	(Y16046) leucine-rich repeat protein [Arabidopsis thaliana]
Seq. No.	158350
Seq. ID	LIB3176-092-P1-K1-C11
Method	BLASTN
NCBI GI	g3985957
BLAST score	142
E value	3.0e-74
Match length	158
% identity	97
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MYN8, complete sequence [Arabidopsis thaliana]
Seq. No.	158351
Seq. ID	LIB3176-092-P1-K1-C12
Method	BLASTX
NCBI GI	g2662469
BLAST score	314
E value	2.0e-29
Match length	72
% identity	86
NCBI Description	(AF034217) ribosomal protein S6 [Arabidopsis thaliana]
Seq. No.	158352
Seq. ID	LIB3176-092-P1-K1-C4
Method	BLASTX
NCBI GI	g131381
BLAST score	472
E value	1.0e-47
Match length	101
% identity	97
NCBI Description	OXYGEN-EVOLVING ENHANCER PROTEIN 1 PRECURSOR (OEE1) (33 KD SUBUNIT OF OXYGEN EVOLVING SYSTEM OF PHOTOSYSTEM II) (33 KD THYLAKOID MEMBRANE PROTEIN) >gi_99745_pir__S11852 photosystem II oxygen-evolving complex protein 1 precursor - Arabidopsis thaliana >gi_22571_emb_CAA36675_ (X52428) 33

kDa oxygen-evolving protein [Arabidopsis thaliana]

Seq. No.	158353
Seq. ID	LIB3176-092-P1-K1-C5
Method	BLASTX
NCBI GI	g119975
BLAST score	477
E value	3.0e-48
Match length	97
% identity	99
NCBI Description	FERREDOXIN PRECURSOR >gi_99692_pir__S09979 ferredoxin [2Fe-2S] precursor - Arabidopsis thaliana >gi_16437_emb_CAA35754_ (X51370) ferredoxin precursor [Arabidopsis thaliana] >gi_166698 (M35868) ferrodoxin A [Arabidopsis thaliana]

Seq. No.	158354
Seq. ID	LIB3176-092-P1-K1-C6
Method	BLASTX
NCBI GI	g3608136
BLAST score	298
E value	1.0e-27
Match length	59
% identity	95
NCBI Description	(AC005314) defender against cell death [Arabidopsis thaliana]

Seq. No.	158355
Seq. ID	LIB3176-092-P1-K1-C7
Method	BLASTX
NCBI GI	g2493045
BLAST score	329
E value	8.0e-43
Match length	136
% identity	68
NCBI Description	ATP SYNTHASE DELTA' CHAIN, MITOCHONDRIAL PRECURSOR >gi_1655484_dbj_BAA13601_ (D88376) delta-prime subunit of mitochondrial F1-ATPase [Arabidopsis thaliana]

Seq. No.	158356
Seq. ID	LIB3176-092-P1-K1-C8
Method	BLASTX
NCBI GI	g3135611
BLAST score	332
E value	4.0e-31
Match length	68
% identity	94
NCBI Description	(AF062485) cellulose synthase [Arabidopsis thaliana]

Seq. No.	158357
Seq. ID	LIB3176-092-P1-K1-C9
Method	BLASTX
NCBI GI	g2088654
BLAST score	448
E value	9.0e-45
Match length	100
% identity	89

NCBI Description	(AF002109) 60S acidic ribosomal protein P0 isolog [Arabidopsis thaliana]
Seq. No.	158358
Seq. ID	LIB3176-092-P1-K1-D1
Method	BLASTX
NCBI GI	g1351082
BLAST score	499
E value	7.0e-51
Match length	95
% identity	100
NCBI Description	SUPEROXIDE DISMUTASE, CHLOROPLAST PRECURSOR (FE) >gi_166700 (M55910) Fe-superoxide dismutase [Arabidopsis thaliana]
Seq. No.	158359
Seq. ID	LIB3176-092-P1-K1-D11
Method	BLASTX
NCBI GI	g3914917
BLAST score	236
E value	7.0e-20
Match length	50
% identity	90
NCBI Description	40S RIBOSOMAL PROTEIN S3A
Seq. No.	158360
Seq. ID	LIB3176-092-P1-K1-D12
Method	BLASTX
NCBI GI	g3522936
BLAST score	300
E value	2.0e-27
Match length	81
% identity	75
NCBI Description	(AC004411) putative alcohol dehydrogenase [Arabidopsis thaliana]
Seq. No.	158361
Seq. ID	LIB3176-092-P1-K1-D2
Method	BLASTN
NCBI GI	g3402671
BLAST score	370
E value	0.0e+00
Match length	411
% identity	97
NCBI Description	Arabidopsis thaliana chromosome II BAC T16B24 genomic sequence, complete sequence [Arabidopsis thaliana]
Seq. No.	158362
Seq. ID	LIB3176-092-P1-K1-D3
Method	BLASTX
NCBI GI	g4582787
BLAST score	329
E value	8.0e-31
Match length	77
% identity	86
NCBI Description	(AJ012281) adenosine kinase [Zea mays]
Seq. No.	158363

Seq. ID	LIB3176-092-P1-K1-D4
Method	BLASTN
NCBI GI	g3849811
BLAST score	108
E value	3.0e-54
Match length	124
% identity	97
NCBI Description	Arabidopsis thaliana chromosome I BAC T2P11 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	158364
Seq. ID	LIB3176-092-P1-K1-D5
Method	BLASTX
NCBI GI	g3914996
BLAST score	380
E value	7.0e-37
Match length	100
% identity	74
NCBI Description	PHOSPHOSERINE AMINOTRANSFERASE PRECURSOR (PSAT) >gi_1665831_dbj_BAA13640_ (D88541) phosphoserine aminotransferase [Arabidopsis thaliana] >gi_2804260_dbj_BAA24441_ (AB010408) phosphoserine aminotransferase [Arabidopsis thaliana] >gi_3367581_emb_CAA20033_ (AL031135) phosphoserine aminotransferase [Arabidopsis thaliana]

Seq. No.	158365
Seq. ID	LIB3176-092-P1-K1-D6
Method	BLASTX
NCBI GI	g1170503
BLAST score	267
E value	1.0e-23
Match length	55
% identity	95
NCBI Description	EUKARYOTIC INITIATION FACTOR 4A-1 (EIF-4A-1) >gi_322503_pir__JC1452 translation initiation factor eIF-4A1 - Arabidopsis thaliana >gi_16554_emb_CAA46188_ (X65052) eukaryotic translation initiation factor 4A-1 [Arabidopsis thaliana]

Seq. No.	158366
Seq. ID	LIB3176-092-P1-K1-D7
Method	BLASTN
NCBI GI	g2182286
BLAST score	136
E value	1.0e-70
Match length	139
% identity	99
NCBI Description	Sequence of BAC F20P5 from Arabidopsis thaliana chromosome 1, complete sequence [Arabidopsis thaliana]

Seq. No.	158367
Seq. ID	LIB3176-092-P1-K1-D9
Method	BLASTX
NCBI GI	g2529680
BLAST score	588
E value	4.0e-61

Match length	121
% identity	47
NCBI Description	(AC002535) putative protein disulfide-isomerase precursor [Arabidopsis thaliana]

Seq. No.	158368
Seq. ID	LIB3176-092-P1-K1-E1
Method	BLASTX
NCBI GI	g4454037
BLAST score	722
E value	9.0e-77
Match length	138
% identity	96
NCBI Description	(AL035394) putative major latex protein [Arabidopsis thaliana]

Seq. No.	158369
Seq. ID	LIB3176-092-P1-K1-E10
Method	BLASTN
NCBI GI	g4691223
BLAST score	116
E value	2.0e-58
Match length	116
% identity	100
NCBI Description	Arabidopsis thaliana DNA chromosome 3, BAC clone F4F15 (ESSA project)

Seq. No.	158370
Seq. ID	LIB3176-092-P1-K1-E11
Method	BLASTX
NCBI GI	g4056502
BLAST score	624
E value	3.0e-65
Match length	136
% identity	89
NCBI Description	(AC005896) 40S ribosomal protein S5 [Arabidopsis thaliana]

Seq. No.	158371
Seq. ID	LIB3176-092-P1-K1-E12
Method	BLASTX
NCBI GI	g4559369
BLAST score	286
E value	3.0e-26
Match length	57
% identity	95
NCBI Description	(AC006585) putative Rieske iron-sulfur protein [Arabidopsis thaliana]

Seq. No.	158372
Seq. ID	LIB3176-092-P1-K1-E4
Method	BLASTX
NCBI GI	g3046696
BLAST score	429
E value	2.0e-42
Match length	79
% identity	100
NCBI Description	(AL022224) CTP synthase like protein [Arabidopsis thaliana]

Seq. No.	158373
Seq. ID	LIB3176-092-P1-K1-E5
Method	BLASTN
NCBI GI	g166771
BLAST score	57
E value	2.0e-23
Match length	65
% identity	97
NCBI Description	A.thaliana isocitrate lyase gene, 5' end

Seq. No.	158374
Seq. ID	LIB3176-092-P1-K1-E6
Method	BLASTN
NCBI GI	g3785968
BLAST score	100
E value	3.0e-49
Match length	173
% identity	97
NCBI Description	Arabidopsis thaliana chromosome II BAC F2I9 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	158375
Seq. ID	LIB3176-092-P1-K1-E7
Method	BLASTX
NCBI GI	g2146797
BLAST score	475
E value	9.0e-48
Match length	138
% identity	45
NCBI Description	protein disulfide-isomerase (EC 5.3.4.1) - Castor bean >gi_1134968 (U41385) protein disulphide isomerase PDI [Ricinus communis] >gi_1587210_prf__2206331A protein disulfide isomerase [Ricinus communis]

Seq. No.	158376
Seq. ID	LIB3176-092-P1-K1-E8
Method	BLASTX
NCBI GI	g1363489
BLAST score	699
E value	5.0e-74
Match length	131
% identity	98
NCBI Description	thioglucosidase (EC 3.2.3.1) 3D precursor - Arabidopsis thaliana >gi_984052_emb_CAA61592_ (X89413) thioglucoside glucohydrolase [Arabidopsis thaliana]

Seq. No.	158377
Seq. ID	LIB3176-092-P1-K1-F1
Method	BLASTX
NCBI GI	g3688799
BLAST score	542
E value	1.0e-55
Match length	114
% identity	96
NCBI Description	(AF057137) gamma tonoplast intrinsic protein 2 [Arabidopsis thaliana]

Seq. No.	158378
Seq. ID	LIB3176-092-P1-K1-F10
Method	BLASTX
NCBI GI	g2827552
BLAST score	608
E value	2.0e-63
Match length	125
% identity	70
NCBI Description	(AL021635) predicted protein [Arabidopsis thaliana]

Seq. No.	158379
Seq. ID	LIB3176-092-P1-K1-F11
Method	BLASTX
NCBI GI	g2791423
BLAST score	183
E value	2.0e-13
Match length	62
% identity	55
NCBI Description	(AL021185) bcp [Mycobacterium tuberculosis]

Seq. No.	158380
Seq. ID	LIB3176-092-P1-K1-F12
Method	BLASTN
NCBI GI	g484109
BLAST score	122
E value	5.0e-62
Match length	444
% identity	98
NCBI Description	Arabidopsis thaliana chloroplast glyceraldehyde-3-phosphate dehydrogenase B subunit gene, 5'end

Seq. No.	158381
Seq. ID	LIB3176-092-P1-K1-F2
Method	BLASTN
NCBI GI	g3047074
BLAST score	97
E value	2.0e-47
Match length	177
% identity	99
NCBI Description	Arabidopsis thaliana BAC F21E10

Seq. No.	158382
Seq. ID	LIB3176-092-P1-K1-F3
Method	BLASTX
NCBI GI	g4704766
BLAST score	304
E value	8.0e-28
Match length	86
% identity	45
NCBI Description	(AF131223) protein disulfide isomerase homolog; PDI [Datisca glomerata]

Seq. No.	158383
Seq. ID	LIB3176-092-P1-K1-F4
Method	BLASTX
NCBI GI	g2500347

BLAST score	425
E value	7.0e-42
Match length	128
% identity	69
NCBI Description	NHP2/RS6 FAMILY PROTEIN YEL026W HOMOLOG >gi_3878691_emb_CAA90127_ (Z49911) similar to ribosomal protein (L7AE family); cDNA EST EMBL:D73957 comes from this gene; cDNA EST EMBL:D71298 comes from this gene; cDNA EST EMBL:D74077 comes from this gene; cDNA EST EMBL:D71393 comes from this gene; cD

Seq. No.	158384
Seq. ID	LIB3176-092-P1-K1-F5
Method	BLASTN
NCBI GI	g4454447
BLAST score	200
E value	1.0e-109
Match length	212
% identity	99
NCBI Description	Arabidopsis thaliana chromosome II BAC F5H14 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	158385
Seq. ID	LIB3176-092-P1-K1-F8
Method	BLASTX
NCBI GI	g1621268
BLAST score	400
E value	5.0e-39
Match length	120
% identity	62
NCBI Description	(Z81012) unknown [Ricinus communis]

Seq. No.	158386
Seq. ID	LIB3176-092-P1-K1-F9
Method	BLASTX
NCBI GI	g3264759
BLAST score	211
E value	2.0e-17
Match length	60
% identity	70
NCBI Description	(AF071889) 40S ribosomal protein S8 [Prunus armeniaca]

Seq. No.	158387
Seq. ID	LIB3176-092-P1-K1-G10
Method	BLASTX
NCBI GI	g127041
BLAST score	504
E value	2.0e-51
Match length	109
% identity	91
NCBI Description	S-ADENOSYLMETHIONINE SYNTHETASE 1 (METHIONINE ADENOSYLTRANSFERASE 1) (ADOMET SYNTHETASE 1) >gi_81647_pir__JN0131 methionine adenosyltransferase (EC 2.5.1.6) - Arabidopsis thaliana >gi_166872 (M55077) S-adenosylmethionine synthetase [Arabidopsis thaliana]

Seq. No. 158388

Seq. ID	LIB3176-092-P1-K1-G11
Method	BLASTN
NCBI GI	g2351070
BLAST score	93
E value	1.0e-44
Match length	162
% identity	93
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MTH12, complete sequence [Arabidopsis thaliana]

Seq. No.	158389
Seq. ID	LIB3176-092-P1-K1-G12
Method	BLASTN
NCBI GI	g3687221
BLAST score	366
E value	0.0e+00
Match length	405
% identity	98
NCBI Description	Arabidopsis thaliana chromosome II BAC F6F22 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	158390
Seq. ID	LIB3176-092-P1-K1-G2
Method	BLASTN
NCBI GI	g2914688
BLAST score	261
E value	1.0e-145
Match length	265
% identity	100
NCBI Description	Arabidopsis thaliana chromosome II BAC F24L7 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	158391
Seq. ID	LIB3176-092-P1-K1-G4
Method	BLASTX
NCBI GI	g4056502
BLAST score	527
E value	6.0e-54
Match length	106
% identity	98
NCBI Description	(AC005896) 40S ribosomal protein S5 [Arabidopsis thaliana]

Seq. No.	158392
Seq. ID	LIB3176-092-P1-K1-G7
Method	BLASTX
NCBI GI	g3386611
BLAST score	141
E value	7.0e-09
Match length	66
% identity	48
NCBI Description	(AC004665) unknown protein [Arabidopsis thaliana]

Seq. No.	158393
Seq. ID	LIB3176-092-P1-K1-G8
Method	BLASTX
NCBI GI	g1346194
BLAST score	280

E value	4.0e-38
Match length	106
% identity	81
NCBI Description	GLUTATHIONE REDUCTASE, CYTOSOLIC (GR) (GRASE) (OBP29) >gi_1022797 (U37697) glutathione reductase [Arabidopsis thaliana]

Seq. No.	158394
Seq. ID	LIB3176-092-P1-K1-G9
Method	BLASTX
NCBI GI	g129960
BLAST score	183
E value	6.0e-14
Match length	60
% identity	55
NCBI Description	4-NITROPHENYLPHOSPHATASE (PNPPASE)

Seq. No.	158395
Seq. ID	LIB3176-092-P1-K1-H1
Method	BLASTN
NCBI GI	g3449322
BLAST score	156
E value	1.0e-82
Match length	160
% identity	99
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MXC17, complete sequence [Arabidopsis thaliana]

Seq. No.	158396
Seq. ID	LIB3176-092-P1-K1-H12
Method	BLASTN
NCBI GI	g3522932
BLAST score	296
E value	1.0e-166
Match length	349
% identity	96
NCBI Description	Arabidopsis thaliana chromosome II BAC F14M4 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	158397
Seq. ID	LIB3176-092-P1-K1-H3
Method	BLASTN
NCBI GI	g405130
BLAST score	345
E value	0.0e+00
Match length	345
% identity	100
NCBI Description	Arabidopsis thaliana nuclear-encoded chloroplast stromal cyclophilin (ROC4) mRNA, complete cds

Seq. No.	158398
Seq. ID	LIB3176-092-P1-K1-H4
Method	BLASTN
NCBI GI	g4580744
BLAST score	38
E value	1.0e-12
Match length	56

% identity	91
NCBI Description	Sequence of BAC F15I1 from Arabidopsis thaliana chromosome 1, complete sequence

Seq. No.	158399
Seq. ID	LIB3176-092-P1-K1-H6
Method	BLASTX
NCBI GI	g1708107
BLAST score	53
E value	3.0e-14
Match length	81
% identity	58
NCBI Description	HISTONE H2B >gi_473605 (U08226) histone H2B [Zea mays]

Seq. No.	158400
Seq. ID	LIB3176-092-P1-K1-H7
Method	BLASTX
NCBI GI	g132863
BLAST score	502
E value	3.0e-51
Match length	98
% identity	95
NCBI Description	CHLOROPLAST 50S RIBOSOMAL PROTEIN L2 >gi_12214_emb_CAA46568_ (X65615) ribosomal protein L2 [Sinapis alba]

Seq. No.	158401
Seq. ID	LIB3176-092-P1-K1-H8
Method	BLASTN
NCBI GI	g2618601
BLAST score	216
E value	1.0e-118
Match length	220
% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MHJ24, complete sequence [Arabidopsis thaliana]

Seq. No.	158402
Seq. ID	LIB3176-092-P1-K1-H9
Method	BLASTN
NCBI GI	g1490552
BLAST score	279
E value	1.0e-156
Match length	287
% identity	99
NCBI Description	Arabidopsis thaliana S-adenosylmethionine decarboxylase (SAMdc) mRNA, complete cds

Seq. No.	158403
Seq. ID	LIB3176-093-P1-K1-A1
Method	BLASTX
NCBI GI	g1706749
BLAST score	114
E value	1.0e-15
Match length	51
% identity	88
NCBI Description	3-OXOACYL-[ACYL-CARRIER-PROTEIN] SYNTHASE I PRECURSOR

	(BETA-KETOACYL-ACP SYNTHASE I) (KAS I) >gi_780814 (U24177) 3-ketoacyl-acyl carrier protein synthase I [Arabidopsis thaliana]
Seq. No.	158404
Seq. ID	LIB3176-093-P1-K1-A10
Method	BLASTX
NCBI GI	g2062161
BLAST score	203
E value	2.0e-16
Match length	48
% identity	83
NCBI Description	(AC001645) jasmonate inducible protein isolog [Arabidopsis thaliana]
Seq. No.	158405
Seq. ID	LIB3176-093-P1-K1-A12
Method	BLASTX
NCBI GI	g2317911
BLAST score	370
E value	9.0e-36
Match length	94
% identity	85
NCBI Description	(U89959) similar to GTP-binding protein [Arabidopsis thaliana]
Seq. No.	158406
Seq. ID	LIB3176-093-P1-K1-A2
Method	BLASTN
NCBI GI	g414340
BLAST score	146
E value	1.0e-76
Match length	187
% identity	95
NCBI Description	A.thaliana rd21A gene for thiol protease, complete cds
Seq. No.	158407
Seq. ID	LIB3176-093-P1-K1-A3
Method	BLASTN
NCBI GI	g4262221
BLAST score	32
E value	9.0e-09
Match length	84
% identity	92
NCBI Description	Arabidopsis thaliana chromosome II BAC F10A8 genomic sequence, complete sequence [Arabidopsis thaliana]
Seq. No.	158408
Seq. ID	LIB3176-093-P1-K1-A4
Method	BLASTN
NCBI GI	g4490291
BLAST score	102
E value	1.0e-50
Match length	130
% identity	95
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F17M5 (ESSA project)

09504-0074

Seq. No.	158409
Seq. ID	LIB3176-093-P1-K1-A7
Method	BLASTX
NCBI GI	g2583108
BLAST score	553
E value	6.0e-57
Match length	120
% identity	93
NCBI Description	(AC002387) putative surface protein [Arabidopsis thaliana]

Seq. No.	158410
Seq. ID	LIB3176-093-P1-K1-A8
Method	BLASTN
NCBI GI	g2828188
BLAST score	79
E value	8.0e-37
Match length	130
% identity	96
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K3K3, complete sequence [Arabidopsis thaliana]

Seq. No.	158411
Seq. ID	LIB3176-093-P1-K1-B11
Method	BLASTN
NCBI GI	g2317728
BLAST score	104
E value	1.0e-51
Match length	120
% identity	97
NCBI Description	Arabidopsis thaliana reversibly glycosylated polypeptide-1 (AtRGP) mRNA, complete cds

Seq. No.	158412
Seq. ID	LIB3176-093-P1-K1-B12
Method	BLASTN
NCBI GI	g4337186
BLAST score	253
E value	1.0e-140
Match length	274
% identity	98
NCBI Description	Arabidopsis thaliana chromosome II BAC T28I24 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	158413
Seq. ID	LIB3176-093-P1-K1-B2
Method	BLASTX
NCBI GI	g3355468
BLAST score	156
E value	7.0e-11
Match length	59
% identity	59
NCBI Description	(AC004218) putative ribosomal protein L35 [Arabidopsis thaliana]

Seq. No.	158414
Seq. ID	LIB3176-093-P1-K1-B3

Method	BLASTX
NCBI GI	g3128228
BLAST score	396
E value	5.0e-39
Match length	77
% identity	96
NCBI Description	(AC004077) putative ribosomal protein L18A [Arabidopsis thaliana] >gi_3337376 (AC004481) putative ribosomal protein L18A [Arabidopsis thaliana]

Seq. No.	158415
Seq. ID	LIB3176-093-P1-K1-B4
Method	BLASTN
NCBI GI	g3193311
BLAST score	79
E value	6.0e-37
Match length	115
% identity	92
NCBI Description	Arabidopsis thaliana BAC F6N15

Seq. No.	158416
Seq. ID	LIB3176-093-P1-K1-B7
Method	BLASTX
NCBI GI	g2583135
BLAST score	50
E value	5.0e-51
Match length	111
% identity	93
NCBI Description	(AC002387) hypothetical protein [Arabidopsis thaliana] >gi_3822216 (AF074948) FIL [Arabidopsis thaliana] >gi_4322477_gb_AAD16053_ (AF087015) abnormal floral organs protein [Arabidopsis thaliana]

Seq. No.	158417
Seq. ID	LIB3176-093-P1-K1-B8
Method	BLASTN
NCBI GI	g4539290
BLAST score	86
E value	4.0e-41
Match length	102
% identity	97
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F14M19 (ESSA project)

Seq. No.	158418
Seq. ID	LIB3176-093-P1-K1-C1
Method	BLASTX
NCBI GI	g542005
BLAST score	204
E value	1.0e-16
Match length	57
% identity	65
NCBI Description	endoxyloglucan transferase - adzuki bean >gi_469510_dbj_BAA03925_ (D16458) endo-xyloglucan transferase [Vigna angularis]

Seq. No.	158419

Seq. ID	LIB3176-093-P1-K1-C10
Method	BLASTN
NCBI GI	g2113824
BLAST score	48
E value	4.0e-18
Match length	76
% identity	91
NCBI Description	Brassica juncea mRNA for glyoxalase I

Seq. No.	158420
Seq. ID	LIB3176-093-P1-K1-C11
Method	BLASTN
NCBI GI	g4567193
BLAST score	125
E value	7.0e-64
Match length	336
% identity	97
NCBI Description	Arabidopsis thaliana chromosome II BAC T26C19 genomic sequence, complete sequence

Seq. No.	158421
Seq. ID	LIB3176-093-P1-K1-C12
Method	BLASTN
NCBI GI	g4490717
BLAST score	82
E value	9.0e-39
Match length	118
% identity	92
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone (ESSA project)

Seq. No.	158422
Seq. ID	LIB3176-093-P1-K1-C2
Method	BLASTN
NCBI GI	g2191126
BLAST score	103
E value	5.0e-51
Match length	192
% identity	96
NCBI Description	Arabidopsis thaliana BAC IG002N01

Seq. No.	158423
Seq. ID	LIB3176-093-P1-K1-C5
Method	BLASTX
NCBI GI	g1546698
BLAST score	232
E value	7.0e-20
Match length	43
% identity	100
NCBI Description	(X98808) peroxidase ATP3a [Arabidopsis thaliana]

Seq. No.	158424
Seq. ID	LIB3176-093-P1-K1-C6
Method	BLASTX
NCBI GI	g1363489
BLAST score	60
E value	6.0e-37

Match length	83
% identity	88
NCBI Description	thioglucosidase (EC 3.2.3.1) 3D precursor - Arabidopsis thaliana >gi_984052_emb_CAA61592_ (X89413) thioglucoside glucohydrolase [Arabidopsis thaliana]

Seq. No.	158425
Seq. ID	LIB3176-093-P1-K1-C7
Method	BLASTN
NCBI GI	g4567237
BLAST score	197
E value	1.0e-107
Match length	261
% identity	94
NCBI Description	Arabidopsis thaliana chromosome II BAC T22F11 genomic sequence, complete sequence

Seq. No.	158426
Seq. ID	LIB3176-093-P1-K1-C8
Method	BLASTN
NCBI GI	g3298532
BLAST score	125
E value	3.0e-64
Match length	129
% identity	99
NCBI Description	Arabidopsis thaliana chromosome II BAC T26B15 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	158427
Seq. ID	LIB3176-093-P1-K1-C9
Method	BLASTN
NCBI GI	g166761
BLAST score	140
E value	4.0e-73
Match length	188
% identity	94
NCBI Description	A.thaliana heat shock protein HSP70-1 gene, exon 1

Seq. No.	158428
Seq. ID	LIB3176-093-P1-K1-D12
Method	BLASTN
NCBI GI	g2182287
BLAST score	112
E value	1.0e-56
Match length	128
% identity	97
NCBI Description	Genomic sequence for Arabidopsis thaliana BAC T7N9, complete sequence [Arabidopsis thaliana]

Seq. No.	158429
Seq. ID	LIB3176-093-P1-K1-D3
Method	BLASTN
NCBI GI	g1483149
BLAST score	34
E value	8.0e-10
Match length	102
% identity	84

NCBI Description	Arabidopsis thaliana mRNA for monodehydroascorbate reductase, complete cds
Seq. No.	158430
Seq. ID	LIB3176-093-P1-K1-D4
Method	BLASTX
NCBI GI	g4741952
BLAST score	268
E value	5.0e-24
Match length	59
% identity	90
NCBI Description	(AF134126) Lhcb3 protein [Arabidopsis thaliana]
Seq. No.	158431
Seq. ID	LIB3176-093-P1-K1-D5
Method	BLASTN
NCBI GI	g16255
BLAST score	95
E value	2.0e-46
Match length	99
% identity	54
NCBI Description	A.thaliana A2 and A3 genes encoding elongation factor 1-alpha
Seq. No.	158432
Seq. ID	LIB3176-093-P1-K1-D7
Method	BLASTN
NCBI GI	g4455262
BLAST score	133
E value	5.0e-69
Match length	169
% identity	95
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F17L22 (ESSAII project)
Seq. No.	158433
Seq. ID	LIB3176-093-P1-K1-D8
Method	BLASTN
NCBI GI	g2191181
BLAST score	76
E value	6.0e-35
Match length	188
% identity	70
NCBI Description	Arabidopsis thaliana BAC TM021B04
Seq. No.	158434
Seq. ID	LIB3176-093-P1-K1-D9
Method	BLASTN
NCBI GI	g16562
BLAST score	59
E value	3.0e-25
Match length	59
% identity	100
NCBI Description	A.thaliana gene for tRNA-Phe (P-2-S)
Seq. No.	158435
Seq. ID	LIB3176-093-P1-K1-E2

Method	BLASTX
NCBI GI	g4775271
BLAST score	264
E value	2.0e-23
Match length	55
% identity	87
NCBI Description	(AJ131214) SF2/ASF-like splicing modulator Srp30, variant 1 [Arabidopsis thaliana]

Seq. No.	158436
Seq. ID	LIB3176-093-P1-K1-E3
Method	BLASTX
NCBI GI	g4539297
BLAST score	91
E value	2.0e-27
Match length	103
% identity	66
NCBI Description	(AL049480) putative pathogenesis-related protein [Arabidopsis thaliana]

Seq. No.	158437
Seq. ID	LIB3176-093-P1-K1-E4
Method	BLASTX
NCBI GI	g3676762
BLAST score	149
E value	4.0e-10
Match length	43
% identity	74
NCBI Description	(AF087136) RS6/L7A ribosomal protein homolog [Schizosaccharomyces pombe]

Seq. No.	158438
Seq. ID	LIB3176-093-P1-K1-E5
Method	BLASTN
NCBI GI	g2264312
BLAST score	184
E value	3.0e-99
Match length	250
% identity	92
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MOK16, complete sequence [Arabidopsis thaliana]

Seq. No.	158439
Seq. ID	LIB3176-093-P1-K1-E7
Method	BLASTN
NCBI GI	g16347
BLAST score	94
E value	1.0e-45
Match length	189
% identity	87
NCBI Description	A.thaliana mRNA for inorganic pyrophosphatase

Seq. No.	158440
Seq. ID	LIB3176-093-P1-K1-E8
Method	BLASTN
NCBI GI	g16523
BLAST score	190

E value	1.0e-103
Match length	211
% identity	97
NCBI Description	A.thaliana STP4 mRNA

Seq. No.	158441
Seq. ID	LIB3176-093-P1-K1-E9
Method	BLASTN
NCBI GI	g2864607
BLAST score	32
E value	2.0e-09
Match length	55
% identity	91
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F10M6 (ESSAII project)

Seq. No.	158442
Seq. ID	LIB3176-093-P1-K1-F10
Method	BLASTX
NCBI GI	g2499606
BLAST score	307
E value	2.0e-28
Match length	60
% identity	95
NCBI Description	MITOGEN-ACTIVATED PROTEIN KINASE HOMOLOG 2 (MAP KINASE 2) (ATMPK2) >gi_533281_dbj_BAA03536_ (D14714) ATMPK2 [Arabidopsis thaliana]

Seq. No.	158443
Seq. ID	LIB3176-093-P1-K1-F3
Method	BLASTN
NCBI GI	g3659491
BLAST score	417
E value	0.0e+00
Match length	451
% identity	98
NCBI Description	Sequence of BAC T22H22 from Arabidopsis thaliana chromosome 1, complete sequence [Arabidopsis thaliana]

Seq. No.	158444
Seq. ID	LIB3176-093-P1-K1-F5
Method	BLASTN
NCBI GI	g2289094
BLAST score	95
E value	2.0e-46
Match length	127
% identity	94
NCBI Description	Arabidopsis thaliana WD-40 repeat protein (AtArcA) mRNA, complete cds

Seq. No.	158445
Seq. ID	LIB3176-093-P1-K1-F7
Method	BLASTN
NCBI GI	g4371278
BLAST score	117
E value	2.0e-59
Match length	196

% identity	89
NCBI Description	Arabidopsis thaliana chromosome II BAC T2N18 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	158446
Seq. ID	LIB3176-093-P1-K1-F8
Method	BLASTX
NCBI GI	g2160158
BLAST score	537
E value	4.0e-55
Match length	102
% identity	95
NCBI Description	(AC000132) Similar to elongation factor 1-gamma (gb_EF1G_XENLA). ESTs gb_T20564,gb_T45940,gb_T04527 come from this gene. [Arabidopsis thaliana]

Seq. No.	158447
Seq. ID	LIB3176-093-P1-K1-G1
Method	BLASTX
NCBI GI	g1246768
BLAST score	245
E value	2.0e-21
Match length	55
% identity	82
NCBI Description	(X94299) glutamate--ammonia ligase [Lotus japonicus]

Seq. No.	158448
Seq. ID	LIB3176-093-P1-K1-G12
Method	BLASTX
NCBI GI	g2462929
BLAST score	491
E value	8.0e-50
Match length	99
% identity	97
NCBI Description	(Y12295) glutathione transferase [Arabidopsis thaliana]

Seq. No.	158449
Seq. ID	LIB3176-093-P1-K1-G2
Method	BLASTN
NCBI GI	g3702730
BLAST score	66
E value	9.0e-29
Match length	97
% identity	93
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MAB16, complete sequence [Arabidopsis thaliana]

Seq. No.	158450
Seq. ID	LIB3176-093-P1-K1-G3
Method	BLASTN
NCBI GI	g4115370
BLAST score	190
E value	1.0e-103
Match length	231
% identity	95
NCBI Description	Arabidopsis thaliana chromosome II BAC F27D4 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	158451
Seq. ID	LIB3176-093-P1-K1-G7
Method	BLASTN
NCBI GI	g3928074
BLAST score	106
E value	9.0e-53
Match length	134
% identity	95
NCBI Description	Arabidopsis thaliana chromosome II BAC T7F6 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	158452
Seq. ID	LIB3176-093-P1-K1-G8
Method	BLASTX
NCBI GI	g2497486
BLAST score	307
E value	2.0e-28
Match length	69
% identity	87
NCBI Description	URIDYLATE KINASE (UK) (URIDINE MONOPHOSPHATE KINASE) (UMP KINASE) >gi_2121275 (AF000147) UMP/CMP kinase [Arabidopsis thaliana]

Seq. No.	158453
Seq. ID	LIB3176-093-P1-K1-G9
Method	BLASTX
NCBI GI	g3044212
BLAST score	593
E value	9.0e-62
Match length	111
% identity	99
NCBI Description	(AF057043) acyl-CoA oxidase [Arabidopsis thaliana]

Seq. No.	158454
Seq. ID	LIB3176-093-P1-K1-H1
Method	BLASTN
NCBI GI	g3522932
BLAST score	270
E value	1.0e-150
Match length	287
% identity	98
NCBI Description	Arabidopsis thaliana chromosome II BAC F14M4 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	158455
Seq. ID	LIB3176-093-P1-K1-H10
Method	BLASTN
NCBI GI	g4689466
BLAST score	76
E value	1.0e-34
Match length	131
% identity	98
NCBI Description	Arabidopsis thaliana chromosome II BAC T23O15 genomic sequence, complete sequence

Seq. No.	158456

Seq. ID	LIB3176-093-P1-K1-H12
Method	BLASTX
NCBI GI	g3157937
BLAST score	326
E value	6.0e-31
Match length	83
% identity	90
NCBI Description	(AC002131) Identical to aspartic proteinase cDNA gb_U51036 from A. thaliana. ESTs gb_N96313, gb_T21893, gb_R30158, gb_T21482, gb_T43650, gb_R64749, gb_R65157, gb_T88269, gb_T44552, gb_T22542, gb_T76533, gb_T44350, gb_Z34591, gb_AA728734, gb

Seq. No.	158457
Seq. ID	LIB3176-093-P1-K1-H2
Method	BLASTN
NCBI GI	g2618602
BLAST score	79
E value	2.0e-36
Match length	324
% identity	96
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MSJ1, complete sequence [Arabidopsis thaliana]

Seq. No.	158458
Seq. ID	LIB3176-093-P1-K1-H3
Method	BLASTN
NCBI GI	g414339
BLAST score	104
E value	8.0e-52
Match length	132
% identity	95
NCBI Description	A.thaliana rd19A gene for thiol protease, exon 1, exon 2 and exon

Seq. No.	158459
Seq. ID	LIB3176-093-P1-K1-H4
Method	BLASTN
NCBI GI	g343517
BLAST score	78
E value	7.0e-36
Match length	172
% identity	90
NCBI Description	Tobacco (N.tabacum) chloroplast Met-tRNA, Val-tRNA-uac and flanks

Seq. No.	158460
Seq. ID	LIB3176-093-P1-K1-H7
Method	BLASTX
NCBI GI	g1346526
BLAST score	308
E value	2.0e-28
Match length	67
% identity	85
NCBI Description	S-ADENOSYLMETHIONINE SYNTHETASE 2 (METHIONINE ADENOSYLTRANSFERASE 2) (ADOMET SYNTHETASE 2) >gi_1076533_pir__S52218 methionine adenosyltransferase (EC

2.5.1.6) - garden pea >gi_609225_emb_CAA57581_ (X82077) methionine adenosyltransferase [Pisum sativum] >gi_609559 (L36681) S-adenosylmethionine synthase [Pisum sativum]

Seq. No.	158461
Seq. ID	LIB3176-093-P1-K1-H9
Method	BLASTX
NCBI GI	g2129729
BLAST score	531
E value	2.0e-54
Match length	112
% identity	93
NCBI Description	senescence-associated protein sen1 - Arabidopsis thaliana >gi_1046270 (U26945) senescence-associated protein [Arabidopsis thaliana] >gi_3367595_emb_CAA20047_ (AL031135) senescence-associated protein sen1 [Arabidopsis thaliana] >gi_3805843_emb_CAA21463_ (AL031986) senescence-associated protein sen1 [Arabidopsis thaliana]

Seq. No.	158462
Seq. ID	LIB3176-094-P1-K1-A1
Method	BLASTX
NCBI GI	g4567286
BLAST score	394
E value	1.0e-38
Match length	78
% identity	97
NCBI Description	(AC006841) putative coatomer alpha subunit [Arabidopsis thaliana]

Seq. No.	158463
Seq. ID	LIB3176-094-P1-K1-A10
Method	BLASTN
NCBI GI	g4512656
BLAST score	46
E value	3.0e-17
Match length	58
% identity	95
NCBI Description	Arabidopsis thaliana chromosome II BAC F7D19 genomic sequence, complete sequence

Seq. No.	158464
Seq. ID	LIB3176-094-P1-K1-A11
Method	BLASTX
NCBI GI	g4587542
BLAST score	371
E value	4.0e-36
Match length	75
% identity	91
NCBI Description	(AC006577) Belongs to the PF_00657 Lipase/Acylhydrolase with GDSL-motif family. ESTs gb_T45815, gb_T45130 and gb_Z38046 come from this gene. [Arabidopsis thaliana]

Seq. No.	158465
Seq. ID	LIB3176-094-P1-K1-A3
Method	BLASTN
NCBI GI	g4263774

BLAST score	284
E value	1.0e-159
Match length	343
% identity	99
NCBI Description	Arabidopsis thaliana chromosome II BAC T20F21 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	158466
Seq. ID	LIB3176-094-P1-K1-A6
Method	BLASTX
NCBI GI	g2244749
BLAST score	211
E value	2.0e-17
Match length	46
% identity	89
NCBI Description	(Z97335) hydroxymethyltransferase [Arabidopsis thaliana]

Seq. No.	158467
Seq. ID	LIB3176-094-P1-K1-A7
Method	BLASTX
NCBI GI	g166867
BLAST score	535
E value	7.0e-55
Match length	125
% identity	84
NCBI Description	(J05216) ribosomal protein S11 (probable start codon at bp 67) [Arabidopsis thaliana]

Seq. No.	158468
Seq. ID	LIB3176-094-P1-K1-A8
Method	BLASTX
NCBI GI	g4581146
BLAST score	268
E value	6.0e-24
Match length	68
% identity	82
NCBI Description	(AC006919) putative fructose-bisphosphate aldolase, cytoplasmic [Arabidopsis thaliana]

Seq. No.	158469
Seq. ID	LIB3176-094-P1-K1-A9
Method	BLASTX
NCBI GI	g1350965
BLAST score	263
E value	2.0e-23
Match length	56
% identity	89
NCBI Description	40S RIBOSOMAL PROTEIN S23 (S12)

Seq. No.	158470
Seq. ID	LIB3176-094-P1-K1-B1
Method	BLASTN
NCBI GI	g4106537
BLAST score	219
E value	1.0e-120
Match length	247
% identity	97

NCBI Description	Arabidopsis thaliana gamma-tocopherol methyltransferase (g-TMT) mRNA, nuclear gene encoding plastid protein, complete cds
Seq. No.	158471
Seq. ID	LIB3176-094-P1-K1-B10
Method	BLASTX
NCBI GI	g3023848
BLAST score	314
E value	3.0e-29
Match length	70
% identity	62
NCBI Description	GUANINE NUCLEOTIDE-BINDING PROTEIN BETA SUBUNIT-LIKE PROTEIN (WD-40 REPEAT AUXIN-DEPENDENT PROTEIN ARCA) >gi_2289095 (U77381) WD-40 repeat protein [Arabidopsis thaliana]
Seq. No.	158472
Seq. ID	LIB3176-094-P1-K1-B12
Method	BLASTX
NCBI GI	g3776564
BLAST score	512
E value	3.0e-52
Match length	113
% identity	90
NCBI Description	(AC005388) Similar to hypothetical protein T1D16.16 gi_3075397 from A. thaliana BAC gb_AC004484. [Arabidopsis thaliana]
Seq. No.	158473
Seq. ID	LIB3176-094-P1-K1-B2
Method	BLASTX
NCBI GI	g4106538
BLAST score	473
E value	8.0e-48
Match length	94
% identity	94
NCBI Description	(AF104220) gamma-tocopherol methyltransferase [Arabidopsis thaliana]
Seq. No.	158474
Seq. ID	LIB3176-094-P1-K1-B3
Method	BLASTN
NCBI GI	g3482964
BLAST score	209
E value	1.0e-114
Match length	278
% identity	100
NCBI Description	Arabidopsis thaliana DNA chromosome 2, BAC clone F13D4 (ESSAII project)
Seq. No.	158475
Seq. ID	LIB3176-094-P1-K1-B5
Method	BLASTX
NCBI GI	g1352347
BLAST score	389
E value	6.0e-38

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Match length	78
% identity	99
NCBI Description	ELONGATION FACTOR 1-BETA A1 (EF-1-BETA) >gi_480620_pir__S37103 translation elongation factor eEF-1 beta-A1 chain - Arabidopsis thaliana (cv. Colombia) >gi_398608_emb_CAA52751_ (X74733) elongation factor-1 beta A1 [Arabidopsis thaliana]
Seq. No.	158476
Seq. ID	LIB3176-094-P1-K1-B6
Method	BLASTN
NCBI GI	g3927822
BLAST score	106
E value	1.0e-52
Match length	242
% identity	98
NCBI Description	Arabidopsis thaliana chromosome II BAC F8N16 genomic sequence, complete sequence [Arabidopsis thaliana]
Seq. No.	158477
Seq. ID	LIB3176-094-P1-K1-B7
Method	BLASTN
NCBI GI	g2738247
BLAST score	91
E value	6.0e-44
Match length	134
% identity	93
NCBI Description	Arabidopsis thaliana cobalamin-independent methionine synthase (ATCIMS) mRNA, complete cds
Seq. No.	158478
Seq. ID	LIB3176-094-P1-K1-C1
Method	BLASTX
NCBI GI	g3128228
BLAST score	479
E value	2.0e-48
Match length	94
% identity	95
NCBI Description	(AC004077) putative ribosomal protein L18A [Arabidopsis thaliana] >gi_3337376 (AC004481) putative ribosomal protein L18A [Arabidopsis thaliana]
Seq. No.	158479
Seq. ID	LIB3176-094-P1-K1-C2
Method	BLASTN
NCBI GI	g2979540
BLAST score	84
E value	1.0e-39
Match length	196
% identity	99
NCBI Description	Arabidopsis thaliana chromosome II BAC F17K2 genomic sequence, complete sequence [Arabidopsis thaliana]
Seq. No.	158480
Seq. ID	LIB3176-094-P1-K1-C3
Method	BLASTX
NCBI GI	g3122914

BLAST score 310
E value 5.0e-29
Match length 60
% identity 97
NCBI Description VALYL-TRNA SYNTHETASE (VALINE--TRNA LIGASE) (VALRS) >gi_1890130 (U89986) valyl tRNA synthetase [Arabidopsis thaliana]

Seq. No. 158481
Seq. ID LIB3176-094-P1-K1-C4
Method BLASTX
NCBI GI g1170373
BLAST score 57
E value 7.0e-34
Match length 79
% identity 97
NCBI Description HEAT SHOCK COGNATE 70 KD PROTEIN 1 >gi_1072473_pir__S46302 heat shock cognate protein 70-1 - Arabidopsis thaliana >gi_397482_emb_CAA52684_ (X74604) heat shock protein 70 cognate [Arabidopsis thaliana]

Seq. No. 158482
Seq. ID LIB3176-094-P1-K1-C7
Method BLASTN
NCBI GI g4512690
BLAST score 108
E value 6.0e-54
Match length 184
% identity 96
NCBI Description Arabidopsis thaliana chromosome II BAC F11A3 genomic sequence, complete sequence

Seq. No. 158483
Seq. ID LIB3176-094-P1-K1-C8
Method BLASTX
NCBI GI g267081
BLAST score 245
E value 3.0e-21
Match length 51
% identity 90
NCBI Description TUBULIN BETA-7 CHAIN >gi_320188_pir__JQ1591 tubulin beta-7 chain - Arabidopsis thaliana >gi_166906 (M84704) beta-7 tubulin [Arabidopsis thaliana] >gi_3980381 (AC004561) tubulin beta-7 chain [Arabidopsis thaliana]

Seq. No. 158484
Seq. ID LIB3176-094-P1-K1-C9
Method BLASTN
NCBI GI g3150006
BLAST score 182
E value 4.0e-98
Match length 202
% identity 66
NCBI Description CIC5B11.1 check: 4870 from: 1 to: 167234, complete sequence [Arabidopsis thaliana]

Seq. No. 158485

Seq. ID	LIB3176-094-P1-K1-D10
Method	BLASTN
NCBI GI	g1709235
BLAST score	52
E value	1.0e-20
Match length	60
% identity	97
NCBI Description	Arabidopsis thaliana kinase associated protein phosphatase mRNA, complete cds

Seq. No.	158486
Seq. ID	LIB3176-094-P1-K1-D11
Method	BLASTN
NCBI GI	g4376087
BLAST score	237
E value	1.0e-131
Match length	249
% identity	99
NCBI Description	Arabidopsis thaliana DNA chromosome 4, ESSA I AP2 contig fragment No

Seq. No.	158487
Seq. ID	LIB3176-094-P1-K1-D12
Method	BLASTX
NCBI GI	g1363489
BLAST score	165
E value	5.0e-12
Match length	31
% identity	100
NCBI Description	thioglucosidase (EC 3.2.3.1) 3D precursor - Arabidopsis thaliana >gi_984052_emb_CAA61592_ (X89413) thioglucoside glucohydrolase [Arabidopsis thaliana]

Seq. No.	158488
Seq. ID	LIB3176-094-P1-K1-D2
Method	BLASTX
NCBI GI	g4587542
BLAST score	172
E value	1.0e-12
Match length	34
% identity	100
NCBI Description	(AC006577) Belongs to the PF_00657 Lipase/Acylhydrolase with GDSL-motif family. ESTs gb_T45815, gb_T45130 and gb_Z38046 come from this gene. [Arabidopsis thaliana]

Seq. No.	158489
Seq. ID	LIB3176-094-P1-K1-D3
Method	BLASTN
NCBI GI	g3164131
BLAST score	150
E value	6.0e-79
Match length	158
% identity	99
NCBI Description	Arabidopsis thaliana mRNA for cytochrome P450 monooxygenase, complete cds, clone P450-12

Seq. No.	158490

Seq. ID	LIB3176-094-P1-K1-D4
Method	BLASTN
NCBI GI	g1707363
BLAST score	38
E value	1.0e-12
Match length	64
% identity	92
NCBI Description	A.thaliana mRNA for AATP2

Seq. No.	158491
Seq. ID	LIB3176-094-P1-K1-D5
Method	BLASTX
NCBI GI	g4567207
BLAST score	191
E value	2.0e-15
Match length	52
% identity	92
NCBI Description	(AC007168) unknown protein [Arabidopsis thaliana]

Seq. No.	158492
Seq. ID	LIB3176-094-P1-K1-D6
Method	BLASTX
NCBI GI	g4582468
BLAST score	159
E value	3.0e-11
Match length	39
% identity	85
NCBI Description	(AC007071) putative 40S ribosomal protein; contains C-terminal domain [Arabidopsis thaliana]

Seq. No.	158493
Seq. ID	LIB3176-094-P1-K1-D8
Method	BLASTN
NCBI GI	g4309683
BLAST score	79
E value	8.0e-37
Match length	86
% identity	98
NCBI Description	Arabidopsis thaliana chromosome 1 BAC T31J12 sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	158494
Seq. ID	LIB3176-094-P1-K1-D9
Method	BLASTN
NCBI GI	g2317728
BLAST score	112
E value	2.0e-56
Match length	140
% identity	96
NCBI Description	Arabidopsis thaliana reversibly glycosylated polypeptide-1 (AtRGP) mRNA, complete cds

Seq. No.	158495
Seq. ID	LIB3176-094-P1-K1-E11
Method	BLASTN
NCBI GI	g3046853
BLAST score	94

E value	1.0e-45
Match length	147
% identity	99
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MRA19, complete sequence [Arabidopsis thaliana]

Seq. No.	158496
Seq. ID	LIB3176-094-P1-K1-E12
Method	BLASTX
NCBI GI	g2129533
BLAST score	583
E value	1.0e-60
Match length	119
% identity	97
NCBI Description	adenine nucleotide translocase - Arabidopsis thaliana >gi_1051109_emb_CAA89201_ (Z49227) adenine nucleotide translocase [Arabidopsis thaliana]

Seq. No.	158497
Seq. ID	LIB3176-094-P1-K1-E2
Method	BLASTN
NCBI GI	g166829
BLAST score	31
E value	1.0e-08
Match length	61
% identity	84
NCBI Description	Arabidopsis thaliana proteasome (PSM30) gene, complete cds

Seq. No.	158498
Seq. ID	LIB3176-094-P1-K1-E5
Method	BLASTN
NCBI GI	g313837
BLAST score	159
E value	2.0e-84
Match length	175
% identity	98
NCBI Description	A.thaliana gene for hemC

Seq. No.	158499
Seq. ID	LIB3176-094-P1-K1-E6
Method	BLASTN
NCBI GI	g4760411
BLAST score	238
E value	1.0e-131
Match length	258
% identity	98
NCBI Description	Arabidopsis thaliana chromosome 1 BAC F25C20 sequence, complete sequence

Seq. No.	158500
Seq. ID	LIB3176-094-P1-K1-E7
Method	BLASTN
NCBI GI	g3212846
BLAST score	101
E value	6.0e-50
Match length	152
% identity	97

NCBI Description	Arabidopsis thaliana chromosome II BAC F6E13 genomic sequence, complete sequence [Arabidopsis thaliana]
Seq. No.	158501
Seq. ID	LIB3176-094-P1-K1-E8
Method	BLASTN
NCBI GI	g553039
BLAST score	38
E value	8.0e-13
Match length	63
% identity	87
NCBI Description	Arabidopsis thaliana GF14 mRNA, complete cds
Seq. No.	158502
Seq. ID	LIB3176-094-P1-K1-E9
Method	BLASTN
NCBI GI	g2341023
BLAST score	84
E value	6.0e-40
Match length	108
% identity	95
NCBI Description	Sequence of BAC F19P19 from Arabidopsis thaliana chromosome 1, complete sequence [Arabidopsis thaliana]
Seq. No.	158503
Seq. ID	LIB3176-094-P1-K1-F1
Method	BLASTX
NCBI GI	g1651865
BLAST score	175
E value	1.0e-12
Match length	91
% identity	48
NCBI Description	(D90900) hypothetical protein [Synechocystis sp.]
Seq. No.	158504
Seq. ID	LIB3176-094-P1-K1-F11
Method	BLASTX
NCBI GI	g1363489
BLAST score	373
E value	4.0e-36
Match length	69
% identity	99
NCBI Description	thioglucosidase (EC 3.2.3.1) 3D precursor - Arabidopsis thaliana >gi_984052_emb_CAA61592_ (X89413) thioglucoside glucohydrolase [Arabidopsis thaliana]
Seq. No.	158505
Seq. ID	LIB3176-094-P1-K1-F3
Method	BLASTX
NCBI GI	g3292824
BLAST score	224
E value	6.0e-19
Match length	61
% identity	69
NCBI Description	(AL031018) putative protein [Arabidopsis thaliana]
Seq. No.	158506

Seq. ID	LIB3176-094-P1-K1-F4
Method	BLASTX
NCBI GI	g4538963
BLAST score	60
E value	1.0e-14
Match length	49
% identity	78
NCBI Description	(AL049488) chlorophyll a/b-binding protein-like [Arabidopsis thaliana] >gi_4741958_gb_AAD28776.1_AF134129_1 (AF134129) Lhcb5 protein [Arabidopsis thaliana]

Seq. No.	158507
Seq. ID	LIB3176-094-P1-K1-G10
Method	BLASTX
NCBI GI	g2738248
BLAST score	440
E value	5.0e-44
Match length	85
% identity	99
NCBI Description	(U97200) cobalamin-independent methionine synthase [Arabidopsis thaliana]

Seq. No.	158508
Seq. ID	LIB3176-094-P1-K1-G11
Method	BLASTX
NCBI GI	g2244970
BLAST score	613
E value	7.0e-64
Match length	148
% identity	83
NCBI Description	(Z97340) hypothetical protein [Arabidopsis thaliana] >gi_2326365_emb_CAA74765_ (Y14423) putative cell wall protein [Arabidopsis thaliana]

Seq. No.	158509
Seq. ID	LIB3176-094-P1-K1-G2
Method	BLASTN
NCBI GI	g4559344
BLAST score	129
E value	3.0e-66
Match length	233
% identity	5
NCBI Description	Arabidopsis thaliana chromosome II BAC F27C12 genomic sequence, complete sequence

Seq. No.	158510
Seq. ID	LIB3176-094-P1-K1-G3
Method	BLASTX
NCBI GI	g1946361
BLAST score	197
E value	8.0e-16
Match length	54
% identity	69
NCBI Description	(U93215) C3HC4 zinc finger protein isolog [Arabidopsis thaliana]

Seq. No.	158511

Seq. ID	LIB3176-094-P1-K1-G5
Method	BLASTN
NCBI GI	g4490701
BLAST score	70
E value	1.0e-31
Match length	133
% identity	98
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone T24A18 (ESSA project)

Seq. No.	158512
Seq. ID	LIB3176-094-P1-K1-G8
Method	BLASTN
NCBI GI	g2760167
BLAST score	89
E value	2.0e-42
Match length	216
% identity	92
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MCO15, complete sequence [Arabidopsis thaliana]

Seq. No.	158513
Seq. ID	LIB3176-094-P1-K1-G9
Method	BLASTN
NCBI GI	g4678315
BLAST score	112
E value	1.0e-56
Match length	131
% identity	97
NCBI Description	Arabidopsis thaliana DNA chromosome 3, BAC clone T17F15 (ESSA project)

Seq. No.	158514
Seq. ID	LIB3176-094-P1-K1-H1
Method	BLASTN
NCBI GI	g3201608
BLAST score	43
E value	1.0e-15
Match length	75
% identity	89
NCBI Description	Arabidopsis thaliana chromosome II BAC F7F1 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	158515
Seq. ID	LIB3176-094-P1-K1-H10
Method	BLASTX
NCBI GI	g267069
BLAST score	269
E value	2.0e-26
Match length	61
% identity	98
NCBI Description	TUBULIN ALPHA-2/ALPHA-4 CHAIN >gi_320183_pir__JQ1594 tubulin alpha chain - Arabidopsis thaliana >gi_166914 (M84696) apha-2 tubulin [Arabidopsis thaliana] >gi_166916 (M84697) alpha-4 tubulin [Arabidopsis thaliana]

Seq. No.	158516

Seq. ID	LIB3176-094-P1-K1-H11
Method	BLASTX
NCBI GI	g1710525
BLAST score	206
E value	1.0e-16
Match length	47
% identity	85
NCBI Description	60S RIBOSOMAL PROTEIN L26

Seq. No.	158517
Seq. ID	LIB3176-094-P1-K1-H12
Method	BLASTX
NCBI GI	g1175010
BLAST score	356
E value	4.0e-34
Match length	83
% identity	86
NCBI Description	PLASMA MEMBRANE INTRINSIC PROTEIN 1A >gi_629540_pir__S44082 plasma membrane intrinsic protein 1a - Arabidopsis thaliana >gi_472873_emb_CAA53475_ (X75881) plasma membrane intrinsic protein 1a [Arabidopsis thaliana]

Seq. No.	158518
Seq. ID	LIB3176-094-P1-K1-H3
Method	BLASTN
NCBI GI	g4741961
BLAST score	254
E value	1.0e-141
Match length	258
% identity	100
NCBI Description	Arabidopsis thaliana PsbS protein (PsbS) mRNA, complete cds

Seq. No.	158519
Seq. ID	LIB3176-094-P1-K1-H5
Method	BLASTN
NCBI GI	g4519191
BLAST score	67
E value	5.0e-30
Match length	79
% identity	96
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K9P8, complete sequence

Seq. No.	158520
Seq. ID	LIB3176-094-P1-K1-H9
Method	BLASTX
NCBI GI	g232033
BLAST score	221
E value	1.0e-18
Match length	71
% identity	56
NCBI Description	ELONGATION FACTOR 1 BETA' >gi_479830_pir__S35501 translation elongation factor eEF-1 beta' chain - wheat >gi_218341_dbj_BAA02436_ (D13147) elongation factor 1 beta' [Triticum aestivum]

Seq. No.	158521

Seq. ID	LIB3176-095-P1-K1-A10
Method	BLASTN
NCBI GI	g2961335
BLAST score	144
E value	2.0e-75
Match length	237
% identity	94
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F1N20 (ESSAII project)

Seq. No.	158522
Seq. ID	LIB3176-095-P1-K1-A11
Method	BLASTN
NCBI GI	g4220633
BLAST score	111
E value	2.0e-55
Match length	434
% identity	99
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K7J8, complete sequence [Arabidopsis thaliana]

Seq. No.	158523
Seq. ID	LIB3176-095-P1-K1-A2
Method	BLASTX
NCBI GI	g3122673
BLAST score	311
E value	5.0e-29
Match length	59
% identity	98
NCBI Description	60S RIBOSOMAL PROTEIN L15 >gi_2245027_emb_CAB10447_ (Z97341) ribosomal protein [Arabidopsis thaliana]

Seq. No.	158524
Seq. ID	LIB3176-095-P1-K1-A3
Method	BLASTN
NCBI GI	g3449317
BLAST score	45
E value	2.0e-16
Match length	82
% identity	96
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MKM21, complete sequence [Arabidopsis thaliana]

Seq. No.	158525
Seq. ID	LIB3176-095-P1-K1-A4
Method	BLASTX
NCBI GI	g1429209
BLAST score	412
E value	1.0e-40
Match length	87
% identity	97
NCBI Description	(X99111) beta-fructosidase [Arabidopsis thaliana]

Seq. No.	158526
Seq. ID	LIB3176-095-P1-K1-A5
Method	BLASTX
NCBI GI	g2829899

BLAST score	62
E value	1.0e-15
Match length	93
% identity	55
NCBI Description	(AC002311) similar to ripening-induced protein, gp_AJ001449_2465015 and major#latex protein, gp_X91961_1107495 [Arabidopsis thaliana]

Seq. No.	158527
Seq. ID	LIB3176-095-P1-K1-A9
Method	BLASTX
NCBI GI	g3123188
BLAST score	477
E value	3.0e-48
Match length	96
% identity	96
NCBI Description	CATALASE 3 >gi_2347178 (U43147) catalase 3 [Arabidopsis thaliana] >gi_2511726 (AF021937) catalase 3 [Arabidopsis thaliana]

Seq. No.	158528
Seq. ID	LIB3176-095-P1-K1-B10
Method	BLASTX
NCBI GI	g3236248
BLAST score	278
E value	5.0e-25
Match length	84
% identity	68
NCBI Description	(AC004684) unknown protein [Arabidopsis thaliana]

Seq. No.	158529
Seq. ID	LIB3176-095-P1-K1-B11
Method	BLASTN
NCBI GI	g2833627
BLAST score	53
E value	3.0e-21
Match length	61
% identity	97
NCBI Description	Arabidopsis thaliana chromosome 1 BAC F17O7 complete sequence [Arabidopsis thaliana]

Seq. No.	158530
Seq. ID	LIB3176-095-P1-K1-B2
Method	BLASTN
NCBI GI	g4582444
BLAST score	126
E value	8.0e-65
Match length	176
% identity	93
NCBI Description	Arabidopsis thaliana chromosome II BAC T9H9 genomic sequence, complete sequence

Seq. No.	158531
Seq. ID	LIB3176-095-P1-K1-B4
Method	BLASTN
NCBI GI	g4185120
BLAST score	57

E value	9.0e-24
Match length	57
% identity	50
NCBI Description	Arabidopsis thaliana chromosome 1 BAC F5F19 sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	158532
Seq. ID	LIB3176-095-P1-K1-B7
Method	BLASTX
NCBI GI	g4455214
BLAST score	200
E value	1.0e-25
Match length	80
% identity	83
NCBI Description	(AL035440) putative dihydrolipoamide succinyltransferase [Arabidopsis thaliana]

Seq. No.	158533
Seq. ID	LIB3176-095-P1-K1-B8
Method	BLASTX
NCBI GI	g1480347
BLAST score	183
E value	1.0e-13
Match length	90
% identity	46
NCBI Description	(X99419) ferrodoxin NADP oxidoreductase [Pisum sativum]

Seq. No.	158534
Seq. ID	LIB3176-095-P1-K1-B9
Method	BLASTX
NCBI GI	g544242
BLAST score	349
E value	2.0e-33
Match length	81
% identity	89
NCBI Description	ENDOPLASMIN HOMOLOG PRECURSOR (GRP94 HOMOLOG) >gi_485498_pir__S33533 heat shock protein 90 homolog precursor - barley >gi_22652_emb_CAA48143_ (X67960) GRP94 homologue [Hordeum vulgare]

Seq. No.	158535
Seq. ID	LIB3176-095-P1-K1-C1
Method	BLASTN
NCBI GI	g1145694
BLAST score	86
E value	5.0e-41
Match length	130
% identity	97
NCBI Description	Arabidopsis thaliana actin (ACT3) gene, complete cds

Seq. No.	158536
Seq. ID	LIB3176-095-P1-K1-C12
Method	BLASTX
NCBI GI	g2117424
BLAST score	579
E value	6.0e-60
Match length	115

% identity	98
NCBI Description	thioredoxin - Arabidopsis thaliana >gi_992962_emb_CAA84611_ (Z35474) thioredoxin [Arabidopsis thaliana] >gi_1388076 (U35640) thioredoxin h [Arabidopsis thaliana]

Seq. No.	158537
Seq. ID	LIB3176-095-P1-K1-C2
Method	BLASTX
NCBI GI	g4704730
BLAST score	173
E value	6.0e-13
Match length	50
% identity	72
NCBI Description	(AF121355) peroxiredoxin TPx1 [Arabidopsis thaliana]

Seq. No.	158538
Seq. ID	LIB3176-095-P1-K1-C9
Method	BLASTX
NCBI GI	g2244750
BLAST score	56
E value	3.0e-13
Match length	65
% identity	67
NCBI Description	(Z97335) adenosylhomocysteinase [Arabidopsis thaliana] >gi_3088579 (AF059581) S-adenosyl-L-homocysteine hydrolase [Arabidopsis thaliana]

Seq. No.	158539
Seq. ID	LIB3176-095-P1-K1-D10
Method	BLASTN
NCBI GI	g4713943
BLAST score	40
E value	1.0e-13
Match length	128
% identity	83
NCBI Description	Arabidopsis thaliana chromosome 1 BAC T8K14 sequence, complete sequence

Seq. No.	158540
Seq. ID	LIB3176-095-P1-K1-D11
Method	BLASTN
NCBI GI	g1946354
BLAST score	112
E value	2.0e-56
Match length	128
% identity	97
NCBI Description	Arabidopsis thaliana chromosome II BAC T06B20 genomic sequence, complete sequence

Seq. No.	158541
Seq. ID	LIB3176-095-P1-K1-D12
Method	BLASTX
NCBI GI	g2342722
BLAST score	342
E value	3.0e-32
Match length	84
% identity	80

NCBI Description (AC002341) unknown protein [Arabidopsis thaliana]

Seq. No. 158542
Seq. ID LIB3176-095-P1-K1-D4
Method BLASTN
NCBI GI g2143226
BLAST score 38
E value 8.0e-13
Match length 50
% identity 94
NCBI Description Brassica napus mRNA for glyoxysomal isocitrate lyase

Seq. No. 158543
Seq. ID LIB3176-095-P1-K1-D7
Method BLASTX
NCBI GI g4567303
BLAST score 190
E value 6.0e-15
Match length 39
% identity 95
NCBI Description (AC005956) unknown protein [Arabidopsis thaliana]

Seq. No. 158544
Seq. ID LIB3176-095-P1-K1-D9
Method BLASTX
NCBI GI g1363489
BLAST score 352
E value 7.0e-34
Match length 74
% identity 95
NCBI Description thioglucosidase (EC 3.2.3.1) 3D precursor - Arabidopsis thaliana >gi_984052_emb_CAA61592_ (X89413) thioglucoside glucohydrolase [Arabidopsis thaliana]

Seq. No. 158545
Seq. ID LIB3176-095-P1-K1-E10
Method BLASTX
NCBI GI g1170503
BLAST score 164
E value 6.0e-12
Match length 53
% identity 70
NCBI Description EUKARYOTIC INITIATION FACTOR 4A-1 (EIF-4A-1) >gi_322503_pir__JC1452 translation initiation factor eIF-4A1 - Arabidopsis thaliana >gi_16554_emb_CAA46188_ (X65052) eukaryotic translation initiation factor 4A-1 [Arabidopsis thaliana]

Seq. No. 158546
Seq. ID LIB3176-095-P1-K1-E12
Method BLASTN
NCBI GI g3510345
BLAST score 281
E value 1.0e-157
Match length 377
% identity 94
NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:

MNJ8, complete sequence [Arabidopsis thaliana]

Seq. No.	158547
Seq. ID	LIB3176-095-P1-K1-E2
Method	BLASTN
NCBI GI	g3088578
BLAST score	39
E value	3.0e-13
Match length	49
% identity	94
NCBI Description	Arabidopsis thaliana S-adenosyl-L-homocysteine hydrolase (SAHH) mRNA, complete cds

Seq. No.	158548
Seq. ID	LIB3176-095-P1-K1-E3
Method	BLASTN
NCBI GI	g3098611
BLAST score	45
E value	8.0e-17
Match length	57
% identity	95
NCBI Description	Arabidopsis thaliana senescence associated gene (SAG20) mRNA, partial cds

Seq. No.	158549
Seq. ID	LIB3176-095-P1-K1-E4
Method	BLASTN
NCBI GI	g2760168
BLAST score	35
E value	3.0e-10
Match length	106
% identity	83
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MEE6, complete sequence [Arabidopsis thaliana]

Seq. No.	158550
Seq. ID	LIB3176-095-P1-K1-E5
Method	BLASTN
NCBI GI	g1480028
BLAST score	58
E value	3.0e-24
Match length	118
% identity	87
NCBI Description	Brassica rapa mRNA

Seq. No.	158551
Seq. ID	LIB3176-095-P1-K1-E7
Method	BLASTN
NCBI GI	g3860243
BLAST score	51
E value	4.0e-20
Match length	117
% identity	66
NCBI Description	Arabidopsis thaliana chromosome II BAC F15K20 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No. 158552

Seq. ID	LIB3176-095-P1-K1-F1
Method	BLASTN
NCBI GI	g3450888
BLAST score	49
E value	4.0e-19
Match length	61
% identity	97
NCBI Description	Arabidopsis thaliana 19S proteosome subunit 9 mRNA, complete cds

Seq. No.	158553
Seq. ID	LIB3176-095-P1-K1-F12
Method	BLASTN
NCBI GI	g2815519
BLAST score	145
E value	4.0e-76
Match length	169
% identity	96
NCBI Description	Arabidopsis thaliana BAC T5J8 from chromosome IV, top arm, complete sequence [Arabidopsis thaliana]

Seq. No.	158554
Seq. ID	LIB3176-095-P1-K1-F5
Method	BLASTN
NCBI GI	g3421071
BLAST score	32
E value	5.0e-09
Match length	52
% identity	90
NCBI Description	Arabidopsis thaliana 20S proteasome subunit PAA2 (PAA2) mRNA, complete cds

Seq. No.	158555
Seq. ID	LIB3176-095-P1-K1-F6
Method	BLASTX
NCBI GI	g3915823
BLAST score	279
E value	2.0e-25
Match length	58
% identity	95
NCBI Description	[Segment 1 of 2] 60S RIBOSOMAL PROTEIN L5

Seq. No.	158556
Seq. ID	LIB3176-095-P1-K1-F7
Method	BLASTX
NCBI GI	g4337027
BLAST score	327
E value	7.0e-31
Match length	78
% identity	86
NCBI Description	(AF123254) MFP2 [Arabidopsis thaliana]

Seq. No.	158557
Seq. ID	LIB3176-095-P1-K1-F8
Method	BLASTN
NCBI GI	g3282170
BLAST score	193

E value	1.0e-104
Match length	236
% identity	95
NCBI Description	Arabidopsis thaliana chromosome 1 BAC F8K4 sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	158558
Seq. ID	LIB3176-095-P1-K1-F9
Method	BLASTX
NCBI GI	g4263525
BLAST score	426
E value	3.0e-42
Match length	101
% identity	86
NCBI Description	(AC004044) putative photosystem I reaction center subunit II precursor [Arabidopsis thaliana]

Seq. No.	158559
Seq. ID	LIB3176-095-P1-K1-G10
Method	BLASTN
NCBI GI	g1107488
BLAST score	56
E value	3.0e-23
Match length	108
% identity	88
NCBI Description	A.thaliana mRNA for 60S ribosomal protein L9

Seq. No.	158560
Seq. ID	LIB3176-095-P1-K1-G11
Method	BLASTX
NCBI GI	g401169
BLAST score	188
E value	1.0e-14
Match length	35
% identity	100
NCBI Description	TRANSLATIONALLY CONTROLLED TUMOR PROTEIN HOMOLOG (TCTP)

Seq. No.	158561
Seq. ID	LIB3176-095-P1-K1-G2
Method	BLASTX
NCBI GI	g119143
BLAST score	191
E value	6.0e-15
Match length	43
% identity	88
NCBI Description	ELONGATION FACTOR 1-ALPHA (EF-1-ALPHA) >gi_81606_pir__S06724 translation elongation factor eEF-1 alpha chain - Arabidopsis thaliana >gi_295788_emb_CAA34453_ (X16430) elongation factor 1-alpha [Arabidopsis thaliana] >gi_1369927_emb_CAA34454_ (X16431) elongation factor 1-alpha [Arabidopsis thaliana] >gi_1369928_emb_CAA34455_ (X16431) elongation factor 1-alpha [Arabidopsis thaliana] >gi_1532172 (U63815) EF-1alpha-A1 [Arabidopsis thaliana] >gi_1532173 (U63815) EF-1alpha-A2 [Arabidopsis thaliana] >gi_1532174 (U63815) EF-1alpha-A3 [Arabidopsis thaliana]

Seq. No.	158562

Seq. ID	LIB3176-095-P1-K1-G3
Method	BLASTX
NCBI GI	g99735
BLAST score	250
E value	5.0e-22
Match length	54
% identity	93
NCBI Description	L-ascorbate peroxidase (EC 1.11.1.11) precursor - Arabidopsis thaliana (fragment)

Seq. No.	158563
Seq. ID	LIB3176-095-P1-K1-G4
Method	BLASTX
NCBI GI	g4469408
BLAST score	266
E value	2.0e-23
Match length	104
% identity	53
NCBI Description	(AF116527) MADS box protein FLOWERING LOCUS F [Arabidopsis thaliana] >gi_4469410_gb_AAD21249_ (AF116528) MADS box protein FLOWERING LOCUS F [Arabidopsis thaliana]

Seq. No.	158564
Seq. ID	LIB3176-095-P1-K1-G6
Method	BLASTX
NCBI GI	g2506496
BLAST score	546
E value	4.0e-56
Match length	107
% identity	97
NCBI Description	GLUTATHIONE S-TRANSFERASE ERD11 (CLASS PHI) >gi_1890156_emb_CAA72413_ (Y11727) gluthatione S-transferase [Arabidopsis thaliana]

Seq. No.	158565
Seq. ID	LIB3176-095-P1-K1-G7
Method	BLASTN
NCBI GI	g16506
BLAST score	49
E value	6.0e-19
Match length	104
% identity	88
NCBI Description	Arabidopsis thaliana 18S rRNA gene

Seq. No.	158566
Seq. ID	LIB3176-095-P1-K1-G8
Method	BLASTN
NCBI GI	g3510331
BLAST score	159
E value	2.0e-84
Match length	231
% identity	93
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K13P22, complete sequence [Arabidopsis thaliana]

Seq. No.	158567
Seq. ID	LIB3176-095-P1-K1-G9

Method	BLASTN
NCBI GI	g3894156
BLAST score	35
E value	5.0e-11
Match length	35
% identity	100
NCBI Description	Arabidopsis thaliana chromosome II BAC T16F16 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	158568
Seq. ID	LIB3176-095-P1-K1-H1
Method	BLASTN
NCBI GI	g4206762
BLAST score	83
E value	8.0e-39
Match length	246
% identity	83
NCBI Description	Arabidopsis thaliana cell wall-plasma membrane linker protein homolog (CWLP) mRNA, complete cds

Seq. No.	158569
Seq. ID	LIB3176-095-P1-K1-H10
Method	BLASTN
NCBI GI	g4519195
BLAST score	58
E value	3.0e-24
Match length	114
% identity	91
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MQC12, complete sequence

Seq. No.	158570
Seq. ID	LIB3176-095-P1-K1-H11
Method	BLASTN
NCBI GI	g3169718
BLAST score	199
E value	1.0e-108
Match length	250
% identity	95
NCBI Description	Arabidopsis thaliana mRNA, similar to yeast dcp1, complete cds

Seq. No.	158571
Seq. ID	LIB3176-095-P1-K1-H2
Method	BLASTX
NCBI GI	g3236246
BLAST score	284
E value	5.0e-26
Match length	62
% identity	89
NCBI Description	(AC004684) putative expansin protein [Arabidopsis thaliana]

Seq. No.	158572
Seq. ID	LIB3176-095-P1-K1-H5
Method	BLASTN
NCBI GI	g4538949
BLAST score	53

E value	3.0e-21
Match length	57
% identity	98
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F24G24 (ESSA project)

Seq. No.	158573
Seq. ID	LIB3176-095-P1-K1-H8
Method	BLASTX
NCBI GI	g3913650
BLAST score	427
E value	2.0e-42
Match length	91
% identity	86
NCBI Description	FERREDOXIN--NADP REDUCTASE, ROOT-TYPE ISOZYME PRECURSOR (FNR) >gi_2190038_dbj_BAA20365_ (AB004307) ferredoxin-NADP oxidoreductase [Nicotiana tabacum]

Seq. No.	158574
Seq. ID	LIB3176-095-P1-K1-H9
Method	BLASTN
NCBI GI	g4539448
BLAST score	155
E value	9.0e-82
Match length	380
% identity	100
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone T5C23 (ESSA project)

Seq. No.	158575
Seq. ID	LIB3176-096-P1-K1-A1
Method	BLASTN
NCBI GI	g2696018
BLAST score	57
E value	1.0e-23
Match length	157
% identity	97
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MXC9, complete sequence [Arabidopsis thaliana]

Seq. No.	158576
Seq. ID	LIB3176-096-P1-K1-A10
Method	BLASTN
NCBI GI	g2062153
BLAST score	101
E value	8.0e-50
Match length	163
% identity	62
NCBI Description	Arabidopsis thaliana chromosome III BAC T02O04 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	158577
Seq. ID	LIB3176-096-P1-K1-A11
Method	BLASTN
NCBI GI	g3128136
BLAST score	133
E value	6.0e-69

Match length	169
% identity	95
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K1F13, complete sequence [Arabidopsis thaliana]

Seq. No.	158578
Seq. ID	LIB3176-096-P1-K1-A2
Method	BLASTX
NCBI GI	g2062160
BLAST score	177
E value	2.0e-16
Match length	79
% identity	66
NCBI Description	(AC001645) jasmonate inducible protein isolog [Arabidopsis thaliana]

Seq. No.	158579
Seq. ID	LIB3176-096-P1-K1-A3
Method	BLASTN
NCBI GI	g2351062
BLAST score	128
E value	8.0e-66
Match length	177
% identity	97
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MAH20, complete sequence [Arabidopsis thaliana]

Seq. No.	158580
Seq. ID	LIB3176-096-P1-K1-B1
Method	BLASTN
NCBI GI	g4512646
BLAST score	111
E value	7.0e-56
Match length	157
% identity	94
NCBI Description	Arabidopsis thaliana chromosome II BAC F23N11 genomic sequence, complete sequence

Seq. No.	158581
Seq. ID	LIB3176-096-P1-K1-B11
Method	BLASTX
NCBI GI	g4406816
BLAST score	365
E value	2.0e-35
Match length	72
% identity	99
NCBI Description	(AC006201) 60S ribosomal protein L2 [Arabidopsis thaliana]

Seq. No.	158582
Seq. ID	LIB3176-096-P1-K1-B12
Method	BLASTN
NCBI GI	g4757392
BLAST score	105
E value	4.0e-52
Match length	121
% identity	97
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, TAC clone:

K14A17, complete sequence

Seq. No.	158583
Seq. ID	LIB3176-096-P1-K1-B3
Method	BLASTN
NCBI GI	g4589445
BLAST score	34
E value	2.0e-10
Match length	34
% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MWL2, complete sequence

Seq. No.	158584
Seq. ID	LIB3176-096-P1-K1-C1
Method	BLASTX
NCBI GI	g119143
BLAST score	356
E value	2.0e-34
Match length	71
% identity	96
NCBI Description	ELONGATION FACTOR 1-ALPHA (EF-1-ALPHA) >gi_81606_pir__S06724 translation elongation factor eEF-1 alpha chain - Arabidopsis thaliana >gi_295788_emb_CAA34453_ (X16430) elongation factor 1-alpha [Arabidopsis thaliana] >gi_1369927_emb_CAA34454_ (X16431) elongation factor 1-alpha [Arabidopsis thaliana] >gi_1369928_emb_CAA34455_ (X16431) elongation factor 1-alpha [Arabidopsis thaliana] >gi_1532172 (U63815) EF-1alpha-A1 [Arabidopsis thaliana] >gi_1532173 (U63815) EF-1alpha-A2 [Arabidopsis thaliana] >gi_1532174 (U63815) EF-1alpha-A3 [Arabidopsis thaliana]

Seq. No.	158585
Seq. ID	LIB3176-096-P1-K1-C11
Method	BLASTX
NCBI GI	g4490705
BLAST score	118
E value	3.0e-16
Match length	55
% identity	89
NCBI Description	(AL035680) ribosomal protein L14-like protein [Arabidopsis thaliana]

Seq. No.	158586
Seq. ID	LIB3176-096-P1-K1-C12
Method	BLASTN
NCBI GI	g4406805
BLAST score	150
E value	3.0e-79
Match length	162
% identity	98
NCBI Description	Arabidopsis thaliana chromosome II BAC T27K22 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	158587
Seq. ID	LIB3176-096-P1-K1-C3
Method	BLASTX

NCBI GI	g2505878
BLAST score	215
E value	7.0e-18
Match length	58
% identity	81
NCBI Description	(Y12776) gene5; most likely [Arabidopsis thaliana]

Seq. No.	158588
Seq. ID	LIB3176-096-P1-K1-C7
Method	BLASTN
NCBI GI	g16375
BLAST score	41
E value	1.0e-14
Match length	60
% identity	92
NCBI Description	A.thaliana gene (LHCP AB 140) for chlorophyll a/b binding protein

Seq. No.	158589
Seq. ID	LIB3176-096-P1-K1-D11
Method	BLASTN
NCBI GI	g2244747
BLAST score	31
E value	1.0e-08
Match length	51
% identity	90
NCBI Description	Arabidopsis thaliana DNA chromosome 4, ESSA I contig fragment No

Seq. No.	158590
Seq. ID	LIB3176-096-P1-K1-E10
Method	BLASTN
NCBI GI	g2288979
BLAST score	161
E value	1.0e-85
Match length	185
% identity	97
NCBI Description	Arabidopsis thaliana chromosome II BAC T01024 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	158591
Seq. ID	LIB3176-096-P1-K1-E11
Method	BLASTN
NCBI GI	g4314374
BLAST score	166
E value	1.0e-88
Match length	214
% identity	98
NCBI Description	Arabidopsis thaliana chromosome II BAC F10A12 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	158592
Seq. ID	LIB3176-096-P1-K1-E12
Method	BLASTN
NCBI GI	g3449334
BLAST score	182
E value	4.0e-98

Match length	202
% identity	98
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MYH9, complete sequence [Arabidopsis thaliana]

Seq. No.	158593
Seq. ID	LIB3176-096-P1-K1-E2
Method	BLASTN
NCBI GI	g2351068
BLAST score	114
E value	1.0e-57
Match length	162
% identity	93
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MRH10, complete sequence [Arabidopsis thaliana]

Seq. No.	158594
Seq. ID	LIB3176-096-P1-K1-F1
Method	BLASTN
NCBI GI	g3152602
BLAST score	234
E value	1.0e-129
Match length	234
% identity	100
NCBI Description	Arabidopsis thaliana chromosome II BAC F27L4 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	158595
Seq. ID	LIB3176-096-P1-K1-F10
Method	BLASTN
NCBI GI	g2264307
BLAST score	45
E value	3.0e-16
Match length	69
% identity	91
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MED24, complete sequence [Arabidopsis thaliana]

Seq. No.	158596
Seq. ID	LIB3176-096-P1-K1-F12
Method	BLASTN
NCBI GI	g4220468
BLAST score	47
E value	6.0e-18
Match length	55
% identity	96
NCBI Description	Arabidopsis thaliana chromosome II BAC T8O11 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	158597
Seq. ID	LIB3176-096-P1-K1-G1
Method	BLASTN
NCBI GI	g2656029
BLAST score	73
E value	3.0e-33
Match length	168
% identity	95

NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MQB2
Seq. No.	158598
Seq. ID	LIB3176-096-P1-K1-G10
Method	BLASTX
NCBI GI	g132074
BLAST score	255
E value	2.0e-22
Match length	73
% identity	77
NCBI Description	RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN 1A PRECURSOR (RUBISCO SMALL SUBUNIT 1A) >gi_68063_pir__RKMUA1 ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain A1 precursor - Arabidopsis thaliana
Seq. No.	158599
Seq. ID	LIB3176-096-P1-K1-G11
Method	BLASTX
NCBI GI	g4263525
BLAST score	361
E value	1.0e-34
Match length	97
% identity	75
NCBI Description	(AC004044) putative photosystem I reaction center subunit II precursor [Arabidopsis thaliana]
Seq. No.	158600
Seq. ID	LIB3176-096-P1-K1-G12
Method	BLASTX
NCBI GI	g120676
BLAST score	275
E value	6.0e-25
Match length	61
% identity	87
NCBI Description	GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE, CYTOSOLIC >gi_82165_pir__C24430 glyceraldehyde-3-phosphate dehydrogenase (NADP+) (phosphorylating) (EC 1.2.1.13) C, cytosolic - common tobacco (fragment) >gi_170241 (M14419) glyceraldehyde-3-phosphate dehydrogenase [Nicotiana tabacum]
Seq. No.	158601
Seq. ID	LIB3176-096-P1-K1-G2
Method	BLASTX
NCBI GI	g2317729
BLAST score	248
E value	9.0e-22
Match length	53
% identity	91
NCBI Description	(AF013627) reversibly glycosylated polypeptide-1 [Arabidopsis thaliana]
Seq. No.	158602
Seq. ID	LIB3176-096-P1-K1-G9
Method	BLASTN
NCBI GI	g166650

BLAST score	32
E value	1.0e-08
Match length	60
% identity	88
NCBI Description	A.thaliana calmodulin-2 (cam2) mRNA, complete cds

Seq. No.	158603
Seq. ID	LIB3176-096-P1-K1-H11
Method	BLASTX
NCBI GI	g4539316
BLAST score	479
E value	2.0e-48
Match length	102
% identity	97
NCBI Description	(AL035679) putative fructose-bisphosphate aldolase [Arabidopsis thaliana]

Seq. No.	158604
Seq. ID	LIB3176-096-P1-K1-H12
Method	BLASTX
NCBI GI	g2961346
BLAST score	388
E value	1.0e-37
Match length	95
% identity	77
NCBI Description	(AL022140) pectinesterase like protein [Arabidopsis thaliana]

Seq. No.	158605
Seq. ID	LIB3176-096-P1-K1-H2
Method	BLASTN
NCBI GI	g166771
BLAST score	51
E value	1.0e-20
Match length	59
% identity	97
NCBI Description	A.thaliana isocitrate lyase gene, 5' end

Seq. No.	158606
Seq. ID	LIB3176-096-P1-K1-H3
Method	BLASTX
NCBI GI	g4559396
BLAST score	561
E value	6.0e-58
Match length	124
% identity	95
NCBI Description	(AC006526) unknown protein [Arabidopsis thaliana]

Seq. No.	158607
Seq. ID	LIB3176-096-P1-K1-H9
Method	BLASTN
NCBI GI	g1732569
BLAST score	48
E value	1.0e-18
Match length	84
% identity	89
NCBI Description	Arabidopsis thaliana beta-glucosidase (psr3.1) mRNA,

complete cds

Seq. No.	158608
Seq. ID	LIB3176-097-P1-K1-A1
Method	BLASTX
NCBI GI	g3342800
BLAST score	329
E value	8.0e-31
Match length	86
% identity	80
NCBI Description	(AF061837) putative cytosolic 6-phosphogluconate dehydrogenase [Zea mays]

Seq. No.	158609
Seq. ID	LIB3176-097-P1-K1-A10
Method	BLASTX
NCBI GI	g126962
BLAST score	93
E value	6.0e-03
Match length	128
% identity	57
NCBI Description	TONOPLAST INTRINSIC PROTEIN, ROOT-SPECIFIC RB7 >gi_99747_pir__S13718 probable membrane channel protein - Arabidopsis thaliana >gi_16492_emb_CAA38633_ (X54854) possible membrane channel protein [Arabidopsis thaliana]

Seq. No.	158610
Seq. ID	LIB3176-097-P1-K1-A11
Method	BLASTX
NCBI GI	g4539408
BLAST score	146
E value	9.0e-10
Match length	29
% identity	100
NCBI Description	(AL049524) putative alpha NAC [Arabidopsis thaliana]

Seq. No.	158611
Seq. ID	LIB3176-097-P1-K1-A12
Method	BLASTX
NCBI GI	g1732570
BLAST score	422
E value	8.0e-42
Match length	97
% identity	85
NCBI Description	(U72153) beta-glucosidase [Arabidopsis thaliana]

Seq. No.	158612
Seq. ID	LIB3176-097-P1-K1-A2
Method	BLASTX
NCBI GI	g1169423
BLAST score	250
E value	5.0e-22
Match length	53
% identity	92
NCBI Description	DIHYDROFOLATE REDUCTASE 2 / THYMIDYLATE SYNTHASE 2 (DHFR-TS) >gi_289195 (L08594) dihydrofolate reductase-thymidylate synthase [Arabidopsis thaliana]

>gi_3096926_emb_CAA18836.1_ (AL023094) dihydrofolate reductase-thymidylate synthase [Arabidopsis thaliana]

Seq. No.	158613
Seq. ID	LIB3176-097-P1-K1-A3
Method	BLASTN
NCBI GI	g2262155
BLAST score	304
E value	1.0e-171
Match length	320
% identity	99
NCBI Description	DNA sequence of Arabidopsis thaliana BAC F5J6 from chromosome IV, complete sequence [Arabidopsis thaliana]

Seq. No.	158614
Seq. ID	LIB3176-097-P1-K1-A4
Method	BLASTX
NCBI GI	g1702987
BLAST score	522
E value	3.0e-53
Match length	116
% identity	91
NCBI Description	14-3-3-LIKE PROTEIN GF14 PHI >gi_1493805 (L09111) GF14 protein phi chain [Arabidopsis thaliana] >gi_2232146 (AF001414) 14-3-3-like protein GF14 phi [Arabidopsis thaliana]

Seq. No.	158615
Seq. ID	LIB3176-097-P1-K1-A5
Method	BLASTN
NCBI GI	g4159705
BLAST score	185
E value	1.0e-100
Match length	255
% identity	83
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MGD8, complete sequence

Seq. No.	158616
Seq. ID	LIB3176-097-P1-K1-A6
Method	BLASTN
NCBI GI	g3201608
BLAST score	174
E value	3.0e-93
Match length	287
% identity	100
NCBI Description	Arabidopsis thaliana chromosome II BAC F7F1 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	158617
Seq. ID	LIB3176-097-P1-K1-A8
Method	BLASTX
NCBI GI	g1644388
BLAST score	233
E value	2.0e-19
Match length	115
% identity	43

NCBI Description	(U72654) flavonoid 3'5'-hydroxylase [Eustoma grandiflorum]

Seq. No.	158618
Seq. ID	LIB3176-097-P1-K1-A9
Method	BLASTN
NCBI GI	g4741184
BLAST score	148
E value	6.0e-78
Match length	160
% identity	98
NCBI Description	Arabidopsis thaliana DNA chromosome 3, BAC clone T23J7 (ESSA project)

Seq. No.	158619
Seq. ID	LIB3176-097-P1-K1-B1
Method	BLASTN
NCBI GI	g3449334
BLAST score	172
E value	6.0e-92
Match length	233
% identity	97
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MYH9, complete sequence [Arabidopsis thaliana]

Seq. No.	158620
Seq. ID	LIB3176-097-P1-K1-B10
Method	BLASTX
NCBI GI	g4567207
BLAST score	292
E value	6.0e-27
Match length	56
% identity	100
NCBI Description	(AC007168) unknown protein [Arabidopsis thaliana]

Seq. No.	158621
Seq. ID	LIB3176-097-P1-K1-B11
Method	BLASTN
NCBI GI	g2828278
BLAST score	98
E value	4.0e-48
Match length	154
% identity	95
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone T18B16 (ESSAII project)

Seq. No.	158622
Seq. ID	LIB3176-097-P1-K1-B2
Method	BLASTN
NCBI GI	g1707006
BLAST score	326
E value	0.0e+00
Match length	406
% identity	100
NCBI Description	Arabidopsis thaliana chromosome II BAC T1B8 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	158623

Seq. ID	LIB3176-097-P1-K1-B3
Method	BLASTX
NCBI GI	g2341034
BLAST score	504
E value	3.0e-51
Match length	102
% identity	99
NCBI Description	(AC000104) F19P19.13 [Arabidopsis thaliana]

Seq. No.	158624
Seq. ID	LIB3176-097-P1-K1-B4
Method	BLASTX
NCBI GI	g99735
BLAST score	792
E value	4.0e-85
Match length	155
% identity	97
NCBI Description	L-ascorbate peroxidase (EC 1.11.1.11) precursor - Arabidopsis thaliana (fragment)

Seq. No.	158625
Seq. ID	LIB3176-097-P1-K1-B7
Method	BLASTN
NCBI GI	g2827513
BLAST score	93
E value	4.0e-45
Match length	193
% identity	98
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F8F16 (ESSAII project)

Seq. No.	158626
Seq. ID	LIB3176-097-P1-K1-B9
Method	BLASTX
NCBI GI	g3004551
BLAST score	156
E value	2.0e-10
Match length	129
% identity	40
NCBI Description	(AC003673) hypothetical protein [Arabidopsis thaliana]

Seq. No.	158627
Seq. ID	LIB3176-097-P1-K1-C10
Method	BLASTN
NCBI GI	g3128136
BLAST score	301
E value	1.0e-169
Match length	337
% identity	98
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K1F13, complete sequence [Arabidopsis thaliana]

Seq. No.	158628
Seq. ID	LIB3176-097-P1-K1-C11
Method	BLASTX
NCBI GI	g2213602
BLAST score	523

E value	2.0e-53
Match length	123
% identity	86
NCBI Description	(AC000348) T7N9.22 [Arabidopsis thaliana]

Seq. No.	158629
Seq. ID	LIB3176-097-P1-K1-C12
Method	BLASTN
NCBI GI	g4585890
BLAST score	131
E value	7.0e-68
Match length	151
% identity	97
NCBI Description	Arabidopsis thaliana chromosome II BAC T3G21 genomic sequence, complete sequence

Seq. No.	158630
Seq. ID	LIB3176-097-P1-K1-C2
Method	BLASTX
NCBI GI	g2262098
BLAST score	323
E value	2.0e-30
Match length	72
% identity	92
NCBI Description	(AC002343) HSP90 isolog [Arabidopsis thaliana]

Seq. No.	158631
Seq. ID	LIB3176-097-P1-K1-C3
Method	BLASTX
NCBI GI	g629557
BLAST score	299
E value	3.0e-27
Match length	62
% identity	55
NCBI Description	RNA-binding protein rnpD - Arabidopsis thaliana (fragment) >gi_510240_emb_CAA43420_ (X61108) RNA binding protein [Arabidopsis thaliana]

Seq. No.	158632
Seq. ID	LIB3176-097-P1-K1-C5
Method	BLASTX
NCBI GI	g1076678
BLAST score	367
E value	2.0e-35
Match length	74
% identity	100
NCBI Description	ubiquitin / ribosomal protein S27a - potato (fragment)

Seq. No.	158633
Seq. ID	LIB3176-097-P1-K1-C6
Method	BLASTN
NCBI GI	g4589421
BLAST score	117
E value	5.0e-59
Match length	273
% identity	95
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, TAC clone:

K5K13, complete sequence

Seq. No.	158634
Seq. ID	LIB3176-097-P1-K1-C7
Method	BLASTX
NCBI GI	g4587542
BLAST score	56
E value	3.0e-12
Match length	40
% identity	54
NCBI Description	(AC006577) Belongs to the PF_00657 Lipase/Acylhydrolase with GDSL-motif family. ESTs gb_T45815, gb_T45130 and gb_Z38046 come from this gene. [Arabidopsis thaliana]

Seq. No.	158635
Seq. ID	LIB3176-097-P1-K1-C8
Method	BLASTX
NCBI GI	g115767
BLAST score	694
E value	2.0e-73
Match length	144
% identity	94
NCBI Description	CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR (CAB-165/180) (LHCP) >gi_81603_pir__A29280 chlorophyll a/b-binding protein ab165 - Arabidopsis thaliana >gi_16368_emb_CAA27540_ (X03907) chlorophyll a/b binding protein (LHCP AB 65) [Arabidopsis thaliana] >gi_16372_emb_CAA27541_ (X03908) chlorophyll a/b binding protein (LHCP AB 180) [Arabidopsis thaliana]

Seq. No.	158636
Seq. ID	LIB3176-097-P1-K1-C9
Method	BLASTN
NCBI GI	g3449331
BLAST score	50
E value	3.0e-19
Match length	163
% identity	89
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MNC17, complete sequence [Arabidopsis thaliana]

Seq. No.	158637
Seq. ID	LIB3176-097-P1-K1-D1
Method	BLASTX
NCBI GI	g2443878
BLAST score	207
E value	6.0e-17
Match length	41
% identity	95
NCBI Description	(AC002294) Unknown protein [Arabidopsis thaliana]

Seq. No.	158638
Seq. ID	LIB3176-097-P1-K1-D10
Method	BLASTX
NCBI GI	g2914700
BLAST score	277
E value	1.0e-24

Match length	63
% identity	90
NCBI Description	(AC003974) tRNA-processing protein SEN3-like [Arabidopsis thaliana]

Seq. No.	158639
Seq. ID	LIB3176-097-P1-K1-D2
Method	BLASTX
NCBI GI	g4567232
BLAST score	354
E value	2.0e-33
Match length	72
% identity	100
NCBI Description	(AC007119) putative 40S ribosomal protein S25 [Arabidopsis thaliana]

Seq. No.	158640
Seq. ID	LIB3176-097-P1-K1-D3
Method	BLASTX
NCBI GI	g267073
BLAST score	271
E value	3.0e-24
Match length	60
% identity	87
NCBI Description	TUBULIN BETA-2/BETA-3 CHAIN >gi_320184_pir__JQ1587 tubulin beta chain - Arabidopsis thaliana >gi_166898 (M84700) beta-2 tubulin [Arabidopsis thaliana] >gi_166900 (M84701) beta-3 tubulin [Arabidopsis thaliana]

Seq. No.	158641
Seq. ID	LIB3176-097-P1-K1-D4
Method	BLASTN
NCBI GI	g4159706
BLAST score	74
E value	4.0e-34
Match length	98
% identity	94
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MGL6, complete sequence

Seq. No.	158642
Seq. ID	LIB3176-097-P1-K1-D5
Method	BLASTX
NCBI GI	g3746071
BLAST score	380
E value	1.0e-36
Match length	122
% identity	63
NCBI Description	(AC005311) putative GTP-binding protein [Arabidopsis thaliana]

Seq. No.	158643
Seq. ID	LIB3176-097-P1-K1-D6
Method	BLASTN
NCBI GI	g4220627
BLAST score	37
E value	2.0e-11

Match length	166
% identity	84
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K20J1, complete sequence [Arabidopsis thaliana]

Seq. No.	158644
Seq. ID	LIB3176-097-P1-K1-D7
Method	BLASTN
NCBI GI	g166771
BLAST score	60
E value	2.0e-25
Match length	105
% identity	96
NCBI Description	A.thaliana isocitrate lyase gene, 5' end

Seq. No.	158645
Seq. ID	LIB3176-097-P1-K1-D8
Method	BLASTN
NCBI GI	g4559344
BLAST score	186
E value	1.0e-100
Match length	427
% identity	9
NCBI Description	Arabidopsis thaliana chromosome II BAC F27C12 genomic sequence, complete sequence

Seq. No.	158646
Seq. ID	LIB3176-097-P1-K1-D9
Method	BLASTX
NCBI GI	g2119846
BLAST score	149
E value	1.0e-09
Match length	34
% identity	94
NCBI Description	chlorophyll a/b-binding protein type I precursor Lhb1B2 - Arabidopsis thaliana >gi_16364_emb_CAA45790_ (X64460) photosystem II type I chlorophyll a /b binding protein [Arabidopsis thaliana] >gi_3128230 (AC004077) photosystem II type I chlorophyll a/b binding protein [Arabidopsis thaliana] >gi_3337371 (AC004481) photosystem II type I chlorophyll a/b binding protein [Arabidopsis thaliana]

Seq. No.	158647
Seq. ID	LIB3176-097-P1-K1-E1
Method	BLASTX
NCBI GI	g3377797
BLAST score	370
E value	8.0e-36
Match length	81
% identity	89
NCBI Description	(AF075597) Similar to 60S ribosome protein L19; coded for by A. thaliana cDNA T04719; coded for by A. thaliana cDNA H36046; coded for by A. thaliana cDNA T44067; coded for by A. thaliana cDNA T14056; coded for by A. thaliana cDNA R90691 [Ara

Seq. No.	158648

Seq. ID	LIB3176-097-P1-K1-E10
Method	BLASTN
NCBI GI	g414340
BLAST score	110
E value	2.0e-55
Match length	138
% identity	96
NCBI Description	A.thaliana rd21A gene for thiol protease, complete cds

Seq. No.	158649
Seq. ID	LIB3176-097-P1-K1-E12
Method	BLASTN
NCBI GI	g4589440
BLAST score	83
E value	2.0e-39
Match length	115
% identity	99
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MSD21, complete sequence

Seq. No.	158650
Seq. ID	LIB3176-097-P1-K1-E2
Method	BLASTX
NCBI GI	g2062158
BLAST score	240
E value	3.0e-20
Match length	51
% identity	47
NCBI Description	(AC001645) jasmonate inducible protein isolog [Arabidopsis thaliana]

Seq. No.	158651
Seq. ID	LIB3176-097-P1-K1-E3
Method	BLASTX
NCBI GI	g4115387
BLAST score	353
E value	5.0e-34
Match length	71
% identity	99
NCBI Description	(AC005967) putative NADP-dependent glyceraldehyde-3-phosphate dehydrogenase [Arabidopsis thaliana]

Seq. No.	158652
Seq. ID	LIB3176-097-P1-K1-E5
Method	BLASTN
NCBI GI	g4185120
BLAST score	141
E value	1.0e-73
Match length	173
% identity	97
NCBI Description	Arabidopsis thaliana chromosome 1 BAC F5F19 sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	158653
Seq. ID	LIB3176-097-P1-K1-E6
Method	BLASTX

NCBI GI	g2143227
BLAST score	592
E value	1.0e-61
Match length	116
% identity	95
NCBI Description	(Y13356) glyoxysomal isocitrate lyase [Brassica napus]

Seq. No.	158654
Seq. ID	LIB3176-097-P1-K1-E9
Method	BLASTX
NCBI GI	g135442
BLAST score	281
E value	4.0e-25
Match length	55
% identity	95
NCBI Description	TUBULIN BETA-1 CHAIN >gi_71590_pir__UBMUBM tubulin beta-1 chain - Arabidopsis thaliana >gi_166922 (M20405) beta-1 tubulin [Arabidopsis thaliana]

Seq. No.	158655
Seq. ID	LIB3176-097-P1-K1-F1
Method	BLASTN
NCBI GI	g3985958
BLAST score	133
E value	5.0e-69
Match length	166
% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MZN1, complete sequence [Arabidopsis thaliana]

Seq. No.	158656
Seq. ID	LIB3176-097-P1-K1-F10
Method	BLASTX
NCBI GI	g1172806
BLAST score	232
E value	4.0e-19
Match length	43
% identity	98
NCBI Description	60S RIBOSOMAL PROTEIN L10 (WILM'S TUMOR SUPPRESSOR PROTEIN HOMOLOG) >gi_478401_pir__JQ2244 ribosomal protein L10.e, cytosolic - Arabidopsis thaliana >gi_17682_emb_CAA78856_ (Z15157) Wilm's tumor suppressor homologue [Arabidopsis thaliana]

Seq. No.	158657
Seq. ID	LIB3176-097-P1-K1-F11
Method	BLASTN
NCBI GI	g4580745
BLAST score	79
E value	4.0e-37
Match length	83
% identity	99
NCBI Description	Arabidopsis thaliana chromosome 1 BAC F10O3 sequence, complete sequence

Seq. No.	158658
Seq. ID	LIB3176-097-P1-K1-F12

Method	BLASTN
NCBI GI	g4585890
BLAST score	114
E value	1.0e-57
Match length	138
% identity	96
NCBI Description	Arabidopsis thaliana chromosome II BAC T3G21 genomic sequence, complete sequence

Seq. No.	158659
Seq. ID	LIB3176-097-P1-K1-F2
Method	BLASTX
NCBI GI	g2494174
BLAST score	580
E value	4.0e-60
Match length	114
% identity	98
NCBI Description	GLUTAMATE DECARBOXYLASE 1 (GAD 1) >gi_497979 (U10034) glutamate decarboxylase [Arabidopsis thaliana]

Seq. No.	158660
Seq. ID	LIB3176-097-P1-K1-F3
Method	BLASTN
NCBI GI	g4220627
BLAST score	154
E value	4.0e-81
Match length	397
% identity	7
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K20J1, complete sequence [Arabidopsis thaliana]

Seq. No.	158661
Seq. ID	LIB3176-097-P1-K1-F4
Method	BLASTX
NCBI GI	g4138179
BLAST score	249
E value	1.0e-21
Match length	54
% identity	93
NCBI Description	(AJ223969) elongation factor 1 alpha subunit [Malus domestica]

Seq. No.	158662
Seq. ID	LIB3176-097-P1-K1-F6
Method	BLASTN
NCBI GI	g2264317
BLAST score	102
E value	2.0e-50
Match length	209
% identity	97
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MUG13, complete sequence [Arabidopsis thaliana]

Seq. No.	158663
Seq. ID	LIB3176-097-P1-K1-F8
Method	BLASTN
NCBI GI	g3873174

BLAST score	271
E value	1.0e-151
Match length	319
% identity	99
NCBI Description	Genomic sequence for Arabidopsis thaliana BAC F14N23, complete sequence [Arabidopsis thaliana]

Seq. No.	158664
Seq. ID	LIB3176-097-P1-K1-F9
Method	BLASTN
NCBI GI	g3702731
BLAST score	390
E value	0.0e+00
Match length	394
% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MFC19, complete sequence [Arabidopsis thaliana]

Seq. No.	158665
Seq. ID	LIB3176-097-P1-K1-G10
Method	BLASTN
NCBI GI	g2213606
BLAST score	401
E value	0.0e+00
Match length	441
% identity	98
NCBI Description	Genomic sequence for Arabidopsis thaliana BAC F21J9, complete sequence [Arabidopsis thaliana]

Seq. No.	158666
Seq. ID	LIB3176-097-P1-K1-G12
Method	BLASTX
NCBI GI	g1709970
BLAST score	420
E value	1.0e-41
Match length	85
% identity	98
NCBI Description	60S RIBOSOMAL PROTEIN L10A

Seq. No.	158667
Seq. ID	LIB3176-097-P1-K1-G2
Method	BLASTN
NCBI GI	g4309719
BLAST score	126
E value	1.0e-64
Match length	270
% identity	95
NCBI Description	Arabidopsis thaliana chromosome II BAC T30D6 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	158668
Seq. ID	LIB3176-097-P1-K1-G3
Method	BLASTX
NCBI GI	g4006924
BLAST score	530
E value	1.0e-54
Match length	91

% identity	99
NCBI Description	(Z99708) beta-galactosidase like protein [Arabidopsis thaliana]

Seq. No.	158669
Seq. ID	LIB3176-097-P1-K1-G4
Method	BLASTX
NCBI GI	g2462781
BLAST score	359
E value	8.0e-35
Match length	71
% identity	97
NCBI Description	(U73175) carbamoyl phosphate synthetase small subunit [Arabidopsis thaliana]

Seq. No.	158670
Seq. ID	LIB3176-097-P1-K1-G6
Method	BLASTX
NCBI GI	g1732570
BLAST score	477
E value	3.0e-48
Match length	99
% identity	94
NCBI Description	(U72153) beta-glucosidase [Arabidopsis thaliana]

Seq. No.	158671
Seq. ID	LIB3176-097-P1-K1-G7
Method	BLASTN
NCBI GI	g4220627
BLAST score	180
E value	1.0e-96
Match length	431
% identity	8
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K20J1, complete sequence [Arabidopsis thaliana]

Seq. No.	158672
Seq. ID	LIB3176-097-P1-K1-G8
Method	BLASTX
NCBI GI	g3962377
BLAST score	551
E value	8.0e-57
Match length	110
% identity	98
NCBI Description	(AJ002551) heat shock protein 70 [Arabidopsis thaliana]

Seq. No.	158673
Seq. ID	LIB3176-097-P1-K1-G9
Method	BLASTN
NCBI GI	g4049332
BLAST score	167
E value	4.0e-89
Match length	267
% identity	95
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F8B4 (ESSAII project)

Seq. No.	158674
Seq. ID	LIB3176-097-P1-K1-H1
Method	BLASTX
NCBI GI	g417148
BLAST score	256
E value	2.0e-22
Match length	76
% identity	61
NCBI Description	PROBABLE GLUTATHIONE S-TRANSFERASE (HEAT SHOCK PROTEIN 26A) (G2-4) >gi_99912_pir__A33654 heat shock protein 26A - soybean >gi_169981 (M20363) Gmhsp26-A [Glycine max]

Seq. No.	158675
Seq. ID	LIB3176-097-P1-K1-H10
Method	BLASTN
NCBI GI	g4589415
BLAST score	60
E value	2.0e-25
Match length	88
% identity	92
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K14A3, complete sequence

Seq. No.	158676
Seq. ID	LIB3176-097-P1-K1-H11
Method	BLASTX
NCBI GI	g3342800
BLAST score	155
E value	8.0e-11
Match length	34
% identity	85
NCBI Description	(AF061837) putative cytosolic 6-phosphogluconate dehydrogenase [Zea mays]

Seq. No.	158677
Seq. ID	LIB3176-097-P1-K1-H12
Method	BLASTN
NCBI GI	g170240
BLAST score	57
E value	3.0e-23
Match length	89
% identity	91
NCBI Description	Tobacco (N.tabacum) GapC mRNA encoding cytosolic glyceraldehyde-3-phosphophate dehydrogenase, partial cds

Seq. No.	158678
Seq. ID	LIB3176-097-P1-K1-H2
Method	BLASTX
NCBI GI	g4572682
BLAST score	603
E value	8.0e-63
Match length	128
% identity	81
NCBI Description	(AC006954) putative APG protein [Arabidopsis thaliana]

Seq. No.	158679
Seq. ID	LIB3176-097-P1-K1-H3

Method	BLASTX
NCBI GI	g119194
BLAST score	253
E value	8.0e-22
Match length	72
% identity	72
NCBI Description	ELONGATION FACTOR TU, CHLOROPLAST PRECURSOR (EF-TU) >gi_81607_pir__S09152 translation elongation factor Tu precursor, chloroplast - Arabidopsis thaliana >gi_22565_emb_CAA36498_ (X52256) elongation factor Tu precursor [Arabidopsis thaliana] >gi_226817_prf__1607332A elongation factor Tu [Arabidopsis thaliana]

Seq. No.	158680
Seq. ID	LIB3176-097-P1-K1-H4
Method	BLASTX
NCBI GI	g224159
BLAST score	475
E value	8.0e-48
Match length	104
% identity	89
NCBI Description	cytochrome b559 [Spinacia oleracea]

Seq. No.	158681
Seq. ID	LIB3176-097-P1-K1-H5
Method	BLASTN
NCBI GI	g2245073
BLAST score	61
E value	1.0e-25
Match length	65
% identity	98
NCBI Description	Arabidopsis thaliana DNA chromosome 4, ESSA I contig fragment No

Seq. No.	158682
Seq. ID	LIB3176-097-P1-K1-H6
Method	BLASTN
NCBI GI	g3668073
BLAST score	96
E value	5.0e-47
Match length	111
% identity	97
NCBI Description	Arabidopsis thaliana chromosome II BAC T4C15 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	158683
Seq. ID	LIB3176-097-P1-K1-H8
Method	BLASTN
NCBI GI	g2828266
BLAST score	119
E value	1.0e-60
Match length	159
% identity	94
NCBI Description	Arabidopsis thaliana mRNA for geranylgeranyl reductase

Seq. No.	158684
Seq. ID	LIB3176-097-P1-K1-H9

Method	BLASTN
NCBI GI	g1353771
BLAST score	54
E value	6.0e-22
Match length	74
% identity	93
NCBI Description	Arabidopsis thaliana profilin 2 mRNA, complete cds

Seq. No.	158685
Seq. ID	LIB3176-098-P1-K1-A1
Method	BLASTN
NCBI GI	g2477521
BLAST score	210
E value	1.0e-115
Match length	246
% identity	14
NCBI Description	Arabidopsis thaliana chromosome I BAC F22K20 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	158686
Seq. ID	LIB3176-098-P1-K1-A10
Method	BLASTN
NCBI GI	g2281081
BLAST score	228
E value	1.0e-125
Match length	244
% identity	98
NCBI Description	Arabidopsis thaliana chromosome II BAC F18O19 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	158687
Seq. ID	LIB3176-098-P1-K1-A12
Method	BLASTX
NCBI GI	g3377797
BLAST score	165
E value	8.0e-12
Match length	54
% identity	69
NCBI Description	(AF075597) Similar to 60S ribosome protein L19; coded for by A. thaliana cDNA T04719; coded for by A. thaliana cDNA H36046; coded for by A. thaliana cDNA T44067; coded for by A. thaliana cDNA T14056; coded for by A. thaliana cDNA R90691 [Ara

Seq. No.	158688
Seq. ID	LIB3176-098-P1-K1-A2
Method	BLASTX
NCBI GI	g3212869
BLAST score	192
E value	3.0e-15
Match length	57
% identity	72
NCBI Description	(AC004005) unknown protein [Arabidopsis thaliana]

Seq. No.	158689
Seq. ID	LIB3176-098-P1-K1-A3
Method	BLASTN

NCBI GI g2264307
BLAST score 72
E value 2.0e-32
Match length 72
% identity 100
NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MED24, complete sequence [Arabidopsis thaliana]

Seq. No. 158690
Seq. ID LIB3176-098-P1-K1-A4
Method BLASTX
NCBI GI g1871577
BLAST score 238
E value 5.0e-20
Match length 80
% identity 56
NCBI Description (Y11553) putative 21kD protein precursor [Medicago sativa]

Seq. No. 158691
Seq. ID LIB3176-098-P1-K1-A5
Method BLASTX
NCBI GI g4006883
BLAST score 598
E value 4.0e-62
Match length 147
% identity 82
NCBI Description (Z99707) cysteine proteinase [Arabidopsis thaliana]

Seq. No. 158692
Seq. ID LIB3176-098-P1-K1-A8
Method BLASTX
NCBI GI g4539007
BLAST score 336
E value 1.0e-31
Match length 63
% identity 100
NCBI Description (AL049481) cytochrome c [Arabidopsis thaliana]

Seq. No. 158693
Seq. ID LIB3176-098-P1-K1-B1
Method BLASTX
NCBI GI g1169277
BLAST score 432
E value 9.0e-43
Match length 131
% identity 69
NCBI Description DEHYDRIN ERD10 (LOW-TEMPERATURE-INDUCED PROTEIN LTI45) >gi_2129638_pir__S60480 low temperature-induced protein lit29 - Arabidopsis thaliana >gi_556472_dbj_BAA04568_ (D17714) ERD10 protein [Arabidopsis thaliana] >gi_975648_emb_CAA62448_ (X90958) lti29 [Arabidopsis thaliana]

Seq. No. 158694
Seq. ID LIB3176-098-P1-K1-B10
Method BLASTX
NCBI GI g1666173

BLAST score	229
E value	1.0e-19
Match length	84
% identity	70
NCBI Description	(Y09106) transcription factor [Nicotiana plumbaginifolia]

Seq. No.	158695
Seq. ID	LIB3176-098-P1-K1-B12
Method	BLASTN
NCBI GI	g1491614
BLAST score	124
E value	2.0e-63
Match length	148
% identity	97
NCBI Description	A.thaliana mRNA for male sterility 2-like protein

Seq. No.	158696
Seq. ID	LIB3176-098-P1-K1-B3
Method	BLASTX
NCBI GI	g2781394
BLAST score	390
E value	5.0e-38
Match length	89
% identity	94
NCBI Description	(U70424) O-methyltransferase 1 [Arabidopsis thaliana]

Seq. No.	158697
Seq. ID	LIB3176-098-P1-K1-B5
Method	BLASTN
NCBI GI	g4519188
BLAST score	151
E value	1.0e-79
Match length	268
% identity	99
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K21L19, complete sequence

Seq. No.	158698
Seq. ID	LIB3176-098-P1-K1-B6
Method	BLASTN
NCBI GI	g397481
BLAST score	40
E value	1.0e-13
Match length	92
% identity	86
NCBI Description	A.thaliana hsc70 mRNA for heat shock cognate protein

Seq. No.	158699
Seq. ID	LIB3176-098-P1-K1-B7
Method	BLASTX
NCBI GI	g2129569
BLAST score	542
E value	1.0e-55
Match length	117
% identity	89
NCBI Description	cytosolic cyclophilin ROC3 - Arabidopsis thaliana >gi_1305455 (U40399) cytosolic cyclophilin [Arabidopsis

thaliana] >gi_4581104_gb_AAD24594.1_AC005825_1 (AC005825) cytosolic cyclophilin (ROC3) [Arabidopsis thaliana]

Seq. No.	158700
Seq. ID	LIB3176-098-P1-K1-B8
Method	BLASTX
NCBI GI	g4589980
BLAST score	228
E value	2.0e-19
Match length	63
% identity	75
NCBI Description	(AC007195) cyclophilin, 3' partial [Arabidopsis thaliana]

Seq. No.	158701
Seq. ID	LIB3176-098-P1-K1-B9
Method	BLASTN
NCBI GI	g2829274
BLAST score	241
E value	1.0e-133
Match length	267
% identity	99
NCBI Description	Arabidopsis thaliana nucleoside diphosphate kinase 3 (ndpk3) mRNA, complete cds

Seq. No.	158702
Seq. ID	LIB3176-098-P1-K1-C1
Method	BLASTX
NCBI GI	g3123264
BLAST score	571
E value	4.0e-59
Match length	113
% identity	100
NCBI Description	60S RIBOSOMAL PROTEIN L27 >gi_2244857_emb_CAB10279_ (Z97337) hypothetical protein [Arabidopsis thaliana]

Seq. No.	158703
Seq. ID	LIB3176-098-P1-K1-C10
Method	BLASTX
NCBI GI	g3023848
BLAST score	50
E value	9.0e-62
Match length	127
% identity	35
NCBI Description	GUANINE NUCLEOTIDE-BINDING PROTEIN BETA SUBUNIT-LIKE PROTEIN (WD-40 REPEAT AUXIN-DEPENDENT PROTEIN ARCA) >gi_2289095 (U77381) WD-40 repeat protein [Arabidopsis thaliana]

Seq. No.	158704
Seq. ID	LIB3176-098-P1-K1-C12
Method	BLASTN
NCBI GI	g4589421
BLAST score	147
E value	3.0e-77
Match length	220
% identity	98
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, TAC clone:

K5K13, complete sequence

Seq. No.	158705
Seq. ID	LIB3176-098-P1-K1-C2
Method	BLASTX
NCBI GI	g1732570
BLAST score	122
E value	2.0e-22
Match length	72
% identity	83
NCBI Description	(U72153) beta-glucosidase [Arabidopsis thaliana]

Seq. No.	158706
Seq. ID	LIB3176-098-P1-K1-C3
Method	BLASTN
NCBI GI	g4581103
BLAST score	59
E value	5.0e-25
Match length	106
% identity	90
NCBI Description	Arabidopsis thaliana chromosome II BAC T24I21 genomic sequence, complete sequence

Seq. No.	158707
Seq. ID	LIB3176-098-P1-K1-C5
Method	BLASTN
NCBI GI	g1107486
BLAST score	34
E value	6.0e-10
Match length	98
% identity	84
NCBI Description	A.thaliana mRNA for 60S ribosomal protein L27a

Seq. No.	158708
Seq. ID	LIB3176-098-P1-K1-C6
Method	BLASTN
NCBI GI	g3395421
BLAST score	221
E value	1.0e-121
Match length	245
% identity	97
NCBI Description	Arabidopsis thaliana chromosome II BAC T19C21 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	158709
Seq. ID	LIB3176-098-P1-K1-C7
Method	BLASTX
NCBI GI	g113026
BLAST score	199
E value	5.0e-16
Match length	55
% identity	73
NCBI Description	ISOCITRATE LYASE (ISOCITRASE) (ISOCITRATASE) (ICL) >gi_68211_pir__WZRPI isocitrate lyase (EC 4.1.3.1) - rape >gi_255220_bbs_112862 isocitrate lyase, threo-D S-isocitrate glyoxylate-lyase, IL {EC 4.1.3.1} [Brassica napus, seedlings, Peptide, 576 aa] >gi_167144 (L08482)

isocitrate lyase [Brassica napus] >gi_447142_prf__1913424A isocitrate lyase [Brassica napus]

Seq. No.	158710
Seq. ID	LIB3176-098-P1-K1-C9
Method	BLASTX
NCBI GI	g1825645
BLAST score	305
E value	5.0e-28
Match length	72
% identity	76
NCBI Description	(U88173) weak similarity to Arabidopsis thaliana ubiquitin-like protein 8 [Caenorhabditis elegans]

Seq. No.	158711
Seq. ID	LIB3176-098-P1-K1-D1
Method	BLASTN
NCBI GI	g166705
BLAST score	74
E value	9.0e-34
Match length	102
% identity	93
NCBI Description	Arabidopsis thaliana glyceraldehyde-3-phosphate dehydrogenase C subunit (GapC) gene, complete cds

Seq. No.	158712
Seq. ID	LIB3176-098-P1-K1-D10
Method	BLASTX
NCBI GI	g4539419
BLAST score	151
E value	2.0e-10
Match length	40
% identity	78
NCBI Description	(AL049171) putative ribosomal protein [Arabidopsis thaliana]

Seq. No.	158713
Seq. ID	LIB3176-098-P1-K1-D12
Method	BLASTN
NCBI GI	g3860243
BLAST score	213
E value	1.0e-116
Match length	225
% identity	99
NCBI Description	Arabidopsis thaliana chromosome II BAC F15K20 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	158714
Seq. ID	LIB3176-098-P1-K1-D3
Method	BLASTN
NCBI GI	g2351062
BLAST score	116
E value	1.0e-58
Match length	218
% identity	98
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MAH20, complete sequence [Arabidopsis thaliana]

Seq. No.	158715
Seq. ID	LIB3176-098-P1-K1-D4
Method	BLASTN
NCBI GI	g16174
BLAST score	59
E value	8.0e-25
Match length	71
% identity	96
NCBI Description	A.thaliana ANT1 mRNA for adenylate translocator

Seq. No.	158716
Seq. ID	LIB3176-098-P1-K1-D5
Method	BLASTX
NCBI GI	g2129548
BLAST score	255
E value	2.0e-22
Match length	70
% identity	73
NCBI Description	calcium-dependent protein kinase (EC 2.7.1.-) - Arabidopsis thaliana >gi_2129556_pir__S71902 calcium-dependent protein kinase 9 - Arabidopsis thaliana >gi_836938 (U20388) calcium-dependent protein kinase [Arabidopsis thaliana] >gi_836946 (U20626) calcium-dependent protein kinase [Arabidopsis thaliana]

Seq. No.	158717
Seq. ID	LIB3176-098-P1-K1-D6
Method	BLASTX
NCBI GI	g1495251
BLAST score	227
E value	3.0e-19
Match length	51
% identity	92
NCBI Description	(Z70314) heat-shock protein [Arabidopsis thaliana]

Seq. No.	158718
Seq. ID	LIB3176-098-P1-K1-D9
Method	BLASTX
NCBI GI	g113026
BLAST score	199
E value	6.0e-16
Match length	61
% identity	70
NCBI Description	ISOCITRATE LYASE (ISOCITRASE) (ISOCITRATASE) (ICL) >gi_68211_pir__WZRPI isocitrate lyase (EC 4.1.3.1) - rape >gi_255220_bbs_112862 isocitrate lyase, threo-D S-isocitrate glyoxylate-lyase, IL {EC 4.1.3.1} [Brassica napus, seedlings, Peptide, 576 aa] >gi_167144 (L08482) isocitrate lyase [Brassica napus] >gi_447142_prf__1913424A isocitrate lyase [Brassica napus]

Seq. No.	158719
Seq. ID	LIB3176-098-P1-K1-E1
Method	BLASTX
NCBI GI	g3913289
BLAST score	242

E value	2.0e-20
Match length	143
% identity	43
NCBI Description	CAFFEIC ACID 3-O-METHYLTRANSFERASE (S-ADENOSYSL-L-METHIONINE:CAFFEIC ACID 3-O-METHYLTRANSFERASE) (COMT) >gi_2240207 (AF006009) caffeic acid O-methyltransferase [Clarkia breweri]

Seq. No.	158720
Seq. ID	LIB3176-098-P1-K1-E10
Method	BLASTX
NCBI GI	g132110
BLAST score	192
E value	3.0e-15
Match length	44
% identity	91
NCBI Description	RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN 3B PRECURSOR (RUBISCO SMALL SUBUNIT 3B) >gi_68060_pir__RKMUB3 ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain B3 precursor - Arabidopsis thaliana >gi_16195_emb_CAA32702_ (X14564) ribulose bisphosphate carboxylase [Arabidopsis thaliana]

Seq. No.	158721
Seq. ID	LIB3176-098-P1-K1-E11
Method	BLASTX
NCBI GI	g2738248
BLAST score	380
E value	8.0e-37
Match length	75
% identity	97
NCBI Description	(U97200) cobalamin-independent methionine synthase [Arabidopsis thaliana]

Seq. No.	158722
Seq. ID	LIB3176-098-P1-K1-E12
Method	BLASTX
NCBI GI	g3600058
BLAST score	248
E value	4.0e-21
Match length	56
% identity	95
NCBI Description	(AF080120) similar to vacuolar ATPases [Arabidopsis thaliana]

Seq. No.	158723
Seq. ID	LIB3176-098-P1-K1-E2
Method	BLASTN
NCBI GI	g166705
BLAST score	63
E value	3.0e-27
Match length	95
% identity	92
NCBI Description	Arabidopsis thaliana glyceraldehyde-3-phosphate dehydrogenase C subunit (GapC) gene, complete cds

Seq. No.	158724

Seq. ID	LIB3176-098-P1-K1-E3
Method	BLASTN
NCBI GI	g1354206
BLAST score	66
E value	9.0e-29
Match length	102
% identity	92
NCBI Description	Arabidopsis thaliana FK506 binding protein FKBP62 (ROF1) mRNA, complete cds

Seq. No.	158725
Seq. ID	LIB3176-098-P1-K1-E5
Method	BLASTN
NCBI GI	g4467094
BLAST score	66
E value	5.0e-29
Match length	130
% identity	95
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F20D10 (ESSA project)

Seq. No.	158726
Seq. ID	LIB3176-098-P1-K1-E7
Method	BLASTX
NCBI GI	g2651314
BLAST score	218
E value	1.0e-17
Match length	65
% identity	69
NCBI Description	(AC002336) putative ribosomal protein S26 [Arabidopsis thaliana]

Seq. No.	158727
Seq. ID	LIB3176-098-P1-K1-E8
Method	BLASTX
NCBI GI	g3860272
BLAST score	389
E value	8.0e-38
Match length	77
% identity	97
NCBI Description	(AC005824) putative suppressor protein [Arabidopsis thaliana] >gi_4314399_gb_AAD15609_ (AC006232) putative skd1 protein [Arabidopsis thaliana]

Seq. No.	158728
Seq. ID	LIB3176-098-P1-K1-F1
Method	BLASTX
NCBI GI	g3122388
BLAST score	407
E value	4.0e-40
Match length	83
% identity	92
NCBI Description	WD-40 REPEAT PROTEIN MSI2 >gi_2394231 (AF016847) WD-40 repeat protein [Arabidopsis thaliana] >gi_4581121_gb_AAD24611.1_AC005825_18 (AC005825) putative WD-40 protein MSI2 [Arabidopsis thaliana]

Seq. No.	158729
Seq. ID	LIB3176-098-P1-K1-F2
Method	BLASTX
NCBI GI	g3421096
BLAST score	200
E value	4.0e-16
Match length	41
% identity	98
NCBI Description	(AF043528) 20S proteasome subunit PAG1 [Arabidopsis thaliana] >gi_3885332 (AC005623) proteasome component [Arabidopsis thaliana]

Seq. No.	158730
Seq. ID	LIB3176-098-P1-K1-F4
Method	BLASTX
NCBI GI	g3928099
BLAST score	410
E value	2.0e-40
Match length	102
% identity	40
NCBI Description	(AC005770) unknown protein [Arabidopsis thaliana]

Seq. No.	158731
Seq. ID	LIB3176-098-P1-K1-F5
Method	BLASTX
NCBI GI	g2244919
BLAST score	240
E value	2.0e-20
Match length	76
% identity	71
NCBI Description	(Z97339) hypothetical protein [Arabidopsis thaliana]

Seq. No.	158732
Seq. ID	LIB3176-098-P1-K1-F7
Method	BLASTX
NCBI GI	g4587542
BLAST score	183
E value	4.0e-14
Match length	39
% identity	92
NCBI Description	(AC006577) Belongs to the PF_00657 Lipase/Acylhydrolase with GDSL-motif family. ESTs gb_T45815, gb_T45130 and gb_Z38046 come from this gene. [Arabidopsis thaliana]

Seq. No.	158733
Seq. ID	LIB3176-098-P1-K1-F9
Method	BLASTN
NCBI GI	g4678291
BLAST score	197
E value	1.0e-107
Match length	229
% identity	97
NCBI Description	Arabidopsis thaliana DNA chromosome 3, BAC clone F28P10 (ESSA project)

Seq. No.	158734
Seq. ID	LIB3176-098-P1-K1-G1

Method	BLASTX
NCBI GI	g2494264
BLAST score	305
E value	7.0e-28
Match length	121
% identity	51
NCBI Description	HYPOTHETICAL 66.0 KD GTP-BINDING PROTEIN SLR1105 >gi_1651837_dbj_BAA16764_ (D90900) elongation factor EF-G [Synechocystis sp.]

Seq. No.	158735
Seq. ID	LIB3176-098-P1-K1-G10
Method	BLASTN
NCBI GI	g3150006
BLAST score	47
E value	9.0e-18
Match length	107
% identity	93
NCBI Description	CIC5B11.1 check: 4870 from: 1 to: 167234, complete sequence [Arabidopsis thaliana]

Seq. No.	158736
Seq. ID	LIB3176-098-P1-K1-G12
Method	BLASTX
NCBI GI	g3983125
BLAST score	510
E value	6.0e-52
Match length	125
% identity	81
NCBI Description	(AF097648) phosphate/triose-phosphate translocator precursor [Arabidopsis thaliana]

Seq. No.	158737
Seq. ID	LIB3176-098-P1-K1-G2
Method	BLASTN
NCBI GI	g3763915
BLAST score	240
E value	1.0e-132
Match length	264
% identity	98
NCBI Description	Arabidopsis thaliana chromosome II BAC F14B2 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	158738
Seq. ID	LIB3176-098-P1-K1-G3
Method	BLASTN
NCBI GI	g4512656
BLAST score	293
E value	1.0e-164
Match length	385
% identity	99
NCBI Description	Arabidopsis thaliana chromosome II BAC F7D19 genomic sequence, complete sequence

Seq. No.	158739
Seq. ID	LIB3176-098-P1-K1-G4
Method	BLASTN

NCBI GI	g4512656
BLAST score	55
E value	2.0e-22
Match length	115
% identity	87
NCBI Description	Arabidopsis thaliana chromosome II BAC F7D19 genomic sequence, complete sequence

Seq. No.	158740
Seq. ID	LIB3176-098-P1-K1-G6
Method	BLASTX
NCBI GI	g4337027
BLAST score	350
E value	1.0e-33
Match length	69
% identity	99
NCBI Description	(AF123254) MFP2 [Arabidopsis thaliana]

Seq. No.	158741
Seq. ID	LIB3176-098-P1-K1-G7
Method	BLASTX
NCBI GI	g3859607
BLAST score	356
E value	6.0e-34
Match length	98
% identity	77
NCBI Description	(AF104919) contains similarity to cysteine proteases (Pfam: PF00112, E=.21, N=1) [Arabidopsis thaliana]

Seq. No.	158742
Seq. ID	LIB3176-098-P1-K1-G8
Method	BLASTN
NCBI GI	g16316
BLAST score	273
E value	1.0e-152
Match length	289
% identity	99
NCBI Description	A.thaliana gene for histone H1-1

Seq. No.	158743
Seq. ID	LIB3176-098-P1-K1-G9
Method	BLASTX
NCBI GI	g416652
BLAST score	254
E value	3.0e-22
Match length	65
% identity	74
NCBI Description	PROBABLE GLUTATHIONE S-TRANSFERASE (AUXIN-INDUCED PROTEIN PCNT107) >gi_19793_emb_CAA39707_ (X56266) auxin-induced protein [Nicotiana tabacum]

Seq. No.	158744
Seq. ID	LIB3176-098-P1-K1-H1
Method	BLASTX
NCBI GI	g113024
BLAST score	349
E value	3.0e-33

Match length	94
% identity	72
NCBI Description	ISOCITRATE LYASE (ISOCITRASE) (ISOCITRATASE) (ICL) >gi_553043 (M83534) isocitrate lyase [Arabidopsis thaliana]

Seq. No.	158745
Seq. ID	LIB3176-098-P1-K1-H10
Method	BLASTX
NCBI GI	g2062158
BLAST score	172
E value	8.0e-13
Match length	43
% identity	39
NCBI Description	(AC001645) jasmonate inducible protein isolog [Arabidopsis thaliana]

Seq. No.	158746
Seq. ID	LIB3176-098-P1-K1-H11
Method	BLASTX
NCBI GI	g3420239
BLAST score	275
E value	6.0e-25
Match length	53
% identity	98
NCBI Description	(AF059484) actin [Gossypium hirsutum]

Seq. No.	158747
Seq. ID	LIB3176-098-P1-K1-H5
Method	BLASTX
NCBI GI	g4193382
BLAST score	278
E value	6.0e-25
Match length	79
% identity	70
NCBI Description	(AF083336) ribosomal protein S27 [Arabidopsis thaliana] >gi_4193384 (AF083337) ribosomal protein S27 [Arabidopsis thaliana]

Seq. No.	158748
Seq. ID	LIB3176-098-P1-K1-H7
Method	BLASTN
NCBI GI	g2266989
BLAST score	82
E value	1.0e-38
Match length	154
% identity	92
NCBI Description	Arabidopsis thaliana vacuolar type ATPase subunit A mRNA, complete cds

Seq. No.	158749
Seq. ID	LIB3176-098-P1-K1-H8
Method	BLASTX
NCBI GI	g4006883
BLAST score	422
E value	1.0e-41
Match length	108
% identity	78

NCBI Description	(Z99707) cysteine proteinase [Arabidopsis thaliana]
Seq. No.	158750
Seq. ID	LIB3176-098-P1-K1-H9
Method	BLASTN
NCBI GI	g3482964
BLAST score	207
E value	1.0e-113
Match length	246
% identity	100
NCBI Description	Arabidopsis thaliana DNA chromosome 2, BAC clone F13D4 (ESSAII project)
Seq. No.	158751
Seq. ID	LIB3176-099-P1-K1-A1
Method	BLASTX
NCBI GI	g4732091
BLAST score	194
E value	5.0e-15
Match length	76
% identity	43
NCBI Description	(AF126742) bundle sheath defective protein 2 [Zea mays]
Seq. No.	158752
Seq. ID	LIB3176-099-P1-K1-A10
Method	BLASTX
NCBI GI	g1170089
BLAST score	271
E value	2.0e-24
Match length	61
% identity	92
NCBI Description	GLUTATHIONE S-TRANSFERASE ERD13 (CLASS PHI) >gi_481822_pir__S39542 probable glutathione transferase (EC 2.5.1.18) (clone ERD13) - Arabidopsis thaliana >gi_497789_dbj_BAA04554_ (D17673) glutathione S-transferase [Arabidopsis thaliana] >gi_3201614 (AC004669) glutathione S-transferase [Arabidopsis thaliana]
Seq. No.	158753
Seq. ID	LIB3176-099-P1-K1-A12
Method	BLASTX
NCBI GI	g4262240
BLAST score	255
E value	1.0e-22
Match length	60
% identity	78
NCBI Description	(AC006200) putative stress protein [Arabidopsis thaliana]
Seq. No.	158754
Seq. ID	LIB3176-099-P1-K1-A4
Method	BLASTX
NCBI GI	g2828296
BLAST score	197
E value	1.0e-15
Match length	42
% identity	90
NCBI Description	(AL021687) RNase L inhibitor [Arabidopsis thaliana]

Seq. No.	158755
Seq. ID	LIB3176-099-P1-K1-A5
Method	BLASTX
NCBI GI	g1350720
BLAST score	226
E value	3.0e-19
Match length	54
% identity	89
NCBI Description	60S RIBOSOMAL PROTEIN L32

Seq. No.	158756
Seq. ID	LIB3176-099-P1-K1-A6
Method	BLASTX
NCBI GI	g4163997
BLAST score	341
E value	1.0e-32
Match length	66
% identity	94
NCBI Description	(AF087483) alpha-xylosidase precursor [Arabidopsis thaliana]

Seq. No.	158757
Seq. ID	LIB3176-099-P1-K1-A7
Method	BLASTX
NCBI GI	g3184073
BLAST score	169
E value	8.0e-12
Match length	100
% identity	40
NCBI Description	(AL023779) hypothetical protein [Schizosaccharomyces pombe]

Seq. No.	158758
Seq. ID	LIB3176-099-P1-K1-A9
Method	BLASTN
NCBI GI	g2924768
BLAST score	31
E value	9.0e-09
Match length	47
% identity	91
NCBI Description	Arabidopsis thaliana chromosome II BAC F25I18 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	158759
Seq. ID	LIB3176-099-P1-K1-B1
Method	BLASTX
NCBI GI	g116392
BLAST score	529
E value	3.0e-54
Match length	100
% identity	100
NCBI Description	CHALCONE SYNTHASE (NARINGENIN-CHALCONE SYNTHASE) >gi_66543_pir__SYMUCN naringenin-chalcone synthase (EC 2.3.1.74) - Arabidopsis thaliana >gi_166670 (M20308) chalcone synthase [Arabidopsis thaliana]

Seq. No.	158760

Seq. ID	LIB3176-099-P1-K1-B11
Method	BLASTN
NCBI GI	g4757405
BLAST score	143
E value	5.0e-75
Match length	143
% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MOJ10, complete sequence

Seq. No.	158761
Seq. ID	LIB3176-099-P1-K1-B12
Method	BLASTX
NCBI GI	g3047107
BLAST score	190
E value	2.0e-14
Match length	46
% identity	80
NCBI Description	(AF058919) Similar to actin binding protein; F6N23.12 [Arabidopsis thaliana]

Seq. No.	158762
Seq. ID	LIB3176-099-P1-K1-B2
Method	BLASTN
NCBI GI	g4662628
BLAST score	321
E value	0.0e+00
Match length	393
% identity	97
NCBI Description	Arabidopsis thaliana chromosome II BAC F27O10 genomic sequence, complete sequence

Seq. No.	158763
Seq. ID	LIB3176-099-P1-K1-B3
Method	BLASTX
NCBI GI	g477280
BLAST score	158
E value	9.0e-11
Match length	55
% identity	58
NCBI Description	mitochondrial processing peptidase (EC 3.4.99.41) 55K protein precursor - potato >gi_410633_bbs_136740 cytochrome c reductase-processing peptidase subunit I, MPP subunit I, P55 [potatoes, var. Marfona, tuber, Peptide Mitochondrial, 534 aa]

Seq. No.	158764
Seq. ID	LIB3176-099-P1-K1-B4
Method	BLASTN
NCBI GI	g170432
BLAST score	41
E value	9.0e-14
Match length	81
% identity	88
NCBI Description	Tomato ATP-dependent protease (CD4A) gene, complete cds

Seq. No. 158765

Seq. ID	LIB3176-099-P1-K1-B5
Method	BLASTN
NCBI GI	g4512656
BLAST score	195
E value	1.0e-105
Match length	401
% identity	97
NCBI Description	Arabidopsis thaliana chromosome II BAC F7D19 genomic sequence, complete sequence

Seq. No.	158766
Seq. ID	LIB3176-099-P1-K1-B6
Method	BLASTX
NCBI GI	g3264759
BLAST score	205
E value	1.0e-16
Match length	59
% identity	73
NCBI Description	(AF071889) 40S ribosomal protein S8 [Prunus armeniaca]

Seq. No.	158767
Seq. ID	LIB3176-099-P1-K1-B7
Method	BLASTX
NCBI GI	g2088654
BLAST score	236
E value	2.0e-20
Match length	56
% identity	86
NCBI Description	(AF002109) 60S acidic ribosomal protein P0 isolog [Arabidopsis thaliana]

Seq. No.	158768
Seq. ID	LIB3176-099-P1-K1-B8
Method	BLASTX
NCBI GI	g3913289
BLAST score	151
E value	4.0e-10
Match length	80
% identity	47
NCBI Description	CAFFEIC ACID 3-O-METHYLTRANSFERASE (S-ADENOSYSL-L-METHIONINE:CAFFEIC ACID 3-O-METHYLTRANSFERASE) (COMT) >gi_2240207 (AF006009) caffeic acid O-methyltransferase [Clarkia breweri]

Seq. No.	158769
Seq. ID	LIB3176-099-P1-K1-B9
Method	BLASTN
NCBI GI	g3228389
BLAST score	105
E value	3.0e-52
Match length	165
% identity	91
NCBI Description	Genomic sequence for Arabidopsis thaliana BAC F17L21, complete sequence [Arabidopsis thaliana]

Seq. No.	158770
Seq. ID	LIB3176-099-P1-K1-C1

Method	BLASTX
NCBI GI	g2244749
BLAST score	259
E value	5.0e-23
Match length	54
% identity	96
NCBI Description	(Z97335) hydroxymethyltransferase [Arabidopsis thaliana]

Seq. No.	158771
Seq. ID	LIB3176-099-P1-K1-C10
Method	BLASTN
NCBI GI	g3449327
BLAST score	75
E value	2.0e-34
Match length	138
% identity	99
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MCA23, complete sequence [Arabidopsis thaliana]

Seq. No.	158772
Seq. ID	LIB3176-099-P1-K1-C12
Method	BLASTN
NCBI GI	g3702731
BLAST score	141
E value	2.0e-73
Match length	157
% identity	97
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MFC19, complete sequence [Arabidopsis thaliana]

Seq. No.	158773
Seq. ID	LIB3176-099-P1-K1-C2
Method	BLASTX
NCBI GI	g282865
BLAST score	496
E value	2.0e-50
Match length	112
% identity	84
NCBI Description	chlorophyll a/b-binding protein - Arabidopsis thaliana >gi_16207_emb_CAA39534_ (X56062) chlorophyll A/B-binding protein [Arabidopsis thaliana] >gi_166644 (M85150) chlorophyll a/b-binding protein [Arabidopsis thaliana] >gi_4678304_emb_CAB41095.1_ (AL049655) chlorophyll a/b-binding protein [Arabidopsis thaliana]

Seq. No.	158774
Seq. ID	LIB3176-099-P1-K1-C4
Method	BLASTX
NCBI GI	g1750376
BLAST score	472
E value	1.0e-47
Match length	100
% identity	92
NCBI Description	(U80808) ubiquitin activating enzyme [Arabidopsis thaliana] >gi_3150409 (AC004165) ubiquitin activating enzyme (UBA1) [Arabidopsis thaliana]

Seq. No.	158775
Seq. ID	LIB3176-099-P1-K1-C6
Method	BLASTN
NCBI GI	g603055
BLAST score	271
E value	1.0e-151
Match length	279
% identity	99
NCBI Description	Arabidopsis thaliana inner mitochondrial membrane protein mRNA, complete cds

Seq. No.	158776
Seq. ID	LIB3176-099-P1-K1-C7
Method	BLASTN
NCBI GI	g3075383
BLAST score	78
E value	2.0e-36
Match length	78
% identity	100
NCBI Description	Arabidopsis thaliana chromosome II BAC T1D16 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	158777
Seq. ID	LIB3176-099-P1-K1-C8
Method	BLASTN
NCBI GI	g2264307
BLAST score	80
E value	1.0e-37
Match length	87
% identity	99
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MED24, complete sequence [Arabidopsis thaliana]

Seq. No.	158778
Seq. ID	LIB3176-099-P1-K1-D10
Method	BLASTX
NCBI GI	g3153205
BLAST score	428
E value	1.0e-42
Match length	92
% identity	88
NCBI Description	(U80922) serine/threonine protein phosphatase type one [Arabidopsis thaliana]

Seq. No.	158779
Seq. ID	LIB3176-099-P1-K1-D11
Method	BLASTX
NCBI GI	g132110
BLAST score	587
E value	6.0e-61
Match length	113
% identity	96
NCBI Description	RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN 3B PRECURSOR (RUBISCO SMALL SUBUNIT 3B) >gi_68060_pir__RKMUB3 ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain B3 precursor - Arabidopsis thaliana >gi_16195_emb_CAA32702_ (X14564) ribulose bisphosphate carboxylase [Arabidopsis

thaliana]

Seq. No.	158780
Seq. ID	LIB3176-099-P1-K1-D12
Method	BLASTX
NCBI GI	g4371298
BLAST score	430
E value	7.0e-43
Match length	87
% identity	57
NCBI Description	(AC006260) putative RNA-binding protein [Arabidopsis thaliana]

Seq. No.	158781
Seq. ID	LIB3176-099-P1-K1-D2
Method	BLASTX
NCBI GI	g1351014
BLAST score	306
E value	6.0e-28
Match length	79
% identity	75
NCBI Description	40S RIBOSOMAL PROTEIN S8 >gi_968902_dbj_BAA07207_ (D38010) ribosomal protein S8 [Oryza sativa]

Seq. No.	158782
Seq. ID	LIB3176-099-P1-K1-D3
Method	BLASTX
NCBI GI	g3158370
BLAST score	344
E value	7.0e-33
Match length	65
% identity	100
NCBI Description	(AF035382) catalase 3 [Arabidopsis thaliana]

Seq. No.	158783
Seq. ID	LIB3176-099-P1-K1-D5
Method	BLASTN
NCBI GI	g4220627
BLAST score	123
E value	1.0e-62
Match length	319
% identity	5
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K20J1, complete sequence [Arabidopsis thaliana]

Seq. No.	158784
Seq. ID	LIB3176-099-P1-K1-D6
Method	BLASTN
NCBI GI	g4757413
BLAST score	70
E value	4.0e-31
Match length	119
% identity	37
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MXO21, complete sequence

Seq. No.	158785

Seq. ID	LIB3176-099-P1-K1-D7
Method	BLASTN
NCBI GI	g4510323
BLAST score	44
E value	9.0e-16
Match length	71
% identity	92
NCBI Description	Arabidopsis thaliana BAC T7B11 from chromosome IV near 10 cM, complete sequence

Seq. No.	158786
Seq. ID	LIB3176-099-P1-K1-D8
Method	BLASTN
NCBI GI	g3785992
BLAST score	102
E value	2.0e-50
Match length	187
% identity	100
NCBI Description	Arabidopsis thaliana chromosome II BAC T6A23 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	158787
Seq. ID	LIB3176-099-P1-K1-D9
Method	BLASTN
NCBI GI	g4455290
BLAST score	317
E value	1.0e-178
Match length	410
% identity	100
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F18A5 (ESSAII project)

Seq. No.	158788
Seq. ID	LIB3176-099-P1-K1-E1
Method	BLASTN
NCBI GI	g3510339
BLAST score	150
E value	3.0e-79
Match length	150
% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K3K7, complete sequence [Arabidopsis thaliana]

Seq. No.	158789
Seq. ID	LIB3176-099-P1-K1-E10
Method	BLASTN
NCBI GI	g4755185
BLAST score	189
E value	1.0e-102
Match length	193
% identity	99
NCBI Description	Arabidopsis thaliana chromosome II BAC F5G3 genomic sequence, complete sequence

Seq. No.	158790
Seq. ID	LIB3176-099-P1-K1-E11
Method	BLASTX

NCBI GI	g135406
BLAST score	215
E value	6.0e-26
Match length	62
% identity	100
NCBI Description	TUBULIN ALPHA-3/ALPHA-5 CHAIN >gi_99768_pir__A32712 tubulin alpha-5 chain - Arabidopsis thaliana >gi_166912 (M17189) alpha-tubulin [Arabidopsis thaliana] >gi_166918 (M84698) alpha-5 tubulin [Arabidopsis thaliana]

Seq. No.	158791
Seq. ID	LIB3176-099-P1-K1-E2
Method	BLASTX
NCBI GI	g2498731
BLAST score	491
E value	6.0e-50
Match length	95
% identity	98
NCBI Description	PROBABLE NADP-DEPENDENT OXIDOREDUCTASE P1 >gi_1362013_pir__S57611 zeta-crystallin homolog - Arabidopsis thaliana >gi_886428_emb_CAA89838_ (Z49768) zeta-crystallin homologue [Arabidopsis thaliana]

Seq. No.	158792
Seq. ID	LIB3176-099-P1-K1-E5
Method	BLASTX
NCBI GI	g1363489
BLAST score	143
E value	2.0e-09
Match length	41
% identity	73
NCBI Description	thioglucosidase (EC 3.2.3.1) 3D precursor - Arabidopsis thaliana >gi_984052_emb_CAA61592_ (X89413) thioglucoside glucohydrolase [Arabidopsis thaliana]

Seq. No.	158793
Seq. ID	LIB3176-099-P1-K1-E6
Method	BLASTX
NCBI GI	g2493129
BLAST score	397
E value	4.0e-39
Match length	80
% identity	96
NCBI Description	VACUOLAR ATP SYNTHASE SUBUNIT B ISOFORM 1 (V-ATPASE B SUBUNIT) >gi_459198 (U07052) vacuolar H+-ATPase subunit B [Gossypium hirsutum]

Seq. No.	158794
Seq. ID	LIB3176-099-P1-K1-E8
Method	BLASTX
NCBI GI	g4558679
BLAST score	506
E value	1.0e-51
Match length	98
% identity	100
NCBI Description	(AC006586) 40S Ribosomal protein S16 [Arabidopsis thaliana]

Seq. No.	158795
Seq. ID	LIB3176-099-P1-K1-E9
Method	BLASTX
NCBI GI	g282833
BLAST score	342
E value	2.0e-32
Match length	83
% identity	82
NCBI Description	phosphoglycerate kinase (EC 2.7.2.3) - spinach (fragment)

Seq. No.	158796
Seq. ID	LIB3176-099-P1-K1-F1
Method	BLASTX
NCBI GI	g730456
BLAST score	300
E value	3.0e-27
Match length	74
% identity	72
NCBI Description	40S RIBOSOMAL PROTEIN S19

Seq. No.	158797
Seq. ID	LIB3176-099-P1-K1-F12
Method	BLASTN
NCBI GI	g1764099
BLAST score	36
E value	2.0e-11
Match length	63
% identity	94
NCBI Description	Arabidopsis thaliana GDP-D-mannose-4,6-dehydratase (MUR1) mRNA, complete cds

Seq. No.	158798
Seq. ID	LIB3176-099-P1-K1-F3
Method	BLASTX
NCBI GI	g1172806
BLAST score	240
E value	3.0e-20
Match length	43
% identity	100
NCBI Description	60S RIBOSOMAL PROTEIN L10 (WILM'S TUMOR SUPPRESSOR PROTEIN HOMOLOG) >gi_478401_pir__JQ2244 ribosomal protein L10.e, cytosolic - Arabidopsis thaliana >gi_17682_emb_CAA78856_ (Z15157) Wilm's tumor suppressor homologue [Arabidopsis thaliana]

Seq. No.	158799
Seq. ID	LIB3176-099-P1-K1-F4
Method	BLASTN
NCBI GI	g4760369
BLAST score	157
E value	7.0e-83
Match length	157
% identity	100
NCBI Description	Arabidopsis thaliana ATP dependent copper transporter (RAN1) mRNA, complete cds

Seq. No.	158800

Seq. ID	LIB3176-099-P1-K1-F6
Method	BLASTN
NCBI GI	g3985954
BLAST score	60
E value	5.0e-25
Match length	84
% identity	48
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MRG21, complete sequence [Arabidopsis thaliana]

Seq. No.	158801
Seq. ID	LIB3176-099-P1-K1-F7
Method	BLASTX
NCBI GI	g3024871
BLAST score	271
E value	3.0e-24
Match length	85
% identity	61
NCBI Description	HYPOTHETICAL 77.3 KD PROTEIN SLL0005 >gi_1001579_dbj_BAA10206_ (D64000) ABC1-like [Synechocystis sp.]

Seq. No.	158802
Seq. ID	LIB3176-099-P1-K1-F8
Method	BLASTN
NCBI GI	g166705
BLAST score	87
E value	2.0e-41
Match length	87
% identity	100
NCBI Description	Arabidopsis thaliana glyceraldehyde-3-phosphate dehydrogenase C subunit (GapC) gene, complete cds

Seq. No.	158803
Seq. ID	LIB3176-099-P1-K1-F9
Method	BLASTX
NCBI GI	g119350
BLAST score	192
E value	4.0e-18
Match length	53
% identity	100
NCBI Description	ENOLASE (2-PHOSPHOGLYCERATE DEHYDRATASE) (2-PHOSPHO-D-GLYCERATE HYDRO-LYASE) >gi_81608_pir__JQ1187 phosphopyruvate hydratase (EC 4.2.1.11) - Arabidopsis thaliana >gi_16271_emb_CAA41114_ (X58107) enolase [Arabidopsis thaliana] >gi_4581151_gb_AAD24635.1_AC006919_13 (AC006919) enolase (2-phospho-D-glycerate hydroylase);identical to P25696 [Arabidopsis thaliana]

Seq. No.	158804
Seq. ID	LIB3176-099-P1-K1-G1
Method	BLASTN
NCBI GI	g3292807
BLAST score	186
E value	1.0e-100
Match length	194

% identity	99
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F7H19 (ESSAII project)

Seq. No.	158805
Seq. ID	LIB3176-099-P1-K1-G11
Method	BLASTX
NCBI GI	g4753651
BLAST score	143
E value	2.0e-09
Match length	35
% identity	83
NCBI Description	(AL049751) ribosomal protein L13a like protein [Arabidopsis thaliana]

Seq. No.	158806
Seq. ID	LIB3176-099-P1-K1-G12
Method	BLASTX
NCBI GI	g4371282
BLAST score	259
E value	5.0e-23
Match length	61
% identity	85
NCBI Description	(AC006260) putative 60S ribosomal protein L12 [Arabidopsis thaliana]

Seq. No.	158807
Seq. ID	LIB3176-099-P1-K1-G2
Method	BLASTX
NCBI GI	g2851508
BLAST score	491
E value	8.0e-50
Match length	100
% identity	94
NCBI Description	60S RIBOSOMAL PROTEIN L21 >gi_2160162 (AC000132) Similar to ribosomal protein L21 (gb_L38826). ESTs gb_AA395597,gb_ATTS5197 come from this gene. [Arabidopsis thaliana] >gi_3482935 (AC003970) Putative ribosomal protein L21 [Arabidopsis thaliana]

Seq. No.	158808
Seq. ID	LIB3176-099-P1-K1-G3
Method	BLASTN
NCBI GI	g3451391
BLAST score	143
E value	5.0e-75
Match length	155
% identity	98
NCBI Description	Arabidopsis thaliana mRNA for mitochondrial uncoupling protein

Seq. No.	158809
Seq. ID	LIB3176-099-P1-K1-G4
Method	BLASTX
NCBI GI	g2062161
BLAST score	213
E value	1.0e-17

Match length	43
% identity	93
NCBI Description	(AC001645) jasmonate inducible protein isolog [Arabidopsis thaliana]

Seq. No.	158810
Seq. ID	LIB3176-099-P1-K1-G5
Method	BLASTX
NCBI GI	g4127456
BLAST score	245
E value	2.0e-21
Match length	53
% identity	100
NCBI Description	(AJ010818) Cpn21 protein [Arabidopsis thaliana]

Seq. No.	158811
Seq. ID	LIB3176-099-P1-K1-G6
Method	BLASTX
NCBI GI	g3885511
BLAST score	347
E value	7.0e-33
Match length	95
% identity	76
NCBI Description	(AF084200) similar to PSI-K subunit of photosystem I from barley [Medicago sativa]

Seq. No.	158812
Seq. ID	LIB3176-099-P1-K1-G7
Method	BLASTN
NCBI GI	g547390
BLAST score	39
E value	1.0e-12
Match length	46
% identity	96
NCBI Description	Arabidopsis thaliana TRAP mRNA, partial cds

Seq. No.	158813
Seq. ID	LIB3176-099-P1-K1-G8
Method	BLASTN
NCBI GI	g4835223
BLAST score	83
E value	4.0e-39
Match length	164
% identity	93
NCBI Description	Arabidopsis thaliana DNA chromosome 3, BAC clone F18B3 (ESSA project)

Seq. No.	158814
Seq. ID	LIB3176-099-P1-K1-H1
Method	BLASTX
NCBI GI	g3355471
BLAST score	178
E value	1.0e-13
Match length	66
% identity	47
NCBI Description	(AC004218) putative lysophospholipase [Arabidopsis thaliana]

Seq. No.	158815
Seq. ID	LIB3176-099-P1-K1-H2
Method	BLASTX
NCBI GI	g2982301
BLAST score	177
E value	5.0e-13
Match length	74
% identity	51
NCBI Description	(AF051235) YGL010w-like protein [Picea mariana]

Seq. No.	158816
Seq. ID	LIB3176-099-P1-K1-H3
Method	BLASTN
NCBI GI	g3985955
BLAST score	35
E value	3.0e-10
Match length	39
% identity	97
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MTH16, complete sequence [Arabidopsis thaliana]

Seq. No.	158817
Seq. ID	LIB3176-099-P1-K1-H5
Method	BLASTN
NCBI GI	g3236234
BLAST score	95
E value	4.0e-46
Match length	202
% identity	98
NCBI Description	Arabidopsis thaliana chromosome II BAC F13M22 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	158818
Seq. ID	LIB3176-099-P1-K1-H7
Method	BLASTX
NCBI GI	g232031
BLAST score	173
E value	6.0e-13
Match length	53
% identity	60
NCBI Description	ELONGATION FACTOR 1 BETA' >gi_322851_pir__S29224 translation elongation factor eEF-1 beta' chain - rice >gi_218161_dbj_BAA02253_ (D12821) elongation factor 1 beta' [Oryza sativa]

Seq. No.	158819
Seq. ID	LIB3176-099-P1-K1-H9
Method	BLASTN
NCBI GI	g3337347
BLAST score	66
E value	2.0e-29
Match length	74
% identity	97
NCBI Description	Arabidopsis thaliana chromosome II BAC F13P17 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	158820
Seq. ID	LIB3176-101-P1-K1-A1
Method	BLASTX
NCBI GI	g464621
BLAST score	169
E value	2.0e-12
Match length	43
% identity	72
NCBI Description	60S RIBOSOMAL PROTEIN L6 (YL16-LIKE) >gi_280374_pir__S28586 ribosomal protein ML16 - common ice plant >gi_19539_emb_CAA49175_ (X69378) ribosomal protein YL16 [Mesembryanthemum crystallinum]

Seq. No.	158821
Seq. ID	LIB3176-101-P1-K1-A10
Method	BLASTX
NCBI GI	g1076366
BLAST score	532
E value	1.0e-54
Match length	104
% identity	96
NCBI Description	peptidylprolyl isomerase (EC 5.2.1.8) - Arabidopsis thaliana >gi_460968 (U07276) peptidyl-prolyl cis-trans isomerase [Arabidopsis thaliana] >gi_992643 (U32186) cyclophilin [Arabidopsis thaliana] >gi_1091580_prf__2021266A peptidyl-Pro cis-trans isomerase [Arabidopsis thaliana]

Seq. No.	158822
Seq. ID	LIB3176-101-P1-K1-A11
Method	BLASTX
NCBI GI	g549056
BLAST score	222
E value	3.0e-18
Match length	67
% identity	67
NCBI Description	T-COMPLEX PROTEIN 1, BETA SUBUNIT (TCP-1-BETA) (CCT-BETA) >gi_631651_pir__S43059 CCT (chaperonin containing TCP-1) beta chain - mouse >gi_468546_emb_CAA83428_ (Z31553) CCT (chaperonin containing TCP-1) beta subunit [Mus musculus]

Seq. No.	158823
Seq. ID	LIB3176-101-P1-K1-A12
Method	BLASTX
NCBI GI	g549056
BLAST score	222
E value	4.0e-18
Match length	70
% identity	66
NCBI Description	T-COMPLEX PROTEIN 1, BETA SUBUNIT (TCP-1-BETA) (CCT-BETA) >gi_631651_pir__S43059 CCT (chaperonin containing TCP-1) beta chain - mouse >gi_468546_emb_CAA83428_ (Z31553) CCT (chaperonin containing TCP-1) beta subunit [Mus musculus]

Seq. No.	158824
Seq. ID	LIB3176-101-P1-K1-A5
Method	BLASTN

NCBI GI	g2335089
BLAST score	107
E value	1.0e-53
Match length	115
% identity	98
NCBI Description	Arabidopsis thaliana chromosome II BAC T11A7 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	158825
Seq. ID	LIB3176-101-P1-K1-A6
Method	BLASTN
NCBI GI	g3668073
BLAST score	398
E value	0.0e+00
Match length	398
% identity	100
NCBI Description	Arabidopsis thaliana chromosome II BAC T4C15 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	158826
Seq. ID	LIB3176-101-P1-K1-A7
Method	BLASTN
NCBI GI	g2564045
BLAST score	132
E value	2.0e-68
Match length	144
% identity	98
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K8K14, complete sequence [Arabidopsis thaliana]

Seq. No.	158827
Seq. ID	LIB3176-101-P1-K1-A8
Method	BLASTN
NCBI GI	g4584387
BLAST score	75
E value	4.0e-34
Match length	127
% identity	98
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F7J7 (ESSA project)

Seq. No.	158828
Seq. ID	LIB3176-101-P1-K1-A9
Method	BLASTX
NCBI GI	g2655420
BLAST score	260
E value	4.0e-23
Match length	50
% identity	98
NCBI Description	(AF035414) heat shock cognate protein HSC70 [Brassica napus]

Seq. No.	158829
Seq. ID	LIB3176-101-P1-K1-B1
Method	BLASTN
NCBI GI	g1769904
BLAST score	229

E value	1.0e-126
Match length	237
% identity	99
NCBI Description	A.thaliana psbP gene

Seq. No.	158830
Seq. ID	LIB3176-101-P1-K1-B10
Method	BLASTX
NCBI GI	g3193285
BLAST score	412
E value	2.0e-40
Match length	90
% identity	91
NCBI Description	(AF069298) T14P8.18 gene product [Arabidopsis thaliana]

Seq. No.	158831
Seq. ID	LIB3176-101-P1-K1-B11
Method	BLASTN
NCBI GI	g4159707
BLAST score	162
E value	3.0e-86
Match length	162
% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MJK13, complete sequence

Seq. No.	158832
Seq. ID	LIB3176-101-P1-K1-B12
Method	BLASTX
NCBI GI	g4585882
BLAST score	483
E value	1.0e-48
Match length	93
% identity	99
NCBI Description	(AC005850) PSI type III chlorophyll a/b-binding protein [Arabidopsis thaliana]

Seq. No.	158833
Seq. ID	LIB3176-101-P1-K1-B2
Method	BLASTX
NCBI GI	g3335365
BLAST score	549
E value	2.0e-56
Match length	136
% identity	80
NCBI Description	(AC003028) high affinity calcium antiporter [Arabidopsis thaliana]

Seq. No.	158834
Seq. ID	LIB3176-101-P1-K1-B3
Method	BLASTN
NCBI GI	g2827142
BLAST score	265
E value	1.0e-147
Match length	301
% identity	97
NCBI Description	Arabidopsis thaliana cellulose synthase catalytic subunit

(Ath-B) mRNA, complete cds

Seq. No.	158835
Seq. ID	LIB3176-101-P1-K1-B4
Method	BLASTX
NCBI GI	g4336756
BLAST score	547
E value	2.0e-56
Match length	107
% identity	97
NCBI Description	(AF104453) catalase [Brassica juncea]

Seq. No.	158836
Seq. ID	LIB3176-101-P1-K1-B5
Method	BLASTN
NCBI GI	g12219
BLAST score	114
E value	3.0e-57
Match length	350
% identity	92
NCBI Description	Mustard chloroplast trnk gene for tRNA-Lys(UUU)

Seq. No.	158837
Seq. ID	LIB3176-101-P1-K1-B7
Method	BLASTX
NCBI GI	g4587541
BLAST score	631
E value	5.0e-66
Match length	132
% identity	94
NCBI Description	(AC006577) Belongs to the PF_00657 Lipase/Acylhydrolase with GDSL-motif family. ESTs gb_T44453, gb_T04815, gb_T45993, gb_R30138, gb_AI099570 and gb_T22281 come from this gene. [Arabidopsis thaliana]

Seq. No.	158838
Seq. ID	LIB3176-101-P1-K1-B8
Method	BLASTX
NCBI GI	g1709446
BLAST score	520
E value	4.0e-53
Match length	113
% identity	93
NCBI Description	PYRUVATE DEHYDROGENASE E1 COMPONENT, ALPHA SUBUNIT PRECURSOR (PDHE1-A) >gi_2117533_pir__JC4358 pyruvate dehydrogenase (lipoamide) (EC 1.2.4.1) complex E1 alpha chain - Arabidopsis thaliana mitochondrion >gi_710400 (U21214) pyruvate dehydrogenase E1 alpha subunit [Arabidopsis thaliana]

Seq. No.	158839
Seq. ID	LIB3176-101-P1-K1-B9
Method	BLASTN
NCBI GI	g4558521
BLAST score	269
E value	1.0e-149
Match length	437

% identity	99
NCBI Description	Genomic sequence for Arabidopsis thaliana BAC T10O24, complete sequence
Seq. No.	158840
Seq. ID	LIB3176-101-P1-K1-C1
Method	BLASTX
NCBI GI	g3176668
BLAST score	544
E value	5.0e-56
Match length	107
% identity	98
NCBI Description	(AC004393) Similar to ribosomal protein L17 gb_X62724 from Hordeum vulgare. ESTs gb_Z34728, gb_F19974, gb_T75677 and gb_Z33937 come from this gene. [Arabidopsis thaliana]
Seq. No.	158841
Seq. ID	LIB3176-101-P1-K1-C10
Method	BLASTN
NCBI GI	g4455168
BLAST score	100
E value	2.0e-49
Match length	136
% identity	92
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F10M10 (ESSAII project)
Seq. No.	158842
Seq. ID	LIB3176-101-P1-K1-C11
Method	BLASTX
NCBI GI	g113379
BLAST score	223
E value	3.0e-18
Match length	73
% identity	62
NCBI Description	ALCOHOL DEHYDROGENASE 2 >gi_65902_pir__DEPOA2 alcohol dehydrogenase (EC 1.1.1.1) 2 - potato >gi_169469 (M25153) alcohol dehydrogenase 2 (EC 1.1.1.1) [Solanum tuberosum]
Seq. No.	158843
Seq. ID	LIB3176-101-P1-K1-C12
Method	BLASTX
NCBI GI	g2911057
BLAST score	622
E value	6.0e-65
Match length	121
% identity	100
NCBI Description	(AL021961) caffeoyl-CoA O-methyltransferase - like protein [Arabidopsis thaliana]
Seq. No.	158844
Seq. ID	LIB3176-101-P1-K1-C2
Method	BLASTX
NCBI GI	g126766
BLAST score	157
E value	4.0e-11
Match length	43

% identity	74
NCBI Description	MALATE SYNTHASE, GLYOXYSOMAL >gi_68216_pir__SYRPMA malate synthase (EC 4.1.3.2), glyoxysomal - rape >gi_167150 (J04468) malate synthase (EC 4.1.3.2) [Brassica napus]

Seq. No.	158845
Seq. ID	LIB3176-101-P1-K1-C3
Method	BLASTX
NCBI GI	g4544419
BLAST score	289
E value	4.0e-26
Match length	90
% identity	70
NCBI Description	(AC006955) unknown protein [Arabidopsis thaliana]

Seq. No.	158846
Seq. ID	LIB3176-101-P1-K1-C4
Method	BLASTN
NCBI GI	g3510247
BLAST score	237
E value	1.0e-130
Match length	342
% identity	97
NCBI Description	Arabidopsis thaliana chromosome II BAC F19D11 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	158847
Seq. ID	LIB3176-101-P1-K1-C5
Method	BLASTX
NCBI GI	g2062161
BLAST score	55
E value	8.0e-41
Match length	94
% identity	50
NCBI Description	(AC001645) jasmonate inducible protein isolog [Arabidopsis thaliana]

Seq. No.	158848
Seq. ID	LIB3176-101-P1-K1-C7
Method	BLASTX
NCBI GI	g4689386
BLAST score	361
E value	2.0e-34
Match length	139
% identity	55
NCBI Description	(AF139468) photosystem I reaction center subunit III [Vigna radiata]

Seq. No.	158849
Seq. ID	LIB3176-101-P1-K1-C8
Method	BLASTN
NCBI GI	g2264307
BLAST score	75
E value	6.0e-34
Match length	75
% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:

MED24, complete sequence [Arabidopsis thaliana]

Seq. No.	158850
Seq. ID	LIB3176-101-P1-K1-C9
Method	BLASTX
NCBI GI	g1370184
BLAST score	214
E value	9.0e-18
Match length	47
% identity	91
NCBI Description	(Z73941) RAB7B [Lotus japonicus]

Seq. No.	158851
Seq. ID	LIB3176-101-P1-K1-D1
Method	BLASTN
NCBI GI	g438450
BLAST score	187
E value	1.0e-101
Match length	223
% identity	96
NCBI Description	Arabidopsis thaliana delta-12 desaturase (Fad2) mRNA, complete cds

Seq. No.	158852
Seq. ID	LIB3176-101-P1-K1-D10
Method	BLASTX
NCBI GI	g1773330
BLAST score	278
E value	3.0e-25
Match length	62
% identity	87
NCBI Description	(U80071) glycolate oxidase [Mesembryanthemum crystallinum]

Seq. No.	158853
Seq. ID	LIB3176-101-P1-K1-D11
Method	BLASTX
NCBI GI	g2911071
BLAST score	252
E value	9.0e-22
Match length	101
% identity	55
NCBI Description	(AL021960) hypothetical protein [Arabidopsis thaliana]

Seq. No.	158854
Seq. ID	LIB3176-101-P1-K1-D12
Method	BLASTX
NCBI GI	g3023848
BLAST score	549
E value	2.0e-56
Match length	119
% identity	34
NCBI Description	GUANINE NUCLEOTIDE-BINDING PROTEIN BETA SUBUNIT-LIKE PROTEIN (WD-40 REPEAT AUXIN-DEPENDENT PROTEIN ARCA) >gi_2289095 (U77381) WD-40 repeat protein [Arabidopsis thaliana]

Seq. No. 158855

Seq. ID	LIB3176-101-P1-K1-D2
Method	BLASTX
NCBI GI	g4544419
BLAST score	304
E value	1.0e-27
Match length	64
% identity	94
NCBI Description	(AC006955) unknown protein [Arabidopsis thaliana]

Seq. No.	158856
Seq. ID	LIB3176-101-P1-K1-D3
Method	BLASTN
NCBI GI	g3522932
BLAST score	152
E value	4.0e-80
Match length	309
% identity	94
NCBI Description	Arabidopsis thaliana chromosome II BAC F14M4 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	158857
Seq. ID	LIB3176-101-P1-K1-D4
Method	BLASTX
NCBI GI	g4417280
BLAST score	547
E value	3.0e-56
Match length	123
% identity	90
NCBI Description	(AC007019) putative ATP synthase [Arabidopsis thaliana]

Seq. No.	158858
Seq. ID	LIB3176-101-P1-K1-D7
Method	BLASTN
NCBI GI	g2656030
BLAST score	110
E value	3.0e-55
Match length	169
% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MUL8

Seq. No.	158859
Seq. ID	LIB3176-101-P1-K1-D8
Method	BLASTN
NCBI GI	g2618683
BLAST score	40
E value	1.0e-13
Match length	81
% identity	96
NCBI Description	Arabidopsis thaliana chromosome II BAC T32G6 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	158860
Seq. ID	LIB3176-101-P1-K1-D9
Method	BLASTX
NCBI GI	g445612
BLAST score	466

E value	8.0e-47
Match length	102
% identity	88
NCBI Description	ribosomal protein S19 [Solanum tuberosum]

Seq. No.	158861
Seq. ID	LIB3176-101-P1-K1-E1
Method	BLASTX
NCBI GI	g119143
BLAST score	316
E value	1.0e-29
Match length	63
% identity	97
NCBI Description	ELONGATION FACTOR 1-ALPHA (EF-1-ALPHA) >gi_81606_pir__S06724 translation elongation factor eEF-1 alpha chain - Arabidopsis thaliana >gi_295788_emb_CAA34453_ (X16430) elongation factor 1-alpha [Arabidopsis thaliana] >gi_1369927_emb_CAA34454_ (X16431) elongation factor 1-alpha [Arabidopsis thaliana] >gi_1369928_emb_CAA34455_ (X16431) elongation factor 1-alpha [Arabidopsis thaliana] >gi_1532172 (U63815) EF-1alpha-A1 [Arabidopsis thaliana] >gi_1532173 (U63815) EF-1alpha-A2 [Arabidopsis thaliana] >gi_1532174 (U63815) EF-1alpha-A3 [Arabidopsis thaliana]

Seq. No.	158862
Seq. ID	LIB3176-101-P1-K1-E10
Method	BLASTX
NCBI GI	g2243120
BLAST score	161
E value	1.0e-11
Match length	32
% identity	100
NCBI Description	(Y10845) O-acetylserine(thiol) lyase [Brassica juncea]

Seq. No.	158863
Seq. ID	LIB3176-101-P1-K1-E11
Method	BLASTN
NCBI GI	g3193282
BLAST score	228
E value	1.0e-125
Match length	285
% identity	99
NCBI Description	Arabidopsis thaliana BAC T14P8

Seq. No.	158864
Seq. ID	LIB3176-101-P1-K1-E2
Method	BLASTX
NCBI GI	g3024022
BLAST score	580
E value	5.0e-60
Match length	127
% identity	85
NCBI Description	INITIATION FACTOR 5A-5 (EIF-5A) (EIF-4D) >gi_2225885_dbj_BAA20879_ (AB004826) eukaryotic initiation factor 5A5 [Solanum tuberosum]

Seq. No.	158865

Seq. ID	LIB3176-101-P1-K1-E3
Method	BLASTX
NCBI GI	g4582468
BLAST score	180
E value	9.0e-14
Match length	39
% identity	95
NCBI Description	(AC007071) putative 40S ribosomal protein; contains C-terminal domain [Arabidopsis thaliana]

Seq. No.	158866
Seq. ID	LIB3176-101-P1-K1-E4
Method	BLASTN
NCBI GI	g2182286
BLAST score	247
E value	1.0e-136
Match length	247
% identity	100
NCBI Description	Sequence of BAC F20P5 from Arabidopsis thaliana chromosome 1, complete sequence [Arabidopsis thaliana]

Seq. No.	158867
Seq. ID	LIB3176-101-P1-K1-E5
Method	BLASTN
NCBI GI	g2182286
BLAST score	186
E value	1.0e-100
Match length	194
% identity	91
NCBI Description	Sequence of BAC F20P5 from Arabidopsis thaliana chromosome 1, complete sequence [Arabidopsis thaliana]

Seq. No.	158868
Seq. ID	LIB3176-101-P1-K1-E7
Method	BLASTX
NCBI GI	g4371282
BLAST score	272
E value	1.0e-24
Match length	57
% identity	93
NCBI Description	(AC006260) putative 60S ribosomal protein L12 [Arabidopsis thaliana]

Seq. No.	158869
Seq. ID	LIB3176-101-P1-K1-F1
Method	BLASTX
NCBI GI	g484656
BLAST score	512
E value	4.0e-52
Match length	134
% identity	74
NCBI Description	monodehydroascorbate reductase (NADH) (EC 1.6.5.4) - cucumber >gi_452165_dbj_BAA05408_ (D26392) monodehydroascorbate reductase [Cucumis sativus]

Seq. No.	158870
Seq. ID	LIB3176-101-P1-K1-F10

Method	BLASTX
NCBI GI	g1352347
BLAST score	472
E value	2.0e-47
Match length	93
% identity	100
NCBI Description	ELONGATION FACTOR 1-BETA A1 (EF-1-BETA) >gi_480620_pir__S37103 translation elongation factor eEF-1 beta-A1 chain - Arabidopsis thaliana (cv. Colombia) >gi_398608_emb_CAA52751_ (X74733) elongation factor-1 beta A1 [Arabidopsis thaliana]

Seq. No.	158871
Seq. ID	LIB3176-101-P1-K1-F11
Method	BLASTN
NCBI GI	g3004543
BLAST score	251
E value	1.0e-139
Match length	324
% identity	99
NCBI Description	Arabidopsis thaliana chromosome II BAC F19F24 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	158872
Seq. ID	LIB3176-101-P1-K1-F12
Method	BLASTN
NCBI GI	g2275194
BLAST score	106
E value	1.0e-52
Match length	273
% identity	95
NCBI Description	Arabidopsis thaliana chromosome II BAC T08I13 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	158873
Seq. ID	LIB3176-101-P1-K1-F2
Method	BLASTX
NCBI GI	g113024
BLAST score	399
E value	3.0e-54
Match length	114
% identity	94
NCBI Description	ISOCITRATE LYASE (ISOCITRASE) (ISOCITRATASE) (ICL) >gi_553043 (M83534) isocitrate lyase [Arabidopsis thaliana]

Seq. No.	158874
Seq. ID	LIB3176-101-P1-K1-F3
Method	BLASTX
NCBI GI	g166765
BLAST score	337
E value	8.0e-32
Match length	71
% identity	92
NCBI Description	(M23106) heat shock protein HSP70-1 [Arabidopsis thaliana]

Seq. No.	158875
Seq. ID	LIB3176-101-P1-K1-F4

Method	BLASTN
NCBI GI	g2924733
BLAST score	249
E value	1.0e-138
Match length	289
% identity	96
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MUF9, complete sequence [Arabidopsis thaliana]

Seq. No.	158876
Seq. ID	LIB3176-101-P1-K1-F5
Method	BLASTN
NCBI GI	g2264312
BLAST score	172
E value	3.0e-92
Match length	176
% identity	99
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MOK16, complete sequence [Arabidopsis thaliana]

Seq. No.	158877
Seq. ID	LIB3176-101-P1-K1-F6
Method	BLASTX
NCBI GI	g2306917
BLAST score	454
E value	1.0e-45
Match length	85
% identity	100
NCBI Description	(AF003728) plasma membrane intrinsic protein [Arabidopsis thaliana]

Seq. No.	158878
Seq. ID	LIB3176-101-P1-K1-F7
Method	BLASTX
NCBI GI	g2738248
BLAST score	284
E value	6.0e-26
Match length	60
% identity	90
NCBI Description	(U97200) cobalamin-independent methionine synthase [Arabidopsis thaliana]

Seq. No.	158879
Seq. ID	LIB3176-101-P1-K1-F8
Method	BLASTX
NCBI GI	g728873
BLAST score	335
E value	6.0e-32
Match length	71
% identity	92
NCBI Description	L-ASCORBATE PEROXIDASE, CYTOSOLIC (AP) >gi_322534_pir__S28856 L-ascorbate peroxidase (EC 1.11.1.11), cytosolic - Arabidopsis thaliana >gi_16173_emb_CAA42168_ (X59600) L-ascorbate peroxidase [Arabidopsis thaliana] >gi_217833_dbj_BAA03334_ (D14442) ascorbate peroxidase [Arabidopsis thaliana] >gi_1532170 (U63815) ascorbate peroxidase [Arabidopsis thaliana]

Seq. No.	158880
Seq. ID	LIB3176-101-P1-K1-F9
Method	BLASTX
NCBI GI	g3193323
BLAST score	382
E value	4.0e-37
Match length	80
% identity	95
NCBI Description	(AF069299) similar to ribosomal protein S13 (Pfam; S15.hmm, score: 78.35); identical to Arabidopsis 40S ribosomal protein S13 (fragment) (SW: P49203A) except the first 32 amino acids are different [Arabidopsis thaliana]

Seq. No.	158881
Seq. ID	LIB3176-101-P1-K1-G1
Method	BLASTX
NCBI GI	g3219271
BLAST score	292
E value	1.0e-26
Match length	63
% identity	90
NCBI Description	(AB015315) MAP kinase kinase 4 [Arabidopsis thaliana]

Seq. No.	158882
Seq. ID	LIB3176-101-P1-K1-G10
Method	BLASTX
NCBI GI	g2651314
BLAST score	186
E value	2.0e-14
Match length	53
% identity	70
NCBI Description	(AC002336) putative ribosomal protein S26 [Arabidopsis thaliana]

Seq. No.	158883
Seq. ID	LIB3176-101-P1-K1-G11
Method	BLASTX
NCBI GI	g1524280
BLAST score	188
E value	1.0e-14
Match length	71
% identity	54
NCBI Description	(Z79702) rocE [Mycobacterium tuberculosis]

Seq. No.	158884
Seq. ID	LIB3176-101-P1-K1-G12
Method	BLASTX
NCBI GI	g4587544
BLAST score	521
E value	2.0e-53
Match length	110
% identity	95
NCBI Description	(AC006577) Belongs to the PF_00657 Lipase/Acylhydrolase with GDSL-motif family. ESTs gb_T75865, gb_R30449, gb_AI239373, gb_F19931 and gb_F19930 come from this gene. [Arabidopsis thaliana]

Seq. No.	158885
Seq. ID	LIB3176-101-P1-K1-G2
Method	BLASTX
NCBI GI	g400983
BLAST score	221
E value	5.0e-18
Match length	49
% identity	88
NCBI Description	50S RIBOSOMAL PROTEIN L11, CHLOROPLAST PRECURSOR (CL11) >gi_279648_pir__R5SP11 ribosomal protein L11 precursor - spinach >gi_21313_emb_CAA39950_ (X56615) ribosomal protein L11 [Spinacia oleracea]

Seq. No.	158886
Seq. ID	LIB3176-101-P1-K1-G4
Method	BLASTX
NCBI GI	g4455253
BLAST score	637
E value	1.0e-66
Match length	151
% identity	81
NCBI Description	(AL035523) superoxide dismutase (EC 1.15.1.1) (Fe)(fragment) [Arabidopsis thaliana]

Seq. No.	158887
Seq. ID	LIB3176-101-P1-K1-G5
Method	BLASTX
NCBI GI	g4469023
BLAST score	499
E value	1.0e-50
Match length	125
% identity	78
NCBI Description	(AL035602) putative protein [Arabidopsis thaliana]

Seq. No.	158888
Seq. ID	LIB3176-101-P1-K1-G6
Method	BLASTX
NCBI GI	g3021506
BLAST score	241
E value	1.0e-20
Match length	93
% identity	54
NCBI Description	(X96727) isocitrate dehydrogenase (NAD+) [Nicotiana tabacum]

Seq. No.	158889
Seq. ID	LIB3176-101-P1-K1-G7
Method	BLASTX
NCBI GI	g2529682
BLAST score	289
E value	5.0e-26
Match length	118
% identity	53
NCBI Description	(AC002535) unknown protein [Arabidopsis thaliana]

Seq. No.	158890

Seq. ID	LIB3176-101-P1-K1-G8
Method	BLASTN
NCBI GI	g4191771
BLAST score	282
E value	1.0e-157
Match length	294
% identity	99
NCBI Description	Arabidopsis thaliana chromosome II BAC F3P11 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	158891
Seq. ID	LIB3176-101-P1-K1-G9
Method	BLASTN
NCBI GI	g4102581
BLAST score	148
E value	9.0e-78
Match length	214
% identity	100
NCBI Description	Arabidopsis thaliana CAO gene, nuclear gene encoding chloroplast protein, complete cds

Seq. No.	158892
Seq. ID	LIB3176-101-P1-K1-H1
Method	BLASTN
NCBI GI	g21142
BLAST score	38
E value	1.0e-12
Match length	50
% identity	94
NCBI Description	Mustard mRNA for cytosolic glyceraldehyde-3-phosphate dehydrogenase (GAPDH, NAD-specific; EC 1.2.1.12)

Seq. No.	158893
Seq. ID	LIB3176-101-P1-K1-H10
Method	BLASTX
NCBI GI	g1673395
BLAST score	181
E value	3.0e-13
Match length	60
% identity	55
NCBI Description	(Z82044) hypothetical 9.1 kd protein [Bacillus subtilis] >gi_2633195_emb_CAB12700_ (Z99108) similar to thiol-specific antioxidant protein [Bacillus subtilis]

Seq. No.	158894
Seq. ID	LIB3176-101-P1-K1-H11
Method	BLASTX
NCBI GI	g584825
BLAST score	297
E value	2.0e-27
Match length	63
% identity	87
NCBI Description	B2 PROTEIN >gi_322726_pir__S32124 B2 protein - carrot >gi_297889_emb_CAA51078_ (X72385) B2 protein [Daucus carota]

Seq. No.	158895

Seq. ID	LIB3176-101-P1-K1-H12
Method	BLASTX
NCBI GI	g584825
BLAST score	443
E value	2.0e-44
Match length	94
% identity	86
NCBI Description	B2 PROTEIN >gi_322726_pir__S32124 B2 protein - carrot >gi_297889_emb_CAA51078_ (X72385) B2 protein [Daucus carota]

Seq. No.	158896
Seq. ID	LIB3176-101-P1-K1-H2
Method	BLASTX
NCBI GI	g4218120
BLAST score	308
E value	3.0e-28
Match length	85
% identity	74
NCBI Description	(AL035353) Proline-rich APG-like protein [Arabidopsis thaliana]

Seq. No.	158897
Seq. ID	LIB3176-101-P1-K1-H5
Method	BLASTX
NCBI GI	g3776575
BLAST score	340
E value	6.0e-32
Match length	83
% identity	80
NCBI Description	(AC005388) Similar to Schizosaccharomyces CCAAT-binding factor F7G19.16 gi_1922964 from Arabidopsis thaliana BAC gb_AC000106. EST gb_H36963 comes from this gene. [Arabidopsis thaliana]

Seq. No.	158898
Seq. ID	LIB3176-101-P1-K1-H6
Method	BLASTX
NCBI GI	g1350768
BLAST score	356
E value	5.0e-34
Match length	99
% identity	76
NCBI Description	60S RIBOSOMAL PROTEIN L7A

Seq. No.	158899
Seq. ID	LIB3176-101-P1-K1-H7
Method	BLASTN
NCBI GI	g3193282
BLAST score	60
E value	1.0e-25
Match length	68
% identity	97
NCBI Description	Arabidopsis thaliana BAC T14P8

Seq. No.	158900
Seq. ID	LIB3176-101-P1-K1-H8

Method	BLASTX
NCBI GI	g1172977
BLAST score	337
E value	4.0e-32
Match length	76
% identity	92
NCBI Description	60S RIBOSOMAL PROTEIN L18 >gi_606970 (U15741) cytoplasmic ribosomal protein L18 [Arabidopsis thaliana]

Seq. No.	158901
Seq. ID	LIB3176-101-P1-K1-H9
Method	BLASTN
NCBI GI	g2143226
BLAST score	85
E value	2.0e-40
Match length	133
% identity	91
NCBI Description	Brassica napus mRNA for glyoxysomal isocitrate lyase

Seq. No.	158902
Seq. ID	LIB3176-102-P1-K1-A1
Method	BLASTX
NCBI GI	g2911068
BLAST score	350
E value	2.0e-33
Match length	64
% identity	100
NCBI Description	(AL021960) G10-like protein [Arabidopsis thaliana]

Seq. No.	158903
Seq. ID	LIB3176-102-P1-K1-A11
Method	BLASTN
NCBI GI	g2815404
BLAST score	245
E value	1.0e-135
Match length	249
% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MMG4, complete sequence [Arabidopsis thaliana]

Seq. No.	158904
Seq. ID	LIB3176-102-P1-K1-A3
Method	BLASTX
NCBI GI	g2160174
BLAST score	563
E value	3.0e-58
Match length	113
% identity	97
NCBI Description	(AC000132) Identical to A. thaliana PUR2 (gb_X74766). ESTs gb_ATTS3927,gb_N96446 come from this gene. [Arabidopsis thaliana]

Seq. No.	158905
Seq. ID	LIB3176-102-P1-K1-A4
Method	BLASTX
NCBI GI	g543841
BLAST score	342

E value	2.0e-32
Match length	70
% identity	97
NCBI Description	ADP-RIBOSYLATION FACTOR 1 >gi_322518_pir__S28875 ADP-ribosylation factor 1 - Arabidopsis thaliana >gi_166586 (M95166) ADP-ribosylation factor [Arabidopsis thaliana] >gi_2275195 (AC002337) ADP-ribosylation factor [Arabidopsis thaliana] >gi_4630747_gb_AAD26597.1_AC007236_2 (AC007236) ADP-ribosylation factor [Arabidopsis thaliana]

Seq. No.	158906
Seq. ID	LIB3176-102-P1-K1-A5
Method	BLASTX
NCBI GI	g2129648
BLAST score	275
E value	6.0e-25
Match length	51
% identity	54
NCBI Description	MYB-related protein 33,3K - Arabidopsis thaliana >gi_1263095_emb_CAA90809_ (Z54136) MYB-related protein [Arabidopsis thaliana]

Seq. No.	158907
Seq. ID	LIB3176-102-P1-K1-A6
Method	BLASTX
NCBI GI	g2129569
BLAST score	439
E value	1.0e-43
Match length	104
% identity	83
NCBI Description	cytosolic cyclophilin ROC3 - Arabidopsis thaliana >gi_1305455 (U40399) cytosolic cyclophilin [Arabidopsis thaliana] >gi_4581104_gb_AAD24594.1_AC005825_1 (AC005825) cytosolic cyclophilin (ROC3) [Arabidopsis thaliana]

Seq. No.	158908
Seq. ID	LIB3176-102-P1-K1-A8
Method	BLASTN
NCBI GI	g1695716
BLAST score	51
E value	4.0e-20
Match length	71
% identity	93
NCBI Description	Arabidopsis thaliana DNA for luminal binding protein, complete cds

Seq. No.	158909
Seq. ID	LIB3176-102-P1-K1-B10
Method	BLASTX
NCBI GI	g1518540
BLAST score	636
E value	1.0e-66
Match length	132
% identity	90
NCBI Description	(U53418) UDP-glucose dehydrogenase [Glycine max]

Seq. No.	158910

Seq. ID	LIB3176-102-P1-K1-B11
Method	BLASTX
NCBI GI	g1518540
BLAST score	505
E value	3.0e-53
Match length	124
% identity	86
NCBI Description	(U53418) UDP-glucose dehydrogenase [Glycine max]

Seq. No.	158911
Seq. ID	LIB3176-102-P1-K1-B12
Method	BLASTN
NCBI GI	g2245031
BLAST score	121
E value	2.0e-61
Match length	181
% identity	92
NCBI Description	Arabidopsis thaliana DNA chromosome 4, ESSA I contig fragment No

Seq. No.	158912
Seq. ID	LIB3176-102-P1-K1-B2
Method	BLASTX
NCBI GI	g115783
BLAST score	549
E value	2.0e-56
Match length	106
% identity	97
NCBI Description	CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR (CAB-140) (LHCP) >gi_16376_emb_CAA27543_ (X03909) chlorophyll a/b binding protein (LHCP AB 140) [Arabidopsis thaliana]

Seq. No.	158913
Seq. ID	LIB3176-102-P1-K1-B3
Method	BLASTX
NCBI GI	g134025
BLAST score	550
E value	2.0e-56
Match length	131
% identity	83
NCBI Description	CHLOROPLAST 30S RIBOSOMAL PROTEIN S8 >gi_70913_pir__R3NT8 ribosomal protein S8 - common tobacco chloroplast >gi_11863_emb_CAA77378_ (Z00044) ribosomal protein S8 [Nicotiana tabacum] >gi_225232_prf__1211235BP ribosomal protein S8 [Nicotiana tabacum]

Seq. No.	158914
Seq. ID	LIB3176-102-P1-K1-B4
Method	BLASTX
NCBI GI	g1710530
BLAST score	533
E value	8.0e-55
Match length	99
% identity	96
NCBI Description	60S RIBOSOMAL PROTEIN L27A >gi_2129719_pir__S71256 ribosomal protein L27a - Arabidopsis thaliana

	>gi_1107487_emb_CAA63025_ (X91959) 60S ribosomal protein L27a [Arabidopsis thaliana]
Seq. No.	158915
Seq. ID	LIB3176-102-P1-K1-B5
Method	BLASTX
NCBI GI	g1710530
BLAST score	149
E value	6.0e-10
Match length	42
% identity	67
NCBI Description	60S RIBOSOMAL PROTEIN L27A >gi_2129719_pir__S71256 ribosomal protein L27a - Arabidopsis thaliana >gi_1107487_emb_CAA63025_ (X91959) 60S ribosomal protein L27a [Arabidopsis thaliana]
Seq. No.	158916
Seq. ID	LIB3176-102-P1-K1-B6
Method	BLASTX
NCBI GI	g3551052
BLAST score	465
E value	8.0e-56
Match length	115
% identity	96
NCBI Description	(AB011545) GF14 mu [Arabidopsis thaliana] >gi_4559343_gb_AAD23005.1_AC007087_24 (AC007087) DNA regulatory protein GF14 mu [Arabidopsis thaliana]
Seq. No.	158917
Seq. ID	LIB3176-102-P1-K1-B7
Method	BLASTN
NCBI GI	g2264306
BLAST score	155
E value	6.0e-82
Match length	183
% identity	96
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MBK5, complete sequence [Arabidopsis thaliana]
Seq. No.	158918
Seq. ID	LIB3176-102-P1-K1-C1
Method	BLASTX
NCBI GI	g4741940
BLAST score	235
E value	5.0e-20
Match length	46
% identity	96
NCBI Description	(AF134120) Lhca2 protein [Arabidopsis thaliana]
Seq. No.	158919
Seq. ID	LIB3176-102-P1-K1-C10
Method	BLASTN
NCBI GI	g2182286
BLAST score	38
E value	1.0e-12
Match length	58
% identity	91

NCBI Description	Sequence of BAC F20P5 from Arabidopsis thaliana chromosome 1, complete sequence [Arabidopsis thaliana]
Seq. No.	158920
Seq. ID	LIB3176-102-P1-K1-C11
Method	BLASTX
NCBI GI	g1408473
BLAST score	423
E value	1.0e-41
Match length	85
% identity	95
NCBI Description	(U48939) actin depolymerizing factor 2 [Arabidopsis thaliana]
Seq. No.	158921
Seq. ID	LIB3176-102-P1-K1-C12
Method	BLASTX
NCBI GI	g3882081
BLAST score	457
E value	8.0e-46
Match length	95
% identity	35
NCBI Description	(AJ012552) polyubiquitin [Vicia faba]
Seq. No.	158922
Seq. ID	LIB3176-102-P1-K1-C2
Method	BLASTX
NCBI GI	g2160168
BLAST score	337
E value	1.0e-32
Match length	75
% identity	91
NCBI Description	(AC000132) Strong similarity to R. communis phosphoglycerate mutase (gb_X70652). ESTs gb_T41853,gb_T76648 come from this gene. [Arabidopsis thaliana]
Seq. No.	158923
Seq. ID	LIB3176-102-P1-K1-C3
Method	BLASTX
NCBI GI	g99772
BLAST score	444
E value	3.0e-44
Match length	117
% identity	80
NCBI Description	ubiquitin 81-aa extension protein 2 - Arabidopsis thaliana >gi_166936 (J05540) ubiquitin extension protein (UBQ6) [Arabidopsis thaliana] >gi_3522953 (AC004411) ubiquitin extension protein (UBQ6) [Arabidopsis thaliana]
Seq. No.	158924
Seq. ID	LIB3176-102-P1-K1-C4
Method	BLASTN
NCBI GI	g166935
BLAST score	86
E value	1.0e-40
Match length	146

% identity	90
NCBI Description	A.thaliana ubiquitin extension protein (UBQ6) gene, complete cds

Seq. No.	158925
Seq. ID	LIB3176-102-P1-K1-C5
Method	BLASTN
NCBI GI	g2444276
BLAST score	102
E value	3.0e-50
Match length	122
% identity	96
NCBI Description	Arabidopsis thaliana GSK3/shaggy-like protein kinase (GSK1) mRNA, complete cds

Seq. No.	158926
Seq. ID	LIB3176-102-P1-K1-C6
Method	BLASTX
NCBI GI	g3688799
BLAST score	485
E value	4.0e-49
Match length	99
% identity	98
NCBI Description	(AF057137) gamma tonoplast intrinsic protein 2 [Arabidopsis thaliana]

Seq. No.	158927
Seq. ID	LIB3176-102-P1-K1-C7
Method	BLASTX
NCBI GI	g1709970
BLAST score	458
E value	7.0e-46
Match length	114
% identity	81
NCBI Description	60S RIBOSOMAL PROTEIN L10A

Seq. No.	158928
Seq. ID	LIB3176-102-P1-K1-C8
Method	BLASTN
NCBI GI	g4589432
BLAST score	268
E value	1.0e-149
Match length	276
% identity	99
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MMJ24, complete sequence

Seq. No.	158929
Seq. ID	LIB3176-102-P1-K1-D1
Method	BLASTX
NCBI GI	g1946367
BLAST score	530
E value	2.0e-54
Match length	111
% identity	94
NCBI Description	(U93215) unknown protein [Arabidopsis thaliana]

Seq. No.	158930
Seq. ID	LIB3176-102-P1-K1-D10
Method	BLASTX
NCBI GI	g267083
BLAST score	321
E value	6.0e-30
Match length	63
% identity	92
NCBI Description	TUBULIN BETA-9 CHAIN >gi_320190_pir__JQ1593 tubulin beta-9 chain - Arabidopsis thaliana >gi_166910 (M84706) beta-9 tubulin [Arabidopsis thaliana]

Seq. No.	158931
Seq. ID	LIB3176-102-P1-K1-D11
Method	BLASTX
NCBI GI	g2199574
BLAST score	267
E value	5.0e-24
Match length	52
% identity	94
NCBI Description	(AF004293) aquaporin [Brassica rapa]

Seq. No.	158932
Seq. ID	LIB3176-102-P1-K1-D12
Method	BLASTX
NCBI GI	g2088654
BLAST score	284
E value	1.0e-25
Match length	68
% identity	85
NCBI Description	(AF002109) 60S acidic ribosomal protein P0 isolog [Arabidopsis thaliana]

Seq. No.	158933
Seq. ID	LIB3176-102-P1-K1-D2
Method	BLASTN
NCBI GI	g4589428
BLAST score	191
E value	1.0e-103
Match length	346
% identity	98
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MFH8, complete sequence

Seq. No.	158934
Seq. ID	LIB3176-102-P1-K1-D3
Method	BLASTN
NCBI GI	g1030724
BLAST score	107
E value	2.0e-53
Match length	213
% identity	86
NCBI Description	A.thaliana DNA for pyrroline-5-carboxylase synthetase gene

Seq. No.	158935
Seq. ID	LIB3176-102-P1-K1-D4
Method	BLASTN

NCBI GI	g3080406
BLAST score	344
E value	0.0e+00
Match length	344
% identity	100
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F23E12 (ESSA project)

Seq. No.	158936
Seq. ID	LIB3176-102-P1-K1-D5
Method	BLASTN
NCBI GI	g4454447
BLAST score	40
E value	2.0e-13
Match length	72
% identity	89
NCBI Description	Arabidopsis thaliana chromosome II BAC F5H14 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	158937
Seq. ID	LIB3176-102-P1-K1-D6
Method	BLASTN
NCBI GI	g3869065
BLAST score	229
E value	1.0e-126
Match length	233
% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K24M7, complete sequence [Arabidopsis thaliana]

Seq. No.	158938
Seq. ID	LIB3176-102-P1-K1-D7
Method	BLASTX
NCBI GI	g481821
BLAST score	415
E value	1.0e-40
Match length	96
% identity	83
NCBI Description	probable glutathione transferase (EC 2.5.1.18) (clone ERD11) - Arabidopsis thaliana >gi_497788_dbj_BAA04553_ (D17672) glutathione S-transferase [Arabidopsis thaliana]

Seq. No.	158939
Seq. ID	LIB3176-102-P1-K1-E1
Method	BLASTX
NCBI GI	g4325345
BLAST score	624
E value	3.0e-65
Match length	139
% identity	88
NCBI Description	(AF128393) similar to thioredoxin-like proteins (Pfam: PF00085, Score=42.9, E=1.4e-11, N=1); contains similarity to dihydroorotases (Pfam: PF00744, Score=154.9, E=1.4e-42, N=1) [Arabidopsis thaliana]

Seq. No.	158940
Seq. ID	LIB3176-102-P1-K1-E10

Method	BLASTX
NCBI GI	g464662
BLAST score	247
E value	2.0e-21
Match length	88
% identity	61
NCBI Description	CHLOROPLAST 31 KD RIBONUCLEOPROTEIN PRECURSOR (RNA-BINDING PROTEIN RNP-T) (RNA-BINDING PROTEIN 1) >gi_282884_pir__S28057 RNA-binding protein RNP-T - Arabidopsis thaliana >gi_16490_emb_CAA46347_ (X65255) RNA-binding protein [Arabidopsis thaliana] >gi_387569 (M94554) 31 kDa RNA binding protein [Arabidopsis thaliana] >gi_475718 (U08467) RNA-binding protein 1 [Arabidopsis thaliana] >gi_4220513_emb_CAA22986_ (AL035356) RNA-binding protein RNP-T precursor [Arabidopsis thaliana] >gi_737169_prf__1921382A RNA-binding protein [Arabidopsis thaliana]

Seq. No.	158941
Seq. ID	LIB3176-102-P1-K1-E11
Method	BLASTX
NCBI GI	g132074
BLAST score	465
E value	8.0e-47
Match length	88
% identity	100
NCBI Description	RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN 1A PRECURSOR (RUBISCO SMALL SUBUNIT 1A) >gi_68063_pir__RKMUA1 ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain A1 precursor - Arabidopsis thaliana

Seq. No.	158942
Seq. ID	LIB3176-102-P1-K1-E12
Method	BLASTX
NCBI GI	g4263509
BLAST score	530
E value	2.0e-54
Match length	110
% identity	96
NCBI Description	(AC004044) hypothetical protein [Arabidopsis thaliana]

Seq. No.	158943
Seq. ID	LIB3176-102-P1-K1-E2
Method	BLASTN
NCBI GI	g3869073
BLAST score	266
E value	1.0e-148
Match length	270
% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MKN22, complete sequence [Arabidopsis thaliana]

Seq. No.	158944
Seq. ID	LIB3176-102-P1-K1-E4
Method	BLASTN
NCBI GI	g4510408
BLAST score	201

E value	1.0e-109
Match length	285
% identity	93
NCBI Description	Arabidopsis thaliana chromosome II BAC T1E2 genomic sequence, complete sequence

Seq. No.	158945
Seq. ID	LIB3176-102-P1-K1-E5
Method	BLASTX
NCBI GI	g4539417
BLAST score	158
E value	5.0e-11
Match length	35
% identity	91
NCBI Description	(AL049171) putative protein [Arabidopsis thaliana]

Seq. No.	158946
Seq. ID	LIB3176-102-P1-K1-E6
Method	BLASTX
NCBI GI	g1419090
BLAST score	384
E value	2.0e-37
Match length	95
% identity	75
NCBI Description	(X94968) 37kDa chloroplast inner envelope membrane polypeptide precursor [Nicotiana tabacum]

Seq. No.	158947
Seq. ID	LIB3176-102-P1-K1-E7
Method	BLASTX
NCBI GI	g4587595
BLAST score	227
E value	8.0e-19
Match length	70
% identity	59
NCBI Description	(AC006951) putative proline-rich protein APG [Arabidopsis thaliana]

Seq. No.	158948
Seq. ID	LIB3176-102-P1-K1-E8
Method	BLASTX
NCBI GI	g464621
BLAST score	324
E value	9.0e-35
Match length	107
% identity	68
NCBI Description	60S RIBOSOMAL PROTEIN L6 (YL16-LIKE) >gi_280374_pir__S28586 ribosomal protein ML16 - common ice plant >gi_19539_emb_CAA49175_ (X69378) ribosomal protein YL16 [Mesembryanthemum crystallinum]

Seq. No.	158949
Seq. ID	LIB3176-102-P1-K1-E9
Method	BLASTX
NCBI GI	g266936
BLAST score	269
E value	7.0e-24

Match length	85
% identity	67
NCBI Description	50S RIBOSOMAL PROTEIN L27, CHLOROPLAST PRECURSOR (CL27) >gi_282960_pir__A42840 ribosomal protein L27 - common tobacco >gi_170306 (M98473) ribosomal protein L27 [Nicotiana tabacum] >gi_170326 (M75731) ribosomal protein L27 [Nicotiana tabacum]

Seq. No.	158950
Seq. ID	LIB3176-102-P1-K1-F10
Method	BLASTN
NCBI GI	g2052382
BLAST score	49
E value	9.0e-19
Match length	77
% identity	91
NCBI Description	Arabidopsis thaliana calreticulin (Crt3) mRNA, complete cds

Seq. No.	158951
Seq. ID	LIB3176-102-P1-K1-F11
Method	BLASTX
NCBI GI	g4102703
BLAST score	575
E value	1.0e-59
Match length	122
% identity	94
NCBI Description	(AF015274) ribulose-5-phosphate-3-epimerase [Arabidopsis thaliana]

Seq. No.	158952
Seq. ID	LIB3176-102-P1-K1-F12
Method	BLASTN
NCBI GI	g3068702
BLAST score	265
E value	1.0e-147
Match length	342
% identity	98
NCBI Description	Arabidopsis thaliana putative transmembrane protein G1p (AtG1), putative nuclear DNA-binding protein G2p (AtG2), Em1 protein (ATEM1), putative chlorophyll synthetase (AtG4), putative transmembrane protein G5p (AtG5), put

Seq. No.	158953
Seq. ID	LIB3176-102-P1-K1-F2
Method	BLASTN
NCBI GI	g4757409
BLAST score	71
E value	1.0e-31
Match length	344
% identity	58
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MVC8, complete sequence

Seq. No.	158954
Seq. ID	LIB3176-102-P1-K1-F3
Method	BLASTX
NCBI GI	g2498731

BLAST score	157
E value	3.0e-29
Match length	82
% identity	73
NCBI Description	PROBABLE NADP-DEPENDENT OXIDOREDUCTASE P1 >gi_1362013_pir__S57611 zeta-crystallin homolog - Arabidopsis thaliana >gi_886428_emb_CAA89838_ (Z49768) zeta-crystallin homologue [Arabidopsis thaliana]

Seq. No.	158955
Seq. ID	LIB3176-102-P1-K1-F4
Method	BLASTN
NCBI GI	g3660470
BLAST score	228
E value	1.0e-125
Match length	248
% identity	98
NCBI Description	Arabidopsis thaliana mRNA for Succinate dehydrogenase flavoprotein (alpha) subunit

Seq. No.	158956
Seq. ID	LIB3176-102-P1-K1-F5
Method	BLASTX
NCBI GI	g4755189
BLAST score	398
E value	6.0e-39
Match length	104
% identity	71
NCBI Description	(AC007018) putative cytochrome P450 [Arabidopsis thaliana]

Seq. No.	158957
Seq. ID	LIB3176-102-P1-K1-F6
Method	BLASTX
NCBI GI	g464662
BLAST score	254
E value	8.0e-22
Match length	114
% identity	51
NCBI Description	CHLOROPLAST 31 KD RIBONUCLEOPROTEIN PRECURSOR (RNA-BINDING PROTEIN RNP-T) (RNA-BINDING PROTEIN 1) >gi_282884_pir__S28057 RNA-binding protein RNP-T - Arabidopsis thaliana >gi_16490_emb_CAA46347_ (X65255) RNA-binding protein [Arabidopsis thaliana] >gi_387569 (M94554) 31 kDa RNA binding protein [Arabidopsis thaliana] >gi_475718 (U08467) RNA-binding protein 1 [Arabidopsis thaliana] >gi_4220513_emb_CAA22986_ (AL035356) RNA-binding protein RNP-T precursor [Arabidopsis thaliana] >gi_737169_prf__1921382A RNA-binding protein [Arabidopsis thaliana]

Seq. No.	158958
Seq. ID	LIB3176-102-P1-K1-F7
Method	BLASTN
NCBI GI	g16489
BLAST score	161
E value	2.0e-85
Match length	221

% identity	94
NCBI Description	A.thaliana mRNA for RNA-binding protein (RNP-T)

Seq. No.	158959
Seq. ID	LIB3176-102-P1-K1-F8
Method	BLASTX
NCBI GI	g3024022
BLAST score	320
E value	2.0e-38
Match length	98
% identity	84
NCBI Description	INITIATION FACTOR 5A-5 (EIF-5A) (EIF-4D) >gi_2225885_dbj_BAA20879_ (AB004826) eukaryotic initiation factor 5A5 [Solanum tuberosum]

Seq. No.	158960
Seq. ID	LIB3176-102-P1-K1-F9
Method	BLASTN
NCBI GI	g4454022
BLAST score	66
E value	7.0e-29
Match length	82
% identity	95
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F9D16 (ESSAII project)

Seq. No.	158961
Seq. ID	LIB3176-102-P1-K1-G10
Method	BLASTX
NCBI GI	g115767
BLAST score	619
E value	9.0e-65
Match length	116
% identity	97
NCBI Description	CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR (CAB-165/180) (LHCP) >gi_81603_pir__A29280 chlorophyll a/b-binding protein ab165 - Arabidopsis thaliana >gi_16368_emb_CAA27540_ (X03907) chlorophyll a/b binding protein (LHCP AB 65) [Arabidopsis thaliana] >gi_16372_emb_CAA27541_ (X03908) chlorophyll a/b binding protein (LHCP AB 180) [Arabidopsis thaliana]

Seq. No.	158962
Seq. ID	LIB3176-102-P1-K1-G11
Method	BLASTN
NCBI GI	g3193282
BLAST score	249
E value	1.0e-138
Match length	314
% identity	100
NCBI Description	Arabidopsis thaliana BAC T14P8

Seq. No.	158963
Seq. ID	LIB3176-102-P1-K1-G12
Method	BLASTN
NCBI GI	g3785992
BLAST score	151

E value	9.0e-80
Match length	163
% identity	98
NCBI Description	Arabidopsis thaliana chromosome II BAC T6A23 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	158964
Seq. ID	LIB3176-102-P1-K1-G5
Method	BLASTX
NCBI GI	g2911071
BLAST score	412
E value	2.0e-40
Match length	105
% identity	72
NCBI Description	(AL021960) hypothetical protein [Arabidopsis thaliana]

Seq. No.	158965
Seq. ID	LIB3176-102-P1-K1-G6
Method	BLASTX
NCBI GI	g2244750
BLAST score	546
E value	4.0e-56
Match length	110
% identity	97
NCBI Description	(Z97335) adenosylhomocysteinase [Arabidopsis thaliana] >gi_3088579 (AF059581) S-adenosyl-L-homocysteine hydrolase [Arabidopsis thaliana]

Seq. No.	158966
Seq. ID	LIB3176-102-P1-K1-G7
Method	BLASTX
NCBI GI	g231586
BLAST score	296
E value	2.0e-27
Match length	69
% identity	86
NCBI Description	ATP SYNTHASE BETA CHAIN, MITOCHONDRIAL PRECURSOR >gi_82027_pir__S20504 H+-transporting ATP synthase (EC 3.6.1.34) beta chain, mitochondrial - Para rubber tree >gi_18831_emb_CAA41401_ (X58498) mitochondrial ATP synthase beta-subunit [Hevea brasiliensis]

Seq. No.	158967
Seq. ID	LIB3176-102-P1-K1-H1
Method	BLASTX
NCBI GI	g121357
BLAST score	177
E value	6.0e-13
Match length	107
% identity	39
NCBI Description	GLUTAMINE SYNTHETASE (GLUTAMATE--AMMONIA LIGASE) >gi_68610_pir__AJBSQU glutamate--ammonia ligase (EC 6.3.1.2) - Bacillus cereus >gi_216273_dbj_BAA00403_ (D00513) glutamine synthetase [Bacillus cereus]

Seq. No.	158968
Seq. ID	LIB3176-102-P1-K1-H10

Method	BLASTN
NCBI GI	g4006885
BLAST score	70
E value	2.0e-31
Match length	70
% identity	100
NCBI Description	Arabidopsis thaliana DNA chromosome 4, ESSA I AP2 contig fragment No

Seq. No.	158969
Seq. ID	LIB3176-102-P1-K1-H11
Method	BLASTN
NCBI GI	g4741961
BLAST score	232
E value	1.0e-128
Match length	232
% identity	100
NCBI Description	Arabidopsis thaliana PsbS protein (PsbS) mRNA, complete cds

Seq. No.	158970
Seq. ID	LIB3176-102-P1-K1-H12
Method	BLASTN
NCBI GI	g2358139
BLAST score	65
E value	7.0e-29
Match length	73
% identity	97
NCBI Description	Arabidopsis thaliana chromosome 1 YAC yUP8H12 complete sequence [Arabidopsis thaliana]

Seq. No.	158971
Seq. ID	LIB3176-102-P1-K1-H3
Method	BLASTN
NCBI GI	g3241927
BLAST score	134
E value	3.0e-69
Match length	339
% identity	99
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MTE17, complete sequence [Arabidopsis thaliana]

Seq. No.	158972
Seq. ID	LIB3176-102-P1-K1-H4
Method	BLASTN
NCBI GI	g2264309
BLAST score	161
E value	2.0e-85
Match length	340
% identity	98
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MJJ3, complete sequence [Arabidopsis thaliana]

Seq. No.	158973
Seq. ID	LIB3176-102-P1-K1-H5
Method	BLASTX
NCBI GI	g464987
BLAST score	233

E value	8.0e-20
Match length	47
% identity	94
NCBI Description	UBIQUITIN-CONJUGATING ENZYME E2-17 KD 10 (UBIQUITIN-PROTEIN LIGASE 10) (UBIQUITIN CARRIER PROTEIN 10) >gi_421858_pir__S32672 ubiquitin--protein ligase (EC 6.3.2.19) UBC10 - Arabidopsis thaliana >gi_297878_emb_CAA78715_ (Z14991) ubiquitin conjugating enzyme [Arabidopsis thaliana] >gi_349213 (L00640) ubiquitin conjugating enzyme [Arabidopsis thaliana]

Seq. No.	158974
Seq. ID	LIB3176-102-P1-K1-H8
Method	BLASTX
NCBI GI	g4586041
BLAST score	607
E value	3.0e-63
Match length	129
% identity	51
NCBI Description	(AC007020) hypothetical protein [Arabidopsis thaliana] >gi_4587998_gb_AAD25939.1_AF085279_12 (AF085279) hypothetical protein [Arabidopsis thaliana]

Seq. No.	158975
Seq. ID	LIB3176-103-P1-K1-A1
Method	BLASTX
NCBI GI	g3914740
BLAST score	449
E value	7.0e-45
Match length	98
% identity	90
NCBI Description	60S RIBOSOMAL PROTEIN L26 >gi_2160300_dbj_BAA18941_ (D78495) ribosomal protein [Brassica rapa]

Seq. No.	158976
Seq. ID	LIB3176-103-P1-K1-A11
Method	BLASTX
NCBI GI	g1732570
BLAST score	121
E value	7.0e-11
Match length	61
% identity	72
NCBI Description	(U72153) beta-glucosidase [Arabidopsis thaliana]

Seq. No.	158977
Seq. ID	LIB3176-103-P1-K1-A4
Method	BLASTX
NCBI GI	g120667
BLAST score	260
E value	1.0e-22
Match length	50
% identity	100
NCBI Description	GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE, CYTOSOLIC >gi_81622_pir__JQ1287 glyceraldehyde-3-phosphate dehydrogenase (EC 1.2.1.12), cytosolic - Arabidopsis thaliana >gi_166706 (M64116) cystolic glyceraldehyde-3-phosphate dehydrogenase [Arabidopsis

thaliana] >gi_166710 (M64119) glyceraldehyde-3-phosphate dehydrogenase [Arabidopsis thaliana]

Seq. No.	158978
Seq. ID	LIB3176-103-P1-K1-A6
Method	BLASTX
NCBI GI	g551288
BLAST score	343
E value	1.0e-45
Match length	107
% identity	77
NCBI Description	(Z33611) phosphoglycerate mutase [Zea mays]

Seq. No.	158979
Seq. ID	LIB3176-103-P1-K1-A7
Method	BLASTX
NCBI GI	g1914683
BLAST score	218
E value	8.0e-18
Match length	107
% identity	49
NCBI Description	(Y12013) RAD23, isoform I [Daucus carota]

Seq. No.	158980
Seq. ID	LIB3176-103-P1-K1-A8
Method	BLASTN
NCBI GI	g2459406
BLAST score	129
E value	1.0e-66
Match length	141
% identity	98
NCBI Description	Arabidopsis thaliana chromosome II BAC F4P9 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	158981
Seq. ID	LIB3176-103-P1-K1-A9
Method	BLASTX
NCBI GI	g4454036
BLAST score	404
E value	9.0e-40
Match length	77
% identity	96
NCBI Description	(AL035394) putative major latex protein [Arabidopsis thaliana]

Seq. No.	158982
Seq. ID	LIB3176-103-P1-K1-B1
Method	BLASTX
NCBI GI	g2791834
BLAST score	153
E value	1.0e-10
Match length	32
% identity	91
NCBI Description	(AF041463) elongation factor 1-alpha [Manihot esculenta]

Seq. No.	158983
Seq. ID	LIB3176-103-P1-K1-B12

Method	BLASTX
NCBI GI	g3319349
BLAST score	178
E value	4.0e-13
Match length	52
% identity	71
NCBI Description	(AF077407) No definition line found [Arabidopsis thaliana]

Seq. No.	158984
Seq. ID	LIB3176-103-P1-K1-B2
Method	BLASTN
NCBI GI	g2582638
BLAST score	410
E value	0.0e+00
Match length	434
% identity	99
NCBI Description	Arabidosis thaliana mRNA for a hnRNP-like protein

Seq. No.	158985
Seq. ID	LIB3176-103-P1-K1-B4
Method	BLASTN
NCBI GI	g16174
BLAST score	89
E value	2.0e-42
Match length	176
% identity	92
NCBI Description	A.thaliana ANT1 mRNA for adenylate translocator

Seq. No.	158986
Seq. ID	LIB3176-103-P1-K1-B5
Method	BLASTX
NCBI GI	g2213584
BLAST score	368
E value	1.0e-35
Match length	79
% identity	92
NCBI Description	(AC000348) T7N9.4 [Arabidopsis thaliana]

Seq. No.	158987
Seq. ID	LIB3176-103-P1-K1-B7
Method	BLASTN
NCBI GI	g2244747
BLAST score	163
E value	8.0e-87
Match length	199
% identity	95
NCBI Description	Arabidopsis thaliana DNA chromosome 4, ESSA I contig fragment No

Seq. No.	158988
Seq. ID	LIB3176-103-P1-K1-B8
Method	BLASTN
NCBI GI	g2582638
BLAST score	100
E value	3.0e-49
Match length	174
% identity	91

NCBI Description	Arabidosis thaliana mRNA for a hnRNP-like protein
Seq. No.	158989
Seq. ID	LIB3176-103-P1-K1-B9
Method	BLASTX
NCBI GI	g3023848
BLAST score	649
E value	4.0e-68
Match length	129
% identity	61
NCBI Description	GUANINE NUCLEOTIDE-BINDING PROTEIN BETA SUBUNIT-LIKE PROTEIN (WD-40 REPEAT AUXIN-DEPENDENT PROTEIN ARCA) >gi_2289095 (U77381) WD-40 repeat protein [Arabidopsis thaliana]
Seq. No.	158990
Seq. ID	LIB3176-103-P1-K1-C10
Method	BLASTN
NCBI GI	g860933
BLAST score	48
E value	6.0e-18
Match length	64
% identity	94
NCBI Description	E.robustum gene for 18S small subunit rRNA
Seq. No.	158991
Seq. ID	LIB3176-103-P1-K1-C11
Method	BLASTX
NCBI GI	g3157947
BLAST score	528
E value	4.0e-54
Match length	103
% identity	51
NCBI Description	(AC002131) Similar to protein gb_Z74962 from Brassica oleracea which is similar to bacterial YRN1 and HEAHIO proteins. ESTs gb_T21954, gb_T04283, gb_Z37609, gb_N37366, gb_R90704, gb_F15500 and gb_F14353 come from this gene. [Arabidopsis tha
Seq. No.	158992
Seq. ID	LIB3176-103-P1-K1-C12
Method	BLASTX
NCBI GI	g480450
BLAST score	318
E value	5.0e-30
Match length	73
% identity	84
NCBI Description	ketol-acid reductoisomerase (EC 1.1.1.86) - Arabidopsis thaliana >gi_402552_emb_CAA49506_ (X69880) ketol-acid reductoisomerase [Arabidopsis thaliana]
Seq. No.	158993
Seq. ID	LIB3176-103-P1-K1-C3
Method	BLASTN
NCBI GI	g2618683
BLAST score	98
E value	7.0e-48

Match length	187
% identity	100
NCBI Description	Arabidopsis thaliana chromosome II BAC T32G6 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	158994
Seq. ID	LIB3176-103-P1-K1-C4
Method	BLASTX
NCBI GI	g121357
BLAST score	169
E value	6.0e-12
Match length	122
% identity	36
NCBI Description	GLUTAMINE SYNTHETASE (GLUTAMATE--AMMONIA LIGASE) >gi_68610_pir__AJBSQU glutamate--ammonia ligase (EC 6.3.1.2) - Bacillus cereus >gi_216273_dbj_BAA00403_ (D00513) glutamine synthetase [Bacillus cereus]

Seq. No.	158995
Seq. ID	LIB3176-103-P1-K1-C5
Method	BLASTN
NCBI GI	g1495254
BLAST score	338
E value	0.0e+00
Match length	403
% identity	99
NCBI Description	A.thaliana mRNA for unknown protein, ORF02

Seq. No.	158996
Seq. ID	LIB3176-103-P1-K1-C6
Method	BLASTX
NCBI GI	g3107931
BLAST score	129
E value	5.0e-42
Match length	139
% identity	71
NCBI Description	(AB013353) UDP-glucose pyrophosphorylase [Pyrus pyrifolia]

Seq. No.	158997
Seq. ID	LIB3176-103-P1-K1-C7
Method	BLASTN
NCBI GI	g4587641
BLAST score	106
E value	5.0e-53
Match length	110
% identity	99
NCBI Description	Arabidopsis thaliana chromosome I BAC F20D21 genomic sequence, complete sequence

Seq. No.	158998
Seq. ID	LIB3176-103-P1-K1-C8
Method	BLASTN
NCBI GI	g4559344
BLAST score	42
E value	2.0e-14
Match length	140
% identity	5

NCBI Description	Arabidopsis thaliana chromosome II BAC F27C12 genomic sequence, complete sequence
Seq. No.	158999
Seq. ID	LIB3176-103-P1-K1-D1
Method	BLASTX
NCBI GI	g1546698
BLAST score	678
E value	1.0e-71
Match length	134
% identity	99
NCBI Description	(X98808) peroxidase ATP3a [Arabidopsis thaliana]
Seq. No.	159000
Seq. ID	LIB3176-103-P1-K1-D11
Method	BLASTN
NCBI GI	g968976
BLAST score	109
E value	2.0e-54
Match length	160
% identity	92
NCBI Description	Arabidopsis thaliana light-dependent NADPH:protochlorophyllide oxidoreductase B (PorB) mRNA, nuclear gene encoding chloroplast protein, complete cds
Seq. No.	159001
Seq. ID	LIB3176-103-P1-K1-D12
Method	BLASTX
NCBI GI	g115783
BLAST score	387
E value	1.0e-37
Match length	75
% identity	96
NCBI Description	CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR (CAB-140) (LHCP) >gi_16376_emb_CAA27543_ (X03909) chlorophyll a/b binding protein (LHCP AB 140) [Arabidopsis thaliana]
Seq. No.	159002
Seq. ID	LIB3176-103-P1-K1-D2
Method	BLASTX
NCBI GI	g3913202
BLAST score	362
E value	2.0e-34
Match length	83
% identity	78
NCBI Description	CENTROMERE/MICROTUBULE BINDING PROTEIN CBF5 (CENTROMERE-BINDING FACTOR 5) (NUCLEOLAR PROTEIN CBF5) >gi_2239214_emb_CAB10131_ (Z97210) hypothetical protein [Schizosaccharomyces pombe]
Seq. No.	159003
Seq. ID	LIB3176-103-P1-K1-D4
Method	BLASTX
NCBI GI	g1053047
BLAST score	548
E value	2.0e-56

Match length	114
% identity	96
NCBI Description	(U38425) histone H3 [Glycine max] >gi_1053049 (U38426) histone H3 [Glycine max] >gi_1053051 (U38427) histone H3 [Glycine max]

Seq. No.	159004
Seq. ID	LIB3176-103-P1-K1-D5
Method	BLASTX
NCBI GI	g1053047
BLAST score	370
E value	2.0e-35
Match length	83
% identity	90
NCBI Description	(U38425) histone H3 [Glycine max] >gi_1053049 (U38426) histone H3 [Glycine max] >gi_1053051 (U38427) histone H3 [Glycine max]

Seq. No.	159005
Seq. ID	LIB3176-103-P1-K1-D6
Method	BLASTX
NCBI GI	g1053047
BLAST score	170
E value	1.0e-12
Match length	72
% identity	57
NCBI Description	(U38425) histone H3 [Glycine max] >gi_1053049 (U38426) histone H3 [Glycine max] >gi_1053051 (U38427) histone H3 [Glycine max]

Seq. No.	159006
Seq. ID	LIB3176-103-P1-K1-D7
Method	BLASTX
NCBI GI	g3023848
BLAST score	265
E value	9.0e-24
Match length	53
% identity	64
NCBI Description	GUANINE NUCLEOTIDE-BINDING PROTEIN BETA SUBUNIT-LIKE PROTEIN (WD-40 REPEAT AUXIN-DEPENDENT PROTEIN ARCA) >gi_2289095 (U77381) WD-40 repeat protein [Arabidopsis thaliana]

Seq. No.	159007
Seq. ID	LIB3176-103-P1-K1-D8
Method	BLASTX
NCBI GI	g3334141
BLAST score	504
E value	4.0e-51
Match length	117
% identity	80
NCBI Description	CENTROMERE/MICROTUBULE BINDING PROTEIN CBF5 (CENTROMERE-BINDING FACTOR 5) (NUCLEOLAR PROTEIN CBF5) >gi_2737890 (U59149) nucleolar protein CaCbf5p [Candida albicans]

Seq. No.	159008

Seq. ID	LIB3176-103-P1-K1-D9
Method	BLASTN
NCBI GI	g4662640
BLAST score	410
E value	0.0e+00
Match length	422
% identity	99
NCBI Description	Arabidopsis thaliana chromosome II BAC F15K19 genomic sequence, complete sequence

Seq. No.	159009
Seq. ID	LIB3176-103-P1-K1-E10
Method	BLASTX
NCBI GI	g4262180
BLAST score	217
E value	4.0e-18
Match length	43
% identity	93
NCBI Description	(AC005508) 29621 [Arabidopsis thaliana]

Seq. No.	159010
Seq. ID	LIB3176-103-P1-K1-E2
Method	BLASTX
NCBI GI	g119143
BLAST score	308
E value	1.0e-28
Match length	59
% identity	100
NCBI Description	ELONGATION FACTOR 1-ALPHA (EF-1-ALPHA) >gi_81606_pir__S06724 translation elongation factor eEF-1 alpha chain - Arabidopsis thaliana >gi_295788_emb_CAA34453_ (X16430) elongation factor 1-alpha [Arabidopsis thaliana] >gi_1369927_emb_CAA34454_ (X16431) elongation factor 1-alpha [Arabidopsis thaliana] >gi_1369928_emb_CAA34455_ (X16431) elongation factor 1-alpha [Arabidopsis thaliana] >gi_1532172 (U63815) EF-1alpha-A1 [Arabidopsis thaliana] >gi_1532173 (U63815) EF-1alpha-A2 [Arabidopsis thaliana] >gi_1532174 (U63815) EF-1alpha-A3 [Arabidopsis thaliana]

Seq. No.	159011
Seq. ID	LIB3176-103-P1-K1-E3
Method	BLASTX
NCBI GI	g136739
BLAST score	196
E value	1.0e-15
Match length	53
% identity	74
NCBI Description	UTP--GLUCOSE-1-PHOSPHATE URIDYLYLTRANSFERASE (UDP-GLUCOSE PYROPHOSPHORYLASE) (UDPGP) >gi_67061_pir__XNPOU UTP--glucose-1-phosphate uridylyltransferase (EC 2.7.7.9) - potato >gi_218001_dbj_BAA00570_ (D00667) UDP-glucose pyrophosphorylase precursor [Solanum tuberosum]

Seq. No.	159012
Seq. ID	LIB3176-103-P1-K1-E4
Method	BLASTN
NCBI GI	g4115370

BLAST score	92
E value	3.0e-44
Match length	160
% identity	89
NCBI Description	Arabidopsis thaliana chromosome II BAC F27D4 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	159013
Seq. ID	LIB3176-103-P1-K1-E5
Method	BLASTN
NCBI GI	g2264321
BLAST score	66
E value	5.0e-29
Match length	140
% identity	88
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MXM12, complete sequence [Arabidopsis thaliana]

Seq. No.	159014
Seq. ID	LIB3176-103-P1-K1-E7
Method	BLASTN
NCBI GI	g4678291
BLAST score	123
E value	6.0e-63
Match length	157
% identity	98
NCBI Description	Arabidopsis thaliana DNA chromosome 3, BAC clone F28P10 (ESSA project)

Seq. No.	159015
Seq. ID	LIB3176-103-P1-K1-E8
Method	BLASTX
NCBI GI	g2492952
BLAST score	297
E value	3.0e-27
Match length	64
% identity	89
NCBI Description	CHORISMATE SYNTHASE 1 PRECURSOR (5-ENOLPYRUVYLSHIKIMATE-3-PHOSPHATE PHOSPHOLYASE 1) >gi_542026_pir__S40410 chorismate synthase (EC 4.6.1.4) 1 precursor - tomato >gi_410482_emb_CAA79859_ (Z21796) chorismate synthase 1 [Lycopersicon esculentum]

Seq. No.	159016
Seq. ID	LIB3176-103-P1-K1-E9
Method	BLASTX
NCBI GI	g99752
BLAST score	290
E value	4.0e-26
Match length	119
% identity	62
NCBI Description	protochlorophyllide reductase (EC 1.3.1.33) precursor - Arabidopsis thaliana

Seq. No.	159017
Seq. ID	LIB3176-103-P1-K1-F1
Method	BLASTX

NCBI GI	g3377797
BLAST score	476
E value	4.0e-48
Match length	102
% identity	91
NCBI Description	(AF075597) Similar to 60S ribosome protein L19; coded for by A. thaliana cDNA T04719; coded for by A. thaliana cDNA H36046; coded for by A. thaliana cDNA T44067; coded for by A. thaliana cDNA T14056; coded for by A. thaliana cDNA R90691 [Ara

Seq. No.	159018
Seq. ID	LIB3176-103-P1-K1-F10
Method	BLASTX
NCBI GI	g126962
BLAST score	319
E value	8.0e-30
Match length	73
% identity	89
NCBI Description	TONOPLAST INTRINSIC PROTEIN, ROOT-SPECIFIC RB7 >gi_99747_pir__S13718 probable membrane channel protein - Arabidopsis thaliana >gi_16492_emb_CAA38633_ (X54854) possible membrane channel protein [Arabidopsis thaliana]

Seq. No.	159019
Seq. ID	LIB3176-103-P1-K1-F12
Method	BLASTX
NCBI GI	g3738287
BLAST score	62
E value	2.0e-30
Match length	101
% identity	73
NCBI Description	(AC005309) glutathione s-transferase, GST6 [Arabidopsis thaliana]

Seq. No.	159020
Seq. ID	LIB3176-103-P1-K1-F2
Method	BLASTX
NCBI GI	g586145
BLAST score	323
E value	6.0e-30
Match length	123
% identity	56
NCBI Description	UBIQUINOL-CYTOCHROME C REDUCTASE IRON-SULFUR SUBUNIT PRECURSOR (RIESKE IRON-SULFUR PROTEIN) (RISP) >gi_488848_emb_CAA55894_ (X79332) Rieske iron sulphur protein [Solanum tuberosum]

Seq. No.	159021
Seq. ID	LIB3176-103-P1-K1-F3
Method	BLASTX
NCBI GI	g2695931
BLAST score	223
E value	3.0e-18
Match length	61
% identity	70
NCBI Description	(AJ222779) hypothetical protein [Hordeum vulgare]

Seq. No.	159022
Seq. ID	LIB3176-103-P1-K1-F5
Method	BLASTX
NCBI GI	g2129516
BLAST score	268
E value	1.0e-23
Match length	81
% identity	65
NCBI Description	1-aminocyclopropane-1-carboxylate oxidase homolog (clone 2A6) - Arabidopsis thaliana >gi_599622_emb_CAA58151_ (X83096) 2A6 [Arabidopsis thaliana] >gi_2809261 (AC002560) F21B7.30 [Arabidopsis thaliana]

Seq. No.	159023
Seq. ID	LIB3176-103-P1-K1-F8
Method	BLASTX
NCBI GI	g3023216
BLAST score	151
E value	2.0e-10
Match length	31
% identity	97
NCBI Description	14-3-3-LIKE PROTEIN GF14 MU >gi_1531629 (U60444) GF14 mu [Arabidopsis thaliana]

Seq. No.	159024
Seq. ID	LIB3176-103-P1-K1-F9
Method	BLASTX
NCBI GI	g2827039
BLAST score	319
E value	4.0e-30
Match length	67
% identity	91
NCBI Description	(AF008444) chloroplast processing enzyme [Arabidopsis thaliana]

Seq. No.	159025
Seq. ID	LIB3176-103-P1-K1-G11
Method	BLASTN
NCBI GI	g2244870
BLAST score	276
E value	1.0e-154
Match length	288
% identity	92
NCBI Description	Arabidopsis thaliana DNA chromosome 4, ESSA I contig fragment No

Seq. No.	159026
Seq. ID	LIB3176-103-P1-K1-G12
Method	BLASTX
NCBI GI	g2252857
BLAST score	299
E value	2.0e-27
Match length	67
% identity	94
NCBI Description	(AF013294) similar to acidic ribosomal protein p1 [Arabidopsis thaliana]

Seq. No.	159027
Seq. ID	LIB3176-103-P1-K1-G2
Method	BLASTX
NCBI GI	g4337027
BLAST score	197
E value	2.0e-15
Match length	49
% identity	84
NCBI Description	(AF123254) MFP2 [Arabidopsis thaliana]

Seq. No.	159028
Seq. ID	LIB3176-103-P1-K1-G3
Method	BLASTN
NCBI GI	g4584387
BLAST score	98
E value	5.0e-48
Match length	193
% identity	97
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F7J7 (ESSA project)

Seq. No.	159029
Seq. ID	LIB3176-103-P1-K1-G4
Method	BLASTX
NCBI GI	g3738287
BLAST score	501
E value	7.0e-51
Match length	130
% identity	76
NCBI Description	(AC005309) glutathione s-transferase, GST6 [Arabidopsis thaliana]

Seq. No.	159030
Seq. ID	LIB3176-103-P1-K1-G5
Method	BLASTN
NCBI GI	g2244870
BLAST score	125
E value	8.0e-64
Match length	155
% identity	87
NCBI Description	Arabidopsis thaliana DNA chromosome 4, ESSA I contig fragment No

Seq. No.	159031
Seq. ID	LIB3176-103-P1-K1-G6
Method	BLASTN
NCBI GI	g4079614
BLAST score	236
E value	1.0e-130
Match length	252
% identity	98
NCBI Description	Arabidopsis thaliana chromosome I BAC F21M11 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	159032
Seq. ID	LIB3176-103-P1-K1-G7

Method	BLASTX
NCBI GI	g3281869
BLAST score	372
E value	6.0e-36
Match length	71
% identity	99
NCBI Description	(AL031004) RSZp22 splicing factor [Arabidopsis thaliana] >gi_3435094_gb_AAD12769.1_ (AF033586) 9G8-like SR protein [Arabidopsis thaliana]

Seq. No.	159033
Seq. ID	LIB3176-103-P1-K1-G9
Method	BLASTN
NCBI GI	g2351069
BLAST score	133
E value	5.0e-69
Match length	157
% identity	96
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MSH12, complete sequence [Arabidopsis thaliana]

Seq. No.	159034
Seq. ID	LIB3176-103-P1-K1-H1
Method	BLASTX
NCBI GI	g2244750
BLAST score	120
E value	3.0e-35
Match length	85
% identity	92
NCBI Description	(Z97335) adenosylhomocysteinase [Arabidopsis thaliana] >gi_3088579 (AF059581) S-adenosyl-L-homocysteine hydrolase [Arabidopsis thaliana]

Seq. No.	159035
Seq. ID	LIB3176-103-P1-K1-H10
Method	BLASTN
NCBI GI	g3201608
BLAST score	141
E value	1.0e-73
Match length	195
% identity	93
NCBI Description	Arabidopsis thaliana chromosome II BAC F7F1 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	159036
Seq. ID	LIB3176-103-P1-K1-H2
Method	BLASTX
NCBI GI	g1171978
BLAST score	273
E value	1.0e-24
Match length	71
% identity	28
NCBI Description	POLYADENYLATE-BINDING PROTEIN 2 (POLY(A) BINDING PROTEIN 2) (PABP 2) >gi_304109 (L19418) poly(A)-binding protein [Arabidopsis thaliana] >gi_2911051_emb_CAA17561_ (AL021961) poly(A)-binding protein [Arabidopsis thaliana]

Seq. No.	159037
Seq. ID	LIB3176-103-P1-K1-H3
Method	BLASTX
NCBI GI	g3953471
BLAST score	586
E value	7.0e-61
Match length	120
% identity	92
NCBI Description	(AC002328) F22O2.16 [Arabidopsis thaliana]

Seq. No.	159038
Seq. ID	LIB3176-103-P1-K1-H5
Method	BLASTX
NCBI GI	g1352347
BLAST score	164
E value	6.0e-12
Match length	38
% identity	87
NCBI Description	ELONGATION FACTOR 1-BETA A1 (EF-1-BETA) >gi_480620_pir__S37103 translation elongation factor eEF-1 beta-A1 chain - Arabidopsis thaliana (cv. Colombia) >gi_398608_emb_CAA52751_ (X74733) elongation factor-1 beta A1 [Arabidopsis thaliana]

Seq. No.	159039
Seq. ID	LIB3176-103-P1-K1-H6
Method	BLASTX
NCBI GI	g3377797
BLAST score	121
E value	2.0e-35
Match length	80
% identity	89
NCBI Description	(AF075597) Similar to 60S ribosome protein L19; coded for by A. thaliana cDNA T04719; coded for by A. thaliana cDNA H36046; coded for by A. thaliana cDNA T44067; coded for by A. thaliana cDNA T14056; coded for by A. thaliana cDNA R90691 [Ara

Seq. No.	159040
Seq. ID	LIB3176-103-P1-K1-H7
Method	BLASTX
NCBI GI	g3914535
BLAST score	168
E value	2.0e-12
Match length	39
% identity	87
NCBI Description	60S RIBOSOMAL PROTEIN L13A >gi_2791948_emb_CAA11283_ (AJ223363) ribosomal protein L13a [Lupinus luteus]

Seq. No.	159041
Seq. ID	LIB3176-103-P1-K1-H9
Method	BLASTX
NCBI GI	g3915865
BLAST score	282
E value	2.0e-25
Match length	63
% identity	84

NCBI Description	40S RIBOSOMAL PROTEIN S4

Seq. No.	159042
Seq. ID	LIB3176-104-P1-K1-A1
Method	BLASTX
NCBI GI	g3193323
BLAST score	464
E value	1.0e-46
Match length	96
% identity	93
NCBI Description	(AF069299) similar to ribosomal protein S13 (Pfam; S15.hmm, score: 78.35); identical to Arabidopsis 40S ribosomal protein S13 (fragment) (SW: P49203A) except the first 32 amino acids are different [Arabidopsis thaliana]

Seq. No.	159043
Seq. ID	LIB3176-104-P1-K1-A12
Method	BLASTN
NCBI GI	g3702724
BLAST score	291
E value	1.0e-163
Match length	306
% identity	99
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K17N15, complete sequence [Arabidopsis thaliana]

Seq. No.	159044
Seq. ID	LIB3176-104-P1-K1-A2
Method	BLASTN
NCBI GI	g443819
BLAST score	269
E value	1.0e-150
Match length	297
% identity	98
NCBI Description	A.thaliana pyrB mRNA

Seq. No.	159045
Seq. ID	LIB3176-104-P1-K1-A3
Method	BLASTX
NCBI GI	g2369714
BLAST score	220
E value	2.0e-18
Match length	47
% identity	89
NCBI Description	(Z97178) elongation factor 2 [Beta vulgaris]

Seq. No.	159046
Seq. ID	LIB3176-104-P1-K1-A4
Method	BLASTX
NCBI GI	g3021336
BLAST score	204
E value	7.0e-16
Match length	61
% identity	72
NCBI Description	(AJ224957) RGA-like [Arabidopsis thaliana]

Seq. No.	159047

Seq. ID	LIB3176-104-P1-K1-A5
Method	BLASTX
NCBI GI	g2738248
BLAST score	49
E value	3.0e-19
Match length	76
% identity	72
NCBI Description	(U97200) cobalamin-independent methionine synthase [Arabidopsis thaliana]

Seq. No.	159048
Seq. ID	LIB3176-104-P1-K1-A6
Method	BLASTX
NCBI GI	g544425
BLAST score	221
E value	1.0e-18
Match length	47
% identity	91
NCBI Description	GLYCINE-RICH RNA-BINDING PROTEIN 8 (CCR1 PROTEIN) >gi_419756_pir__S30148 glycine-rich protein (clone AtGRP8) - Arabidopsis thaliana >gi_16305_emb_CAA78712_ (Z14988) glycine rich protein [Arabidopsis thaliana] >gi_166658 (L04171) ORF [Arabidopsis thaliana] >gi_166839 (L00649) RNA-binding protein [Arabidopsis thaliana]

Seq. No.	159049
Seq. ID	LIB3176-104-P1-K1-A7
Method	BLASTN
NCBI GI	g2264313
BLAST score	109
E value	1.0e-54
Match length	211
% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MOP10, complete sequence [Arabidopsis thaliana]

Seq. No.	159050
Seq. ID	LIB3176-104-P1-K1-A8
Method	BLASTN
NCBI GI	g4757662
BLAST score	121
E value	5.0e-62
Match length	121
% identity	100
NCBI Description	Genomic sequence for Arabidopsis thaliana BAC F10B6 from chromosome I, complete sequence

Seq. No.	159051
Seq. ID	LIB3176-104-P1-K1-A9
Method	BLASTN
NCBI GI	g2358139
BLAST score	250
E value	1.0e-138
Match length	344
% identity	95
NCBI Description	Arabidopsis thaliana chromosome 1 YAC yUP8H12 complete sequence [Arabidopsis thaliana]

Seq. No.	159052
Seq. ID	LIB3176-104-P1-K1-B1
Method	BLASTN
NCBI GI	g16304
BLAST score	37
E value	2.0e-11
Match length	49
% identity	94
NCBI Description	A.thaliana mRNA for glycine rich protein >gi_166838_gb_L00649_ATHRBPB Arabidopsis thaliana RNA-binding protein mRNA, complete cds

Seq. No.	159053
Seq. ID	LIB3176-104-P1-K1-B11
Method	BLASTN
NCBI GI	g2275194
BLAST score	71
E value	3.0e-32
Match length	115
% identity	93
NCBI Description	Arabidopsis thaliana chromosome II BAC T08I13 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	159054
Seq. ID	LIB3176-104-P1-K1-B12
Method	BLASTX
NCBI GI	g2131329
BLAST score	148
E value	2.0e-09
Match length	39
% identity	64
NCBI Description	hypothetical protein YDL087c - yeast (Saccharomyces cerevisiae) >gi_1431114_emb_CAA98653_ (Z74135) ORF YDL087c [Saccharomyces cerevisiae]

Seq. No.	159055
Seq. ID	LIB3176-104-P1-K1-B3
Method	BLASTN
NCBI GI	g472876
BLAST score	47
E value	3.0e-18
Match length	67
% identity	93
NCBI Description	A.thaliana mRNA for plasma membrane intrinsic protein 2a

Seq. No.	159056
Seq. ID	LIB3176-104-P1-K1-B4
Method	BLASTX
NCBI GI	g4559396
BLAST score	479
E value	2.0e-48
Match length	112
% identity	91
NCBI Description	(AC006526) unknown protein [Arabidopsis thaliana]

Seq. No.	159057

Seq. ID	LIB3176-104-P1-K1-B6
Method	BLASTN
NCBI GI	g1732569
BLAST score	37
E value	3.0e-12
Match length	53
% identity	94
NCBI Description	Arabidopsis thaliana beta-glucosidase (psr3.1) mRNA, complete cds

Seq. No.	159058
Seq. ID	LIB3176-104-P1-K1-B7
Method	BLASTX
NCBI GI	g4581146
BLAST score	196
E value	1.0e-15
Match length	40
% identity	100
NCBI Description	(AC006919) putative fructose-bisphosphate aldolase, cytoplasmic [Arabidopsis thaliana]

Seq. No.	159059
Seq. ID	LIB3176-104-P1-K1-C10
Method	BLASTX
NCBI GI	g4262174
BLAST score	285
E value	9.0e-26
Match length	58
% identity	93
NCBI Description	(AC005508) 9058 [Arabidopsis thaliana]

Seq. No.	159060
Seq. ID	LIB3176-104-P1-K1-C11
Method	BLASTX
NCBI GI	g2980641
BLAST score	210
E value	3.0e-17
Match length	46
% identity	91
NCBI Description	(Y11250) multi resistance protein [Arabidopsis thaliana]

Seq. No.	159061
Seq. ID	LIB3176-104-P1-K1-C12
Method	BLASTX
NCBI GI	g113024
BLAST score	361
E value	9.0e-35
Match length	69
% identity	99
NCBI Description	ISOCITRATE LYASE (ISOCITRASE) (ISOCITRATASE) (ICL) >gi_553043 (M83534) isocitrate lyase [Arabidopsis thaliana]

Seq. No.	159062
Seq. ID	LIB3176-104-P1-K1-C2
Method	BLASTN
NCBI GI	g2264306
BLAST score	79

E value	4.0e-37
Match length	91
% identity	97
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MBK5, complete sequence [Arabidopsis thaliana]

Seq. No.	159063
Seq. ID	LIB3176-104-P1-K1-C3
Method	BLASTX
NCBI GI	g4567303
BLAST score	329
E value	3.0e-31
Match length	66
% identity	92
NCBI Description	(AC005956) unknown protein [Arabidopsis thaliana]

Seq. No.	159064
Seq. ID	LIB3176-104-P1-K1-C4
Method	BLASTX
NCBI GI	g1709446
BLAST score	459
E value	5.0e-46
Match length	98
% identity	94
NCBI Description	PYRUVATE DEHYDROGENASE E1 COMPONENT, ALPHA SUBUNIT PRECURSOR (PDHE1-A) >gi_2117533_pir__JC4358 pyruvate dehydrogenase (lipoamide) (EC 1.2.4.1) complex E1 alpha chain - Arabidopsis thaliana mitochondrion >gi_710400 (U21214) pyruvate dehydrogenase E1 alpha subunit [Arabidopsis thaliana]

Seq. No.	159065
Seq. ID	LIB3176-104-P1-K1-C5
Method	BLASTX
NCBI GI	g1170373
BLAST score	60
E value	4.0e-18
Match length	56
% identity	93
NCBI Description	HEAT SHOCK COGNATE 70 KD PROTEIN 1 >gi_1072473_pir__S46302 heat shock cognate protein 70-1 - Arabidopsis thaliana >gi_397482_emb_CAA52684_ (X74604) heat shock protein 70 cognate [Arabidopsis thaliana]

Seq. No.	159066
Seq. ID	LIB3176-104-P1-K1-C6
Method	BLASTN
NCBI GI	g414340
BLAST score	108
E value	2.0e-54
Match length	108
% identity	100
NCBI Description	A.thaliana rd21A gene for thiol protease, complete cds

Seq. No.	159067
Seq. ID	LIB3176-104-P1-K1-C7
Method	BLASTX

D0960460 : D0960460

NCBI GI	g134025
BLAST score	386
E value	1.0e-37
Match length	95
% identity	81
NCBI Description	CHLOROPLAST 30S RIBOSOMAL PROTEIN S8 >gi_70913_pir__R3NT8 ribosomal protein S8 - common tobacco chloroplast >gi_11863_emb_CAA77378_ (Z00044) ribosomal protein S8 [Nicotiana tabacum] >gi_225232_prf__1211235BP ribosomal protein S8 [Nicotiana tabacum]

Seq. No.	159068
Seq. ID	LIB3176-104-P1-K1-D1
Method	BLASTX
NCBI GI	g1666173
BLAST score	186
E value	4.0e-14
Match length	69
% identity	61
NCBI Description	(Y09106) transcription factor [Nicotiana plumbaginifolia]

Seq. No.	159069
Seq. ID	LIB3176-104-P1-K1-D10
Method	BLASTX
NCBI GI	g3176668
BLAST score	386
E value	9.0e-38
Match length	75
% identity	99
NCBI Description	(AC004393) Similar to ribosomal protein L17 gb_X62724 from Hordeum vulgare. ESTs gb_Z34728, gb_F19974, gb_T75677 and gb_Z33937 come from this gene. [Arabidopsis thaliana]

Seq. No.	159070
Seq. ID	LIB3176-104-P1-K1-D4
Method	BLASTX
NCBI GI	g4582468
BLAST score	254
E value	3.0e-22
Match length	55
% identity	95
NCBI Description	(AC007071) putative 40S ribosomal protein; contains C-terminal domain [Arabidopsis thaliana]

Seq. No.	159071
Seq. ID	LIB3176-104-P1-K1-D5
Method	BLASTN
NCBI GI	g4220633
BLAST score	201
E value	1.0e-109
Match length	225
% identity	97
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K7J8, complete sequence [Arabidopsis thaliana]

Seq. No.	159072
Seq. ID	LIB3176-104-P1-K1-D7

Method	BLASTX
NCBI GI	g131397
BLAST score	142
E value	2.0e-09
Match length	49
% identity	76
NCBI Description	OXYGEN-EVOLVING ENHANCER PROTEIN 3 PRECURSOR (OEE3) (16 KD SUBUNIT OF OXYGEN-EVOLVING SYSTEM OF PHOTOSYSTEM II) >gi_81480_pir__S00008 photosystem II oxygen-evolving complex protein 3 precursor - spinach >gi_755802_emb_CAA29056_ (X05512) 16 kDa protein of the photosynthetic oxygen- evolving protein (OEC) [Spinacia oleracea] >gi_225597_prf__1307179B luminal protein 16kD [Spinacia oleracea]

Seq. No.	159073
Seq. ID	LIB3176-104-P1-K1-E11
Method	BLASTN
NCBI GI	g2245073
BLAST score	65
E value	1.0e-28
Match length	111
% identity	100
NCBI Description	Arabidopsis thaliana DNA chromosome 4, ESSA I contig fragment No

Seq. No.	159074
Seq. ID	LIB3176-104-P1-K1-E2
Method	BLASTN
NCBI GI	g2264316
BLAST score	65
E value	1.0e-28
Match length	121
% identity	52
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MRO11, complete sequence [Arabidopsis thaliana]

Seq. No.	159075
Seq. ID	LIB3176-104-P1-K1-E3
Method	BLASTN
NCBI GI	g4191771
BLAST score	301
E value	1.0e-169
Match length	301
% identity	100
NCBI Description	Arabidopsis thaliana chromosome II BAC F3P11 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	159076
Seq. ID	LIB3176-104-P1-K1-E4
Method	BLASTN
NCBI GI	g2264307
BLAST score	67
E value	6.0e-30
Match length	67
% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:

MED24, complete sequence [Arabidopsis thaliana]

Seq. No.	159077
Seq. ID	LIB3176-104-P1-K1-E5
Method	BLASTX
NCBI GI	g336392
BLAST score	355
E value	3.0e-34
Match length	74
% identity	97
NCBI Description	(J05215) ribosomal protein S17 [Arabidopsis thaliana]

Seq. No.	159078
Seq. ID	LIB3176-104-P1-K1-E7
Method	BLASTN
NCBI GI	g1732569
BLAST score	118
E value	4.0e-60
Match length	136
% identity	97
NCBI Description	Arabidopsis thaliana beta-glucosidase (psr3.1) mRNA, complete cds

Seq. No.	159079
Seq. ID	LIB3176-104-P1-K1-F1
Method	BLASTN
NCBI GI	g2088638
BLAST score	75
E value	5.0e-34
Match length	114
% identity	96
NCBI Description	Arabidopsis thaliana chromosome II BAC T28M21 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	159080
Seq. ID	LIB3176-104-P1-K1-F10
Method	BLASTX
NCBI GI	g2062157
BLAST score	356
E value	2.0e-34
Match length	69
% identity	34
NCBI Description	(AC001645) jasmonate inducible protein isolog [Arabidopsis thaliana]

Seq. No.	159081
Seq. ID	LIB3176-104-P1-K1-F12
Method	BLASTN
NCBI GI	g2736146
BLAST score	123
E value	8.0e-63
Match length	139
% identity	97
NCBI Description	Arabidopsis thaliana fatty acid hydroxylase Fah1p (FAH1) mRNA, complete cds

Seq. No.	159082

Seq. ID	LIB3176-104-P1-K1-F2
Method	BLASTX
NCBI GI	g2827039
BLAST score	404
E value	1.0e-39
Match length	101
% identity	83
NCBI Description	(AF008444) chloroplast processing enzyme [Arabidopsis thaliana]

Seq. No.	159083
Seq. ID	LIB3176-104-P1-K1-F3
Method	BLASTX
NCBI GI	g2980781
BLAST score	209
E value	3.0e-17
Match length	62
% identity	55
NCBI Description	(AL022198) putative protein [Arabidopsis thaliana]

Seq. No.	159084
Seq. ID	LIB3176-104-P1-K1-F5
Method	BLASTX
NCBI GI	g1346526
BLAST score	332
E value	3.0e-31
Match length	67
% identity	93
NCBI Description	S-ADENOSYLMETHIONINE SYNTHETASE 2 (METHIONINE ADENOSYLTRANSFERASE 2) (ADOMET SYNTHETASE 2) >gi_1076533_pir__S52218 methionine adenosyltransferase (EC 2.5.1.6) - garden pea >gi_609225_emb_CAA57581_ (X82077) methionine adenosyltransferase [Pisum sativum] >gi_609559 (L36681) S-adenosylmethionine synthase [Pisum sativum]

Seq. No.	159085
Seq. ID	LIB3176-104-P1-K1-F8
Method	BLASTX
NCBI GI	g3176676
BLAST score	603
E value	8.0e-63
Match length	120
% identity	99
NCBI Description	(AC003671) Similar to carbonic anhydrase gb_L19255 from Nicotiana tabacum. ESTs gb_AA597643, gb_T45390, gb_T43963 and gb_AA597734 come from this gene. [Arabidopsis thaliana]

Seq. No.	159086
Seq. ID	LIB3176-104-P1-K1-G1
Method	BLASTX
NCBI GI	g2582645
BLAST score	166
E value	4.0e-12
Match length	32
% identity	100
NCBI Description	(AJ002378) RSZp22 protein [Arabidopsis thaliana]

Seq. No.	159087
Seq. ID	LIB3176-104-P1-K1-G10
Method	BLASTN
NCBI GI	g2182286
BLAST score	154
E value	2.0e-81
Match length	166
% identity	98
NCBI Description	Sequence of BAC F20P5 from Arabidopsis thaliana chromosome 1, complete sequence [Arabidopsis thaliana]

Seq. No.	159088
Seq. ID	LIB3176-104-P1-K1-G12
Method	BLASTX
NCBI GI	g2497733
BLAST score	429
E value	1.0e-42
Match length	83
% identity	99
NCBI Description	NONSPECIFIC LIPID-TRANSFER PROTEIN 1 PRECURSOR (LTP 1) >gi_1177796 (M80567) non-specific lipid transfer protein [Arabidopsis thaliana] >gi_3786018 (AC005499) unknown protein [Arabidopsis thaliana]

Seq. No.	159089
Seq. ID	LIB3176-104-P1-K1-G2
Method	BLASTN
NCBI GI	g1488518
BLAST score	151
E value	2.0e-79
Match length	221
% identity	99
NCBI Description	A.thaliana mRNA for cysteine synthase

Seq. No.	159090
Seq. ID	LIB3176-104-P1-K1-G3
Method	BLASTX
NCBI GI	g1732570
BLAST score	365
E value	5.0e-35
Match length	74
% identity	93
NCBI Description	(U72153) beta-glucosidase [Arabidopsis thaliana]

Seq. No.	159091
Seq. ID	LIB3176-104-P1-K1-G4
Method	BLASTN
NCBI GI	g4519190
BLAST score	224
E value	1.0e-123
Match length	227
% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K6A12, complete sequence

Seq. No.	159092
Seq. ID	LIB3176-104-P1-K1-G5

Method	BLASTN
NCBI GI	g1769904
BLAST score	180
E value	7.0e-97
Match length	188
% identity	99
NCBI Description	A.thaliana psbP gene

Seq. No.	159093
Seq. ID	LIB3176-104-P1-K1-G6
Method	BLASTX
NCBI GI	g1769905
BLAST score	246
E value	5.0e-21
Match length	89
% identity	60
NCBI Description	(X98108) 23 kDa polypeptide of oxygen-evolving comlex (OEC) [Arabidopsis thaliana]

Seq. No.	159094
Seq. ID	LIB3176-104-P1-K1-G7
Method	BLASTN
NCBI GI	g4102581
BLAST score	134
E value	2.0e-69
Match length	196
% identity	100
NCBI Description	Arabidopsis thaliana CAO gene, nuclear gene encoding chloroplast protein, complete cds

Seq. No.	159095
Seq. ID	LIB3176-104-P1-K1-G8
Method	BLASTN
NCBI GI	g166645
BLAST score	115
E value	2.0e-58
Match length	135
% identity	96
NCBI Description	Arabidopsis thaliana light-harvesting chlorophyll a/b-binding protein (Cab4) mRNA, complete cds

Seq. No.	159096
Seq. ID	LIB3176-104-P1-K1-G9
Method	BLASTN
NCBI GI	g166771
BLAST score	99
E value	9.0e-49
Match length	115
% identity	97
NCBI Description	A.thaliana isocitrate lyase gene, 5' end

Seq. No.	159097
Seq. ID	LIB3176-104-P1-K1-H1
Method	BLASTX
NCBI GI	g113024
BLAST score	425
E value	4.0e-42

Match length	102
% identity	86
NCBI Description	ISOCITRATE LYASE (ISOCITRASE) (ISOCITRATASE) (ICL) >gi_553043 (M83534) isocitrate lyase [Arabidopsis thaliana]

Seq. No.	159098
Seq. ID	LIB3176-104-P1-K1-H10
Method	BLASTN
NCBI GI	g4586349
BLAST score	65
E value	4.0e-28
Match length	89
% identity	93
NCBI Description	Arabidopsis thaliana DNA for glucose-1-phosphate adenylyltransferase, complete cds

Seq. No.	159099
Seq. ID	LIB3176-104-P1-K1-H11
Method	BLASTX
NCBI GI	g3096931
BLAST score	380
E value	4.0e-37
Match length	77
% identity	96
NCBI Description	(AL023094) putative ribosomal protein S16 [Arabidopsis thaliana]

Seq. No.	159100
Seq. ID	LIB3176-104-P1-K1-H12
Method	BLASTX
NCBI GI	g445612
BLAST score	339
E value	2.0e-33
Match length	86
% identity	88
NCBI Description	ribosomal protein S19 [Solanum tuberosum]

Seq. No.	159101
Seq. ID	LIB3176-104-P1-K1-H2
Method	BLASTX
NCBI GI	g2738248
BLAST score	49
E value	7.0e-42
Match length	95
% identity	96
NCBI Description	(U97200) cobalamin-independent methionine synthase [Arabidopsis thaliana]

Seq. No.	159102
Seq. ID	LIB3176-104-P1-K1-H3
Method	BLASTN
NCBI GI	g4220633
BLAST score	133
E value	5.0e-69
Match length	133
% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:

K7J8, complete sequence [Arabidopsis thaliana]

Seq. No.	159103
Seq. ID	LIB3176-104-P1-K1-H4
Method	BLASTX
NCBI GI	g99735
BLAST score	345
E value	5.0e-33
Match length	67
% identity	99
NCBI Description	L-ascorbate peroxidase (EC 1.11.1.11) precursor - Arabidopsis thaliana (fragment)

Seq. No.	159104
Seq. ID	LIB3176-104-P1-K1-H5
Method	BLASTX
NCBI GI	g4587542
BLAST score	249
E value	1.0e-21
Match length	62
% identity	79
NCBI Description	(AC006577) Belongs to the PF_00657 Lipase/Acylhydrolase with GDSL-motif family. ESTs gb_T45815, gb_T45130 and gb_Z38046 come from this gene. [Arabidopsis thaliana]

Seq. No.	159105
Seq. ID	LIB3176-104-P1-K1-H7
Method	BLASTN
NCBI GI	g3985954
BLAST score	103
E value	3.0e-51
Match length	123
% identity	51
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MRG21, complete sequence [Arabidopsis thaliana]

Seq. No.	159106
Seq. ID	LIB3176-104-P1-K1-H8
Method	BLASTX
NCBI GI	g1946331
BLAST score	297
E value	2.0e-27
Match length	60
% identity	100
NCBI Description	(U69155) prohibitin [Arabidopsis thaliana] >gi_4097692 (U66593) prohibitin 3 [Arabidopsis thaliana]

Seq. No.	159107
Seq. ID	LIB3176-104-P1-K1-H9
Method	BLASTX
NCBI GI	g4454037
BLAST score	390
E value	4.0e-38
Match length	69
% identity	100
NCBI Description	(AL035394) putative major latex protein [Arabidopsis thaliana]

Seq. No.	159108
Seq. ID	LIB3176-105-P1-K1-A1
Method	BLASTN
NCBI GI	g4388714
BLAST score	62
E value	2.0e-26
Match length	94
% identity	93
NCBI Description	Arabidopsis thaliana chromosome II BAC F5K7 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	159109
Seq. ID	LIB3176-105-P1-K1-A11
Method	BLASTN
NCBI GI	g4185128
BLAST score	58
E value	3.0e-24
Match length	117
% identity	91
NCBI Description	Arabidopsis thaliana chromosome II P1 MSF3 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	159110
Seq. ID	LIB3176-105-P1-K1-A2
Method	BLASTN
NCBI GI	g16263
BLAST score	36
E value	4.0e-11
Match length	64
% identity	89
NCBI Description	Arabidopsis thaliana EF-1 alpha-A4 (NAEEFTU 4) gene for elongation factor 1-alpha

Seq. No.	159111
Seq. ID	LIB3176-105-P1-K1-A4
Method	BLASTN
NCBI GI	g3600045
BLAST score	165
E value	6.0e-88
Match length	177
% identity	98
NCBI Description	Arabidopsis thaliana BAC F2P3

Seq. No.	159112
Seq. ID	LIB3176-105-P1-K1-A5
Method	BLASTN
NCBI GI	g4263373
BLAST score	51
E value	3.0e-20
Match length	107
% identity	87
NCBI Description	Arabidopsis thaliana BAC T15G18 from chromosome IV, near 25 cM, complete sequence [Arabidopsis thaliana]

Seq. No.	159113
Seq. ID	LIB3176-105-P1-K1-A6

Method	BLASTN
NCBI GI	g4490701
BLAST score	63
E value	7.0e-27
Match length	79
% identity	96
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone T24A18 (ESSA project)

Seq. No.	159114
Seq. ID	LIB3176-105-P1-K1-A7
Method	BLASTN
NCBI GI	g3128141
BLAST score	116
E value	1.0e-58
Match length	168
% identity	92
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MQD22, complete sequence [Arabidopsis thaliana]

Seq. No.	159115
Seq. ID	LIB3176-105-P1-K1-A9
Method	BLASTN
NCBI GI	g2924653
BLAST score	123
E value	7.0e-63
Match length	258
% identity	97
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MDA7, complete sequence [Arabidopsis thaliana]

Seq. No.	159116
Seq. ID	LIB3176-105-P1-K1-B1
Method	BLASTX
NCBI GI	g1669389
BLAST score	353
E value	6.0e-34
Match length	73
% identity	93
NCBI Description	(U42007) actin 8 [Arabidopsis thaliana]

Seq. No.	159117
Seq. ID	LIB3176-105-P1-K1-B10
Method	BLASTN
NCBI GI	g1107486
BLAST score	99
E value	6.0e-49
Match length	110
% identity	98
NCBI Description	A.thaliana mRNA for 60S ribosomal protein L27a

Seq. No.	159118
Seq. ID	LIB3176-105-P1-K1-B11
Method	BLASTN
NCBI GI	g4757395
BLAST score	162
E value	5.0e-86

Match length	230
% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K21L13, complete sequence

Seq. No.	159119
Seq. ID	LIB3176-105-P1-K1-B4
Method	BLASTX
NCBI GI	g4490732
BLAST score	367
E value	1.0e-35
Match length	71
% identity	100
NCBI Description	(AL035709) phosphoenolpyruvate carboxykinase (ATP)-like protein [Arabidopsis thaliana]

Seq. No.	159120
Seq. ID	LIB3176-105-P1-K1-B6
Method	BLASTX
NCBI GI	g119143
BLAST [illegible]	
E [illegible]	
Mat[illegible]	
% identity	94
NCBI Description	ELONGATION FACTOR 1-ALPHA (EF-1-ALPHA) >gi_81606_pir__S06724 translation elongation factor eEF-1 [illegible] chain - Arab[illegible]is thaliana >gi_295788_emb_CAA34453_ [illegible] thaliana] [illegible] ctor [illegible] AA34455_ (X16[illegible] [illegible] [illegible] [illegible] idopsis thaliana] >gi_1532172 (U63815) EF-1alpha-A1 [Arabidopsis thaliana] >gi_1532173 (U63815) EF-1alpha-A2 [Arabidopsis thaliana] >gi_1532174 (U63815) EF-1alpha-A3 [Arabidopsis thaliana]

Seq. No.	159121
Seq. ID	LIB3176-105-P1-K1-B7
Method	BLASTN
NCBI GI	g2264310
BLAST score	97
E value	1.0e-47
Match length	121
% identity	96
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MKP11, complete sequence [Arabidopsis thaliana]

Seq. No.	159122
Seq. ID	LIB3176-105-P1-K1-B8
Method	BLASTN
NCBI GI	g1143393
BLAST score	81
E value	3.0e-38
Match length	89
% identity	99
NCBI Description	A.thaliana mRNA for vacuolar proton ATPase subunit E

Seq. No.	159123

Seq. ID	LIB3176-105-P1-K1-B9
Method	BLASTX
NCBI GI	g115788
BLAST score	195
E value	4.0e-15
Match length	64
% identity	66
NCBI Description	CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR (CAB-AB80) (LHCP) >gi_72745_pir__CDPM80 chlorophyll a/b-binding protein AB80 precursor - garden pea >gi_169053 (M64619) cab precursor [Pisum sativum] >gi_169055 (K02067) polypeptide 15 precursor [Pisum sativum] >gi_223990_prf__1006296A protein,chlorophyll a/b binding [Pisum sativum]

Seq. No.	159124
Seq. ID	LIB3176-105-P1-K1-C10
Method	BLASTX
NCBI GI	g399013
BLAST score	145
E value	2.0e-09
Match length	37
% identity	76
NCBI Description	ADP,ATP CARRIER PROTEIN 1 PRECURSOR (ADP/ATP TRANSLOCASE 1) (ADENINE NUCLEOTIDE TRANSLOCATOR 1) (ANT 1) >gi_99658_pir__S21313 ADP,ATP carrier protein - Arabidopsis thaliana (fragment) >gi_16175_emb_CAA46518_ (X65549) adenylate translocator [Arabidopsis thaliana] >gi_445607_prf__1909354A adenylate translocator [Arabidopsis thaliana]

Seq. No.	159125
Seq. ID	LIB3176-105-P1-K1-C12
Method	BLASTX
NCBI GI	g3153205
BLAST score	237
E value	2.0e-20
Match length	49
% identity	88
NCBI Description	(U80922) serine/threonine protein phosphatase type one [Arabidopsis thaliana]

Seq. No.	159126
Seq. ID	LIB3176-105-P1-K1-C2
Method	BLASTN
NCBI GI	g2980757
BLAST score	65
E value	6.0e-29
Match length	65
% identity	100
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F6I18 (ESSAII project)

Seq. No.	159127
Seq. ID	LIB3176-105-P1-K1-C3
Method	BLASTX
NCBI GI	g417381

BLAST score	333
E value	2.0e-31
Match length	73
% identity	95
NCBI Description	NITRILASE 1 >gi_99738_pir__S22398 nitrilase (EC 3.5.5.1) - Arabidopsis thaliana >gi_16400_emb_CAA45041_ (X63445) nitrilase I [Arabidopsis thaliana]

Seq. No.	159128
Seq. ID	LIB3176-105-P1-K1-C4
Method	BLASTN
NCBI GI	g4519188
BLAST score	44
E value	6.0e-16
Match length	151
% identity	87
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K21L19, complete sequence

Seq. No.	159129
Seq. ID	LIB3176-105-P1-K1-C5
Method	BLASTN
NCBI GI	g2143226
BLAST score	85
E value	2.0e-40
Match length	125
% identity	92
NCBI Description	Brassica napus mRNA for glyoxysomal isocitrate lyase

Seq. No.	159130
Seq. ID	LIB3176-105-P1-K1-C8
Method	BLASTN
NCBI GI	g1143393
BLAST score	73
E value	7.0e-33
Match length	113
% identity	92
NCBI Description	A.thaliana mRNA for vacuolar proton ATPase subunit E

Seq. No.	159131
Seq. ID	LIB3176-105-P1-K1-C9
Method	BLASTN
NCBI GI	g3046854
BLAST score	216
E value	1.0e-118
Match length	224
% identity	99
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MRG7, complete sequence [Arabidopsis thaliana]

Seq. No.	159132
Seq. ID	LIB3176-105-P1-K1-D1
Method	BLASTX
NCBI GI	g2062157
BLAST score	248
E value	1.0e-21
Match length	47

% identity	38
NCBI Description	(AC001645) jasmonate inducible protein isolog [Arabidopsis thaliana]

Seq. No.	159133
Seq. ID	LIB3176-105-P1-K1-D11
Method	BLASTX
NCBI GI	g401169
BLAST score	180
E value	2.0e-13
Match length	38
% identity	95
NCBI Description	TRANSLATIONALLY CONTROLLED TUMOR PROTEIN HOMOLOG (TCTP)

Seq. No.	159134
Seq. ID	LIB3176-105-P1-K1-D12
Method	BLASTN
NCBI GI	g2264317
BLAST score	170
E value	1.0e-90
Match length	317
% identity	99
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MUG13, complete sequence [Arabidopsis thaliana]

Seq. No.	159135
Seq. ID	LIB3176-105-P1-K1-D2
Method	BLASTN
NCBI GI	g3928074
BLAST score	93
E value	2.0e-45
Match length	109
% identity	96
NCBI Description	Arabidopsis thaliana chromosome II BAC T7F6 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	159136
Seq. ID	LIB3176-105-P1-K1-D3
Method	BLASTX
NCBI GI	g2653879
BLAST score	187
E value	1.0e-14
Match length	55
% identity	58
NCBI Description	(AF026389) adenyl cyclase [Nicotiana tabacum]

Seq. No.	159137
Seq. ID	LIB3176-105-P1-K1-D4
Method	BLASTX
NCBI GI	g4455322
BLAST score	238
E value	3.0e-20
Match length	64
% identity	73
NCBI Description	(AL035525) putative protein kinase [Arabidopsis thaliana]

Seq. No.	159138

Seq. ID	LIB3176-105-P1-K1-D5
Method	BLASTX
NCBI GI	g2246621
BLAST score	147
E value	7.0e-10
Match length	27
% identity	100
NCBI Description	(AF004393) salt-stress induced tonoplast intrinsic protein [Arabidopsis thaliana]

Seq. No.	159139
Seq. ID	LIB3176-105-P1-K1-D7
Method	BLASTX
NCBI GI	g1350720
BLAST score	265
E value	2.0e-23
Match length	56
% identity	93
NCBI Description	60S RIBOSOMAL PROTEIN L32

Seq. No.	159140
Seq. ID	LIB3176-105-P1-K1-E1
Method	BLASTN
NCBI GI	g4757414
BLAST score	208
E value	1.0e-113
Match length	244
% identity	96
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MYF24, complete sequence

Seq. No.	159141
Seq. ID	LIB3176-105-P1-K1-E11
Method	BLASTX
NCBI GI	g1864017
BLAST score	394
E value	3.0e-38
Match length	83
% identity	94
NCBI Description	(D63396) elongation factor-1 alpha [Nicotiana tabacum]

Seq. No.	159142
Seq. ID	LIB3176-105-P1-K1-E12
Method	BLASTX
NCBI GI	g2262167
BLAST score	667
E value	2.0e-70
Match length	131
% identity	98
NCBI Description	(AC002329) cytosolic ribosomal protein S4 [Arabidopsis thaliana]

Seq. No.	159143
Seq. ID	LIB3176-105-P1-K1-E2
Method	BLASTN
NCBI GI	g409183
BLAST score	94

E value	8.0e-46
Match length	114
% identity	96
NCBI Description	Arabidopsis thaliana ribosomal protein S28 mRNA, complete cds

Seq. No.	159144
Seq. ID	LIB3176-105-P1-K1-E3
Method	BLASTN
NCBI GI	g2618602
BLAST score	106
E value	5.0e-53
Match length	117
% identity	98
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MSJ1, complete sequence [Arabidopsis thaliana]

Seq. No.	159145
Seq. ID	LIB3176-105-P1-K1-E7
Method	BLASTN
NCBI GI	g2564050
BLAST score	121
E value	5.0e-62
Match length	125
% identity	99
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MUA22, complete sequence [Arabidopsis thaliana]

Seq. No.	159146
Seq. ID	LIB3176-105-P1-K1-F10
Method	BLASTX
NCBI GI	g4689254
BLAST score	232
E value	2.0e-19
Match length	99
% identity	49
NCBI Description	(AF121857) sorting nexin 7 [Homo sapiens]

Seq. No.	159147
Seq. ID	LIB3176-105-P1-K1-F12
Method	BLASTX
NCBI GI	g3550519
BLAST score	414
E value	9.0e-41
Match length	113
% identity	67
NCBI Description	(AJ007630) oxygenase [Nicotiana tabacum]

Seq. No.	159148
Seq. ID	LIB3176-105-P1-K1-F2
Method	BLASTX
NCBI GI	g3152560
BLAST score	168
E value	3.0e-12
Match length	68
% identity	43
NCBI Description	(AC002986) Strong similarity to ser/thr protein kinases,

especially gb_X97980 from solanum berthaultii, gb_X90990 from solanum tuberosum and gb_D10909 from A. thaliana. [Arabidopsis thaliana]

Seq. No.	159149
Seq. ID	LIB3176-105-P1-K1-F5
Method	BLASTN
NCBI GI	g166833
BLAST score	40
E value	2.0e-13
Match length	44
% identity	98
NCBI Description	Arabidopisis thaliana ribulose bisphosphate carboxylase/oxygenase activase (rca) gene, complete cds

Seq. No.	159150
Seq. ID	LIB3176-105-P1-K1-F6
Method	BLASTX
NCBI GI	g4567207
BLAST score	174
E value	6.0e-13
Match length	47
% identity	70
NCBI Description	(AC007168) unknown protein [Arabidopsis thaliana]

Seq. No.	159151
Seq. ID	LIB3176-105-P1-K1-F7
Method	BLASTN
NCBI GI	g4512646
BLAST score	83
E value	9.0e-39
Match length	135
% identity	94
NCBI Description	Arabidopsis thaliana chromosome II BAC F23N11 genomic sequence, complete sequence

Seq. No.	159152
Seq. ID	LIB3176-105-P1-K1-F8
Method	BLASTN
NCBI GI	g4376087
BLAST score	185
E value	1.0e-99
Match length	197
% identity	98
NCBI Description	Arabidopsis thaliana DNA chromosome 4, ESSA I AP2 contig fragment No

Seq. No.	159153
Seq. ID	LIB3176-105-P1-K1-F9
Method	BLASTN
NCBI GI	g1732569
BLAST score	116
E value	1.0e-58
Match length	143
% identity	96
NCBI Description	Arabidopsis thaliana beta-glucosidase (psr3.1) mRNA, complete cds

Seq. No.	159154
Seq. ID	LIB3176-105-P1-K1-G10
Method	BLASTN
NCBI GI	g4091809
BLAST score	117
E value	1.0e-59
Match length	141
% identity	96
NCBI Description	Arabidopsis thaliana fatty acid elongase 3-ketoacyl-CoA synthase 1 (KCS1) gene, complete cds

Seq. No.	159155
Seq. ID	LIB3176-105-P1-K1-G2
Method	BLASTX
NCBI GI	g4581146
BLAST score	194
E value	4.0e-15
Match length	59
% identity	71
NCBI Description	(AC006919) putative fructose-bisphosphate aldolase, cytoplasmic [Arabidopsis thaliana]

Seq. No.	159156
Seq. ID	LIB3176-105-P1-K1-G3
Method	BLASTN
NCBI GI	g166814
BLAST score	121
E value	6.0e-62
Match length	145
% identity	41
NCBI Description	Arabidopsis thaliana pyrroline carboxylate reductase gene, complete cds

Seq. No.	159157
Seq. ID	LIB3176-105-P1-K1-G4
Method	BLASTX
NCBI GI	g3421157
BLAST score	281
E value	3.0e-25
Match length	65
% identity	92
NCBI Description	(AF045673) arginine decarboxylase [Capsella bursa-pastoris]

Seq. No.	159158
Seq. ID	LIB3176-105-P1-K1-G6
Method	BLASTX
NCBI GI	g2317731
BLAST score	275
E value	6.0e-25
Match length	54
% identity	96
NCBI Description	(AF013628) reversibly glycosylated polypeptide-2 [Arabidopsis thaliana]

Seq. No.	159159
Seq. ID	LIB3176-105-P1-K1-G7

Method	BLASTN
NCBI GI	g4580744
BLAST score	25
E value	4.0e-05
Match length	49
% identity	62
NCBI Description	Sequence of BAC F15I1 from Arabidopsis thaliana chromosome 1, complete sequence

Seq. No.	159160
Seq. ID	LIB3176-105-P1-K1-G8
Method	BLASTN
NCBI GI	g3212846
BLAST score	114
E value	2.0e-57
Match length	146
% identity	95
NCBI Description	Arabidopsis thaliana chromosome II BAC F6E13 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	159161
Seq. ID	LIB3176-105-P1-K1-G9
Method	BLASTX
NCBI GI	g4220527
BLAST score	288
E value	5.0e-26
Match length	67
% identity	72
NCBI Description	(AL035356) putative protein [Arabidopsis thaliana]

Seq. No.	159162
Seq. ID	LIB3176-105-P1-K1-H1
Method	BLASTN
NCBI GI	g313837
BLAST score	57
E value	2.0e-23
Match length	97
% identity	90
NCBI Description	A.thaliana gene for hemC

Seq. No.	159163
Seq. ID	LIB3176-105-P1-K1-H3
Method	BLASTX
NCBI GI	g123656
BLAST score	264
E value	1.0e-23
Match length	53
% identity	96
NCBI Description	CHLOROPLAST ENVELOPE MEMBRANE 70 KD HEAT SHOCK-RELATED PROTEIN >gi_285407_pir__A42582 heat shock protein SCE70 - spinach >gi_21338_emb_CAA43711_ (X61491) 70 kDa heat shock protein [Spinacia oleracea]

Seq. No.	159164
Seq. ID	LIB3176-105-P1-K1-H4
Method	BLASTN
NCBI GI	g2618601

BLAST score	37
E value	2.0e-12
Match length	49
% identity	94
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MHJ24, complete sequence [Arabidopsis thaliana]

Seq. No.	159165
Seq. ID	LIB3176-105-P1-K1-H5
Method	BLASTX
NCBI GI	g3421123
BLAST score	360
E value	1.0e-34
Match length	79
% identity	92
NCBI Description	(AF043538) 20S proteasome beta subunit PBG1 [Arabidopsis thaliana]

Seq. No.	159166
Seq. ID	LIB3176-105-P1-K1-H9
Method	BLASTX
NCBI GI	g2244759
BLAST score	372
E value	9.0e-36
Match length	91
% identity	74
NCBI Description	(Z97335) selenium-binding protein [Arabidopsis thaliana]

Seq. No.	159167
Seq. ID	LIB3176-106-P1-K1-A1
Method	BLASTN
NCBI GI	g3869071
BLAST score	104
E value	2.0e-51
Match length	251
% identity	98
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MIL23, complete sequence [Arabidopsis thaliana]

Seq. No.	159168
Seq. ID	LIB3176-106-P1-K1-A10
Method	BLASTX
NCBI GI	g1170503
BLAST score	390
E value	7.0e-38
Match length	76
% identity	99
NCBI Description	EUKARYOTIC INITIATION FACTOR 4A-1 (EIF-4A-1) >gi_322503_pir__JC1452 translation initiation factor eIF-4A1 - Arabidopsis thaliana >gi_16554_emb_CAA46188_ (X65052) eukaryotic translation initiation factor 4A-1 [Arabidopsis thaliana]

Seq. No.	159169
Seq. ID	LIB3176-106-P1-K1-A11
Method	BLASTN
NCBI GI	g2244950

BLAST score	112
E value	1.0e-56
Match length	128
% identity	97
NCBI Description	Arabidopsis thaliana DNA chromosome 4, ESSA I contig fragment No

Seq. No.	159170
Seq. ID	LIB3176-106-P1-K1-A12
Method	BLASTN
NCBI GI	g4056429
BLAST score	176
E value	2.0e-94
Match length	260
% identity	99
NCBI Description	Arabidopsis thaliana chromosome 1 BAC F5O8 sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	159171
Seq. ID	LIB3176-106-P1-K1-A2
Method	BLASTX
NCBI GI	g122007
BLAST score	223
E value	9.0e-19
Match length	60
% identity	73
NCBI Description	HISTONE H2A >gi_100161_pir__S11498 histone H2A - parsley >gi_20448_emb_CAA37828_ (X53831) H2A histone protein (AA 1 - 149) [Petroselinum crispum]

Seq. No.	159172
Seq. ID	LIB3176-106-P1-K1-A8
Method	BLASTX
NCBI GI	g2262167
BLAST score	523
E value	1.0e-53
Match length	101
% identity	99
NCBI Description	(AC002329) cytosolic ribosomal protein S4 [Arabidopsis thaliana]

Seq. No.	159173
Seq. ID	LIB3176-106-P1-K1-B1
Method	BLASTN
NCBI GI	g2737903
BLAST score	51
E value	2.0e-20
Match length	78
% identity	92
NCBI Description	Arabidopsis thaliana retrotransposon TSCL genomic sequence

Seq. No.	159174
Seq. ID	LIB3176-106-P1-K1-B10
Method	BLASTN
NCBI GI	g2143226
BLAST score	93
E value	3.0e-45

Match length	125
% identity	94
NCBI Description	Brassica napus mRNA for glyoxysomal isocitrate lyase

Seq. No.	159175
Seq. ID	LIB3176-106-P1-K1-B11
Method	BLASTX
NCBI GI	g1710581
BLAST score	185
E value	3.0e-14
Match length	45
% identity	84
NCBI Description	60S RIBOSOMAL PROTEIN L9 >gi_2129720_pir__S71255 ribosomal protein L9 - Arabidopsis thaliana >gi_1107489_emb_CAA63024_ (X91958) 60S ribosomal protein L9 [Arabidopsis thaliana]

Seq. No.	159176
Seq. ID	LIB3176-106-P1-K1-B12
Method	BLASTX
NCBI GI	g2246621
BLAST score	325
E value	8.0e-31
Match length	67
% identity	99
NCBI Description	(AF004393) salt-stress induced tonoplast intrinsic protein [Arabidopsis thaliana]

Seq. No.	159177
Seq. ID	LIB3176-106-P1-K1-B4
Method	BLASTN
NCBI GI	g4159706
BLAST score	74
E value	9.0e-34
Match length	108
% identity	97
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MGL6, complete sequence

Seq. No.	159178
Seq. ID	LIB3176-106-P1-K1-B5
Method	BLASTX
NCBI GI	g2506276
BLAST score	48
E value	8.0e-18
Match length	56
% identity	95
NCBI Description	RUBISCO SUBUNIT BINDING-PROTEIN ALPHA SUBUNIT PRECURSOR (60 KD CHAPERONIN ALPHA SUBUNIT) (CPN-60 ALPHA) >gi_2129561_pir__S71235 chaperonin-60 alpha chain - Arabidopsis thaliana >gi_1223910 (U49357) chaperonin-60 alpha subunit [Arabidopsis thaliana] >gi_4510416_gb_AAD21502.1_ (AC006929) putative rubisco binding protein alpha subunit [Arabidopsis thaliana]

Seq. No.	159179
Seq. ID	LIB3176-106-P1-K1-B6
Method	BLASTN

NCBI GI	g454356
BLAST score	190
E value	1.0e-103
Match length	210
% identity	98
NCBI Description	Arabidopsis thaliana Columbia glutamate-1-semialdehyde-2,1-aminomutase (gsa1) gene

Seq. No.	159180
Seq. ID	LIB3176-106-P1-K1-B7
Method	BLASTX
NCBI GI	g3080435
BLAST score	279
E value	2.0e-25
Match length	61
% identity	93
NCBI Description	(AL022605) putative protein [Arabidopsis thaliana]

Seq. No.	159181
Seq. ID	LIB3176-106-P1-K1-B8
Method	BLASTN
NCBI GI	g4521999
BLAST score	178
E value	2.0e-95
Match length	215
% identity	95
NCBI Description	Arabidopsis thaliana chromosome II BAC F2G1 genomic sequence, complete sequence

Seq. No.	159182
Seq. ID	LIB3176-106-P1-K1-B9
Method	BLASTN
NCBI GI	g1402919
BLAST score	39
E value	2.0e-13
Match length	47
% identity	96
NCBI Description	A.thaliana mRNA for peroxidase, prxr9 >gi_1546703_emb_X98854_ATPEROX7A A.thaliana mRNA for peroxidase ATP7a

Seq. No.	159183
Seq. ID	LIB3176-106-P1-K1-C1
Method	BLASTN
NCBI GI	g2980757
BLAST score	117
E value	5.0e-59
Match length	125
% identity	98
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F6I18 (ESSAII project)

Seq. No.	159184
Seq. ID	LIB3176-106-P1-K1-C10
Method	BLASTN
NCBI GI	g4538949
BLAST score	238

E value	1.0e-131
Match length	254
% identity	98
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F24G24 (ESSA project)

Seq. No.	159185
Seq. ID	LIB3176-106-P1-K1-C12
Method	BLASTN
NCBI GI	g2660661
BLAST score	101
E value	4.0e-50
Match length	126
% identity	99
NCBI Description	Arabidopsis thaliana chromosome V BAC T19K24 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	159186
Seq. ID	LIB3176-106-P1-K1-C2
Method	BLASTX
NCBI GI	g119143
BLAST score	236
E value	1.0e-19
Match length	50
% identity	92
NCBI Description	ELONGATION FACTOR 1-ALPHA (EF-1-ALPHA) >gi_81606_pir__S06724 translation elongation factor eEF-1 alpha chain - Arabidopsis thaliana >gi_295788_emb_CAA34453_ (X16430) elongation factor 1-alpha [Arabidopsis thaliana] >gi_1369927_emb_CAA34454_ (X16431) elongation factor 1-alpha [Arabidopsis thaliana] >gi_1369928_emb_CAA34455_ (X16431) elongation factor 1-alpha [Arabidopsis thaliana] >gi_1532172 (U63815) EF-1alpha-A1 [Arabidopsis thaliana] >gi_1532173 (U63815) EF-1alpha-A2 [Arabidopsis thaliana] >gi_1532174 (U63815) EF-1alpha-A3 [Arabidopsis thaliana]

Seq. No.	159187
Seq. ID	LIB3176-106-P1-K1-C3
Method	BLASTX
NCBI GI	g2654208
BLAST score	392
E value	5.0e-38
Match length	133
% identity	67
NCBI Description	(AF035456) heat shock 70 protein [Spinacia oleracea] >gi_2773050 (AF039083) heat shock 70 protein [Spinacia oleracea]

Seq. No.	159188
Seq. ID	LIB3176-106-P1-K1-C5
Method	BLASTX
NCBI GI	g1669387
BLAST score	633
E value	2.0e-66
Match length	125
% identity	100
NCBI Description	(U41998) actin 2 [Arabidopsis thaliana]

Seq. No.	159189
Seq. ID	LIB3176-106-P1-K1-C6
Method	BLASTX
NCBI GI	g1169278
BLAST score	312
E value	1.0e-28
Match length	129
% identity	56
NCBI Description	DEHYDRIN ERD14 >gi_556474_dbj_BAA04569_ (D17715) ERD14 protein [Arabidopsis thaliana]

Seq. No.	159190
Seq. ID	LIB3176-106-P1-K1-C7
Method	BLASTN
NCBI GI	g3510347
BLAST score	132
E value	4.0e-68
Match length	205
% identity	98
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MSJ11, complete sequence [Arabidopsis thaliana]

Seq. No.	159191
Seq. ID	LIB3176-106-P1-K1-C8
Method	BLASTX
NCBI GI	g3249077
BLAST score	378
E value	2.0e-36
Match length	102
% identity	72
NCBI Description	(AC004473) Similar to prunasin hydrolase precursor gb_U50201 from Prunus serotina. ESTs gb_T21225 and gb_AA586305 come from this gene. [Arabidopsis thaliana]

Seq. No.	159192
Seq. ID	LIB3176-106-P1-K1-C9
Method	BLASTX
NCBI GI	g2654868
BLAST score	273
E value	3.0e-24
Match length	58
% identity	91
NCBI Description	(AF015301) RbohAp108 [Arabidopsis thaliana]

Seq. No.	159193
Seq. ID	LIB3176-106-P1-K1-D10
Method	BLASTX
NCBI GI	g4741962
BLAST score	428
E value	2.0e-42
Match length	104
% identity	87
NCBI Description	(AF134131) PsbS protein [Arabidopsis thaliana]

Seq. No.	159194
Seq. ID	LIB3176-106-P1-K1-D11

Method	BLASTX
NCBI GI	g132074
BLAST score	418
E value	2.0e-41
Match length	76
% identity	97
NCBI Description	RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN 1A PRECURSOR (RUBISCO SMALL SUBUNIT 1A) >gi_68063_pir__RKMUA1 ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain A1 precursor - Arabidopsis thaliana

Seq. No.	159195
Seq. ID	LIB3176-106-P1-K1-D2
Method	BLASTN
NCBI GI	g4733953
BLAST score	96
E value	1.0e-46
Match length	116
% identity	96
NCBI Description	Arabidopsis thaliana chromosome I BAC F13O11 genomic sequence, complete sequence

Seq. No.	159196
Seq. ID	LIB3176-106-P1-K1-D3
Method	BLASTN
NCBI GI	g4432829
BLAST score	92
E value	2.0e-44
Match length	179
% identity	97
NCBI Description	Arabidopsis thaliana chromosome II BAC T1B3 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	159197
Seq. ID	LIB3176-106-P1-K1-D5
Method	BLASTX
NCBI GI	g2130028
BLAST score	246
E value	2.0e-21
Match length	59
% identity	76
NCBI Description	B12D protein - barley >gi_471319_emb_CAA54065.1_ (X76604) HvB12D [Hordeum vulgare] >gi_3445292_emb_CAA70936_ (Y09805) B12Dg1 [Hordeum vulgare]

Seq. No.	159198
Seq. ID	LIB3176-106-P1-K1-D6
Method	BLASTX
NCBI GI	g421826
BLAST score	299
E value	9.0e-28
Match length	71
% identity	82
NCBI Description	chlorophyll a/b-binding protein CP29 - Arabidopsis thaliana >gi_298036_emb_CAA50712_ (X71878) CP29 [Arabidopsis thaliana]

Seq. No.	159199
Seq. ID	LIB3176-106-P1-K1-D7
Method	BLASTN
NCBI GI	g4559319
BLAST score	181
E value	3.0e-97
Match length	356
% identity	99
NCBI Description	Arabidopsis thaliana chromosome II BAC F14N22 genomic sequence, complete sequence

Seq. No.	159200
Seq. ID	LIB3176-106-P1-K1-D8
Method	BLASTX
NCBI GI	g444790
BLAST score	66
E value	5.8e+00
Match length	112
% identity	19
NCBI Description	nucleotide translocator [Arabidopsis thaliana]

Seq. No.	159201
Seq. ID	LIB3176-106-P1-K1-D9
Method	BLASTX
NCBI GI	g2317906
BLAST score	366
E value	1.0e-46
Match length	97
% identity	95
NCBI Description	(U89959) ARA-5 [Arabidopsis thaliana]

Seq. No.	159202
Seq. ID	LIB3176-106-P1-K1-E11
Method	BLASTX
NCBI GI	g131397
BLAST score	148
E value	5.0e-10
Match length	51
% identity	75
NCBI Description	OXYGEN-EVOLVING ENHANCER PROTEIN 3 PRECURSOR (OEE3) (16 KD SUBUNIT OF OXYGEN-EVOLVING SYSTEM OF PHOTOSYSTEM II) >gi_81480_pir__S00008 photosystem II oxygen-evolving complex protein 3 precursor - spinach >gi_755802_emb_CAA29056_ (X05512) 16 kDa protein of the photosynthetic oxygen- evolving protein (OEC) [Spinacia oleracea] >gi_225597_prf__1307179B luminal protein 16kD [Spinacia oleracea]

Seq. No.	159203
Seq. ID	LIB3176-106-P1-K1-E12
Method	BLASTX
NCBI GI	g113026
BLAST score	416
E value	5.0e-41
Match length	97
% identity	84
NCBI Description	ISOCITRATE LYASE (ISOCITRASE) (ISOCITRATASE) (ICL)

	>gi_68211_pir__WZRPI isocitrate lyase (EC 4.1.3.1) - rape >gi_255220_bbs_112862 isocitrate lyase, threo-D S-isocitrate glyoxylate-lyase, IL (EC 4.1.3.1) [Brassica napus, seedlings, Peptide, 576 aa] >gi_167144 (L08482) isocitrate lyase [Brassica napus] >gi_447142_prf__1913424A isocitrate lyase [Brassica napus]
Seq. No.	159204
Seq. ID	LIB3176-106-P1-K1-E3
Method	BLASTN
NCBI GI	g4580454
BLAST score	78
E value	2.0e-36
Match length	82
% identity	99
NCBI Description	Arabidopsis thaliana chromosome II BAC T2G17 genomic sequence, complete sequence
Seq. No.	159205
Seq. ID	LIB3176-106-P1-K1-E4
Method	BLASTX
NCBI GI	g2129636
BLAST score	504
E value	2.0e-51
Match length	98
% identity	100
NCBI Description	lipase - Arabidopsis thaliana >gi_1145627 (U38916) lipase [Arabidopsis thaliana]
Seq. No.	159206
Seq. ID	LIB3176-106-P1-K1-E5
Method	BLASTX
NCBI GI	g730645
BLAST score	392
E value	3.0e-38
Match length	94
% identity	85
NCBI Description	40S RIBOSOMAL PROTEIN S15 >gi_629556_pir__S43412 ribosomal protein S15 - Arabidopsis thaliana >gi_313152_emb_CAA80679_ (Z23161) ribosomal protein S15 [Arabidopsis thaliana] >gi_313188_emb_CAA80681_ (Z23162) ribosomal protein S15 [Arabidopsis thaliana] >gi_1903366_gb_AAB70449_ (AC000104) Strong similarity to Oryza 40S ribosomal protein S15. ESTs gb_R29788,gb_ATTS0365 come from this gene. [Arabidopsis thaliana]
Seq. No.	159207
Seq. ID	LIB3176-106-P1-K1-E7
Method	BLASTX
NCBI GI	g2088654
BLAST score	142
E value	3.0e-09
Match length	37
% identity	76
NCBI Description	(AF002109) 60S acidic ribosomal protein P0 isolog [Arabidopsis thaliana]

Seq. No.	159208
Seq. ID	LIB3176-106-P1-K1-E8
Method	BLASTX
NCBI GI	g4455338
BLAST score	228
E value	8.0e-19
Match length	70
% identity	66
NCBI Description	(AL035525) putative protein [Arabidopsis thaliana]

Seq. No.	159209
Seq. ID	LIB3176-106-P1-K1-E9
Method	BLASTX
NCBI GI	g2832643
BLAST score	174
E value	8.0e-13
Match length	71
% identity	55
NCBI Description	(AL021710) hypothetical protein [Arabidopsis thaliana]

Seq. No.	159210
Seq. ID	LIB3176-106-P1-K1-F1
Method	BLASTN
NCBI GI	g2980787
BLAST score	142
E value	6.0e-74
Match length	169
% identity	97
NCBI Description	Arabidopsis thaliana DNA chromosome 4, P1 clone M7J2 (ESSAII project)

Seq. No.	159211
Seq. ID	LIB3176-106-P1-K1-F10
Method	BLASTN
NCBI GI	g4757409
BLAST score	103
E value	9.0e-51
Match length	342
% identity	88
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MVC8, complete sequence

Seq. No.	159212
Seq. ID	LIB3176-106-P1-K1-F12
Method	BLASTN
NCBI GI	g4587641
BLAST score	246
E value	1.0e-136
Match length	258
% identity	99
NCBI Description	Arabidopsis thaliana chromosome I BAC F20D21 genomic sequence, complete sequence

Seq. No.	159213
Seq. ID	LIB3176-106-P1-K1-F3
Method	BLASTN
NCBI GI	g3367500

BLAST score	103
E value	7.0e-51
Match length	292
% identity	100
NCBI Description	REVERSE-COMPLEMENT OF: F23J3.GCG.SEQ CHECK: 2754 FROM: 1 TO: 93489, complete sequence [Arabidopsis thaliana]

Seq. No.	159214
Seq. ID	LIB3176-106-P1-K1-F4
Method	BLASTN
NCBI GI	g2062153
BLAST score	52
E value	2.0e-20
Match length	87
% identity	19
NCBI Description	Arabidopsis thaliana chromosome III BAC T02O04 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	159215
Seq. ID	LIB3176-106-P1-K1-F5
Method	BLASTX
NCBI GI	g132074
BLAST score	364
E value	4.0e-35
Match length	70
% identity	100
NCBI Description	RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN 1A PRECURSOR (RUBISCO SMALL SUBUNIT 1A) >gi_68063_pir__RKMUA1 ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain A1 precursor - Arabidopsis thaliana

Seq. No.	159216
Seq. ID	LIB3176-106-P1-K1-F6
Method	BLASTX
NCBI GI	g4490732
BLAST score	305
E value	6.0e-56
Match length	114
% identity	99
NCBI Description	(AL035709) phosphoenolpyruvate carboxykinase (ATP)-like protein [Arabidopsis thaliana]

Seq. No.	159217
Seq. ID	LIB3176-106-P1-K1-F7
Method	BLASTN
NCBI GI	g4741955
BLAST score	123
E value	1.0e-62
Match length	135
% identity	98
NCBI Description	Arabidopsis thaliana Lhcb4:3 protein (Lhcb4.3) mRNA, complete cds

Seq. No.	159218
Seq. ID	LIB3176-106-P1-K1-F8
Method	BLASTN
NCBI GI	g4490701

BLAST score	69
E value	1.0e-30
Match length	73
% identity	99
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone T24A18 (ESSA project)

Seq. No.	159219
Seq. ID	LIB3176-106-P1-K1-G1
Method	BLASTN
NCBI GI	g2924652
BLAST score	271
E value	1.0e-151
Match length	274
% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K9L2, complete sequence [Arabidopsis thaliana]

Seq. No.	159220
Seq. ID	LIB3176-106-P1-K1-G10
Method	BLASTN
NCBI GI	g2924654
BLAST score	108
E value	4.0e-54
Match length	152
% identity	99
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MHK7, complete sequence [Arabidopsis thaliana]

Seq. No.	159221
Seq. ID	LIB3176-106-P1-K1-G11
Method	BLASTX
NCBI GI	g2326812
BLAST score	361
E value	2.0e-34
Match length	152
% identity	48
NCBI Description	(Z74955) ORF YOR046c [Saccharomyces cerevisiae]

Seq. No.	159222
Seq. ID	LIB3176-106-P1-K1-G2
Method	BLASTX
NCBI GI	g1172558
BLAST score	285
E value	7.0e-26
Match length	75
% identity	73
NCBI Description	OUTER PLASTIDIAL MEMBRANE PROTEIN PORIN (VOLTAGE-DEPENDENT ANION-SELECTIVE CHANNEL PROTEIN) (VDAC) >gi_480122_pir__S36454 porin por1 - garden pea >gi_396819_emb_CAA80988_ (Z25540) Porin [Pisum sativum]

Seq. No.	159223
Seq. ID	LIB3176-106-P1-K1-G3
Method	BLASTX
NCBI GI	g2119846
BLAST score	455

E value	1.0e-45
Match length	92
% identity	95
NCBI Description	chlorophyll a/b-binding protein type I precursor Lhb1B2 - Arabidopsis thaliana >gi_16364_emb_CAA45790_ (X64460) photosystem II type I chlorophyll a /b binding protein [Arabidopsis thaliana] >gi_3128230 (AC004077) photosystem II type I chlorophyll a/b binding protein [Arabidopsis thaliana] >gi_3337371 (AC004481) photosystem II type I chlorophyll a/b binding protein [Arabidopsis thaliana]

Seq. No.	159224
Seq. ID	LIB3176-106-P1-K1-G6
Method	BLASTN
NCBI GI	g4468976
BLAST score	219
E value	1.0e-120
Match length	296
% identity	93
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F19F18 (ESSA project)

Seq. No.	159225
Seq. ID	LIB3176-106-P1-K1-G7
Method	BLASTX
NCBI GI	g4586244
BLAST score	219
E value	8.0e-18
Match length	103
% identity	40
NCBI Description	(AL049640) putative protein [Arabidopsis thaliana]

Seq. No.	159226
Seq. ID	LIB3176-106-P1-K1-G8
Method	BLASTX
NCBI GI	g3150415
BLAST score	278
E value	4.0e-25
Match length	63
% identity	83
NCBI Description	(AC004165) sec13-related protein [Arabidopsis thaliana] >gi_3420046 (AC004680) sec13-related protein [Arabidopsis thaliana]

Seq. No.	159227
Seq. ID	LIB3176-106-P1-K1-G9
Method	BLASTX
NCBI GI	g2244769
BLAST score	197
E value	3.0e-15
Match length	62
% identity	58
NCBI Description	(Z97335) xyloglucan endotransglycosylase-related protein XTR-7 [Arabidopsis thaliana]

Seq. No.	159228
Seq. ID	LIB3176-106-P1-K1-H1

Method	BLASTX
NCBI GI	g4262147
BLAST score	343
E value	2.0e-32
Match length	74
% identity	89
NCBI Description	(AC005275) putative homolog of transport inhibitor response 1 [Arabidopsis thaliana]

Seq. No.	159229
Seq. ID	LIB3176-106-P1-K1-H10
Method	BLASTN
NCBI GI	g4580454
BLAST score	37
E value	3.0e-11
Match length	41
% identity	98
NCBI Description	Arabidopsis thaliana chromosome II BAC T2G17 genomic sequence, complete sequence

Seq. No.	159230
Seq. ID	LIB3176-106-P1-K1-H11
Method	BLASTN
NCBI GI	g3212846
BLAST score	114
E value	2.0e-57
Match length	275
% identity	97
NCBI Description	Arabidopsis thaliana chromosome II BAC F6E13 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	159231
Seq. ID	LIB3176-106-P1-K1-H12
Method	BLASTX
NCBI GI	g464849
BLAST score	286
E value	3.0e-26
Match length	55
% identity	100
NCBI Description	TUBULIN ALPHA CHAIN >gi_486847_pir__S36232 tubulin alpha chain - almond >gi_20413_emb_CAA47635_ (X67162) alpha-tubulin [Prunus dulcis]

Seq. No.	159232
Seq. ID	LIB3176-106-P1-K1-H2
Method	BLASTN
NCBI GI	g3059018
BLAST score	133
E value	1.0e-68
Match length	296
% identity	98
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F1C12 (ESSAII project)

Seq. No.	159233
Seq. ID	LIB3176-106-P1-K1-H5
Method	BLASTX

NCBI GI	g132074
BLAST score	231
E value	2.0e-19
Match length	84
% identity	55
NCBI Description	RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN 1A PRECURSOR (RUBISCO SMALL SUBUNIT 1A) >gi_68063_pir__RKMUA1 ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain A1 precursor - Arabidopsis thaliana

Seq. No.	159234
Seq. ID	LIB3176-106-P1-K1-H6
Method	BLASTN
NCBI GI	g4741957
BLAST score	124
E value	1.0e-63
Match length	138
% identity	99
NCBI Description	Arabidopsis thaliana Lhcb5 protein (Lhcb5) mRNA, complete cds

Seq. No.	159235
Seq. ID	LIB3176-106-P1-K1-H7
Method	BLASTX
NCBI GI	g119143
BLAST score	196
E value	4.0e-15
Match length	39
% identity	97
NCBI Description	ELONGATION FACTOR 1-ALPHA (EF-1-ALPHA) >gi_81606_pir__S06724 translation elongation factor eEF-1 alpha chain - Arabidopsis thaliana >gi_295788_emb_CAA34453_ (X16430) elongation factor 1-alpha [Arabidopsis thaliana] >gi_1369927_emb_CAA34454_ (X16431) elongation factor 1-alpha [Arabidopsis thaliana] >gi_1369928_emb_CAA34455_ (X16431) elongation factor 1-alpha [Arabidopsis thaliana] >gi_1532172 (U63815) EF-1alpha-A1 [Arabidopsis thaliana] >gi_1532173 (U63815) EF-1alpha-A2 [Arabidopsis thaliana] >gi_1532174 (U63815) EF-1alpha-A3 [Arabidopsis thaliana]

Seq. No.	159236
Seq. ID	LIB3176-106-P1-K1-H8
Method	BLASTN
NCBI GI	g2062153
BLAST score	70
E value	3.0e-31
Match length	90
% identity	52
NCBI Description	Arabidopsis thaliana chromosome III BAC T02O04 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	159237
Seq. ID	LIB3176-108-P1-K1-A1
Method	BLASTN
NCBI GI	g4240115
BLAST score	196
E value	1.0e-106

Match length	220
% identity	97
NCBI Description	Arabidopsis thaliana mRNA for NADH-cytochrome b5 reductase, complete cds

Seq. No.	159238
Seq. ID	LIB3176-108-P1-K1-A10
Method	BLASTX
NCBI GI	g2507421
BLAST score	493
E value	7.0e-50
Match length	97
% identity	99
NCBI Description	PROTEIN TRANSLATION FACTOR SUI1 HOMOLOG >gi_1800277 (U81042) translation initiation factor [Arabidopsis thaliana] >gi_4490709_emb_CAB38843.1_ (AL035680) translation initiation factor [Arabidopsis thaliana]

Seq. No.	159239
Seq. ID	LIB3176-108-P1-K1-A11
Method	BLASTN
NCBI GI	g3785992
BLAST score	91
E value	2.0e-43
Match length	169
% identity	91
NCBI Description	Arabidopsis thaliana chromosome II BAC T6A23 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	159240
Seq. ID	LIB3176-108-P1-K1-A12
Method	BLASTN
NCBI GI	g2264317
BLAST score	77
E value	2.0e-35
Match length	183
% identity	99
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MUG13, complete sequence [Arabidopsis thaliana]

Seq. No.	159241
Seq. ID	LIB3176-108-P1-K1-A2
Method	BLASTX
NCBI GI	g4538987
BLAST score	684
E value	3.0e-72
Match length	144
% identity	96
NCBI Description	(AJ133777) gamma-adaptin 2 [Arabidopsis thaliana]

Seq. No.	159242
Seq. ID	LIB3176-108-P1-K1-A6
Method	BLASTX
NCBI GI	g2062161
BLAST score	636
E value	1.0e-66
Match length	123

% identity	49
NCBI Description	(AC001645) jasmonate inducible protein isolog [Arabidopsis thaliana]

Seq. No.	159243
Seq. ID	LIB3176-108-P1-K1-A7
Method	BLASTX
NCBI GI	g3915823
BLAST score	231
E value	9.0e-20
Match length	46
% identity	96
NCBI Description	[Segment 1 of 2] 60S RIBOSOMAL PROTEIN L5

Seq. No.	159244
Seq. ID	LIB3176-108-P1-K1-A8
Method	BLASTX
NCBI GI	g1864017
BLAST score	460
E value	3.0e-46
Match length	92
% identity	96
NCBI Description	(D63396) elongation factor-1 alpha [Nicotiana tabacum]

Seq. No.	159245
Seq. ID	LIB3176-108-P1-K1-A9
Method	BLASTN
NCBI GI	g4096078
BLAST score	34
E value	1.0e-09
Match length	74
% identity	97
NCBI Description	Arabidopsis thaliana chromosome I BAC T5A14 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	159246
Seq. ID	LIB3176-108-P1-K1-B1
Method	BLASTX
NCBI GI	g3024126
BLAST score	321
E value	5.0e-30
Match length	62
% identity	98
NCBI Description	S-ADENOSYLMETHIONINE SYNTHETASE 1 (METHIONINE ADENOSYLTRANSFERASE 1) (ADOMET SYNTHETASE 1) >gi_1655576_emb_CAA95856_ (Z71271) S-adenosyl-L-methionine synthetase 1 [Catharanthus roseus]

Seq. No.	159247
Seq. ID	LIB3176-108-P1-K1-B10
Method	BLASTN
NCBI GI	g4539331
BLAST score	267
E value	1.0e-148
Match length	385
% identity	98
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F22I13

(ESSA project)

Seq. No.	159248
Seq. ID	LIB3176-108-P1-K1-B3
Method	BLASTX
NCBI GI	g1363489
BLAST score	599
E value	2.0e-62
Match length	114
% identity	95
NCBI Description	thioglucosidase (EC 3.2.3.1) 3D precursor - Arabidopsis thaliana >gi_984052_emb_CAA61592_ (X89413) thioglucoside glucohydrolase [Arabidopsis thaliana]

Seq. No.	159249
Seq. ID	LIB3176-108-P1-K1-B4
Method	BLASTX
NCBI GI	g2687686
BLAST score	394
E value	1.0e-38
Match length	78
% identity	100
NCBI Description	(AJ000110) cystatin [Arabidopsis thaliana]

Seq. No.	159250
Seq. ID	LIB3176-108-P1-K1-B5
Method	BLASTX
NCBI GI	g1755164
BLAST score	568
E value	1.0e-58
Match length	141
% identity	80
NCBI Description	(U75193) germin-like protein [Arabidopsis thaliana] >gi_1755168 (U75195) germin-like protein [Arabidopsis thaliana] >gi_2239042_emb_CAA73213_ (Y12673) GLP3 protein [Arabidopsis thaliana] >gi_4666250_dbj_BAA77208.1_ (D89374) germin-like protein 2 precursor [Arabidopsis thaliana]

Seq. No.	159251
Seq. ID	LIB3176-108-P1-K1-B6
Method	BLASTX
NCBI GI	g1173104
BLAST score	399
E value	3.0e-39
Match length	78
% identity	92
NCBI Description	RIBONUCLEASE 2 PRECURSOR >gi_289210 (M98336) ribonuclease [Arabidopsis thaliana] >gi_2642160 (AC003000) ribonuclease, RNS2 [Arabidopsis thaliana]

Seq. No.	159252
Seq. ID	LIB3176-108-P1-K1-B7
Method	BLASTN
NCBI GI	g4519184
BLAST score	291
E value	1.0e-163
Match length	411

% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K16F13, complete sequence

Seq. No.	159253
Seq. ID	LIB3176-108-P1-K1-B8
Method	BLASTN
NCBI GI	g4646215
BLAST score	67
E value	4.0e-29
Match length	79
% identity	96
NCBI Description	Arabidopsis thaliana chromosome II BAC T22O13 genomic sequence, complete sequence

Seq. No.	159254
Seq. ID	LIB3176-108-P1-K1-B9
Method	BLASTN
NCBI GI	g1167960
BLAST score	186
E value	1.0e-100
Match length	802
% identity	31
NCBI Description	Arabidopsis thaliana extensin (atExt1) gene, complete cds

Seq. No.	159255
Seq. ID	LIB3176-108-P1-K1-C1
Method	BLASTN
NCBI GI	g2244901
BLAST score	283
E value	1.0e-158
Match length	354
% identity	100
NCBI Description	Arabidopsis thaliana DNA chromosome 4, ESSA I contig fragment No

Seq. No.	159256
Seq. ID	LIB3176-108-P1-K1-C11
Method	BLASTX
NCBI GI	g1172873
BLAST score	368
E value	1.0e-35
Match length	74
% identity	100
NCBI Description	CYSTEINE PROTEINASE RD21A PRECURSOR >gi_541857_pir__JN0719 drought-inducible cysteine proteinase (EC 3.4.22.-) RD21A precursor - Arabidopsis thaliana >gi_435619_dbj_BAA02374_ (D13043) thiol protease [Arabidopsis thaliana]

Seq. No.	159257
Seq. ID	LIB3176-108-P1-K1-C12
Method	BLASTX
NCBI GI	g2244785
BLAST score	570
E value	6.0e-59
Match length	131
% identity	86

NCBI Description	(Z97335) hypothetical protein [Arabidopsis thaliana]
Seq. No.	159258
Seq. ID	LIB3176-108-P1-K1-C2
Method	BLASTX
NCBI GI	g2062161
BLAST score	398
E value	6.0e-39
Match length	81
% identity	48
NCBI Description	(AC001645) jasmonate inducible protein isolog [Arabidopsis thaliana]
Seq. No.	159259
Seq. ID	LIB3176-108-P1-K1-C4
Method	BLASTN
NCBI GI	g4159709
BLAST score	92
E value	3.0e-44
Match length	140
% identity	91
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MLN21, complete sequence
Seq. No.	159260
Seq. ID	LIB3176-108-P1-K1-C5
Method	BLASTX
NCBI GI	g4582468
BLAST score	373
E value	4.0e-36
Match length	79
% identity	96
NCBI Description	(AC007071) putative 40S ribosomal protein; contains C-terminal domain [Arabidopsis thaliana]
Seq. No.	159261
Seq. ID	LIB3176-108-P1-K1-C6
Method	BLASTN
NCBI GI	g2098816
BLAST score	206
E value	1.0e-112
Match length	323
% identity	96
NCBI Description	Arabidopsis thaliana BAC F19G10, complete sequence
Seq. No.	159262
Seq. ID	LIB3176-108-P1-K1-C7
Method	BLASTX
NCBI GI	g462013
BLAST score	604
E value	1.0e-64
Match length	150
% identity	85
NCBI Description	ENDOPLASMIN HOMOLOG PRECURSOR (GRP94 HOMOLOG) >gi_542022_pir__S39558 HSP90 homolog - Madagascar periwinkle >gi_348696 (L14594) heat shock protein 90 [Catharanthus roseus]

Seq. No.	159263
Seq. ID	LIB3176-108-P1-K1-C9
Method	BLASTX
NCBI GI	g3182906
BLAST score	149
E value	4.0e-10
Match length	40
% identity	80
NCBI Description	ACTIN, MUSCLE >gi_1526485_dbj_BAA13351_ (D87407) muscle actin [Branchiostoma floridae]

Seq. No.	159264
Seq. ID	LIB3176-108-P1-K1-D10
Method	BLASTX
NCBI GI	g4220470
BLAST score	145
E value	1.0e-09
Match length	44
% identity	64
NCBI Description	(AC006069) hypothetical protein [Arabidopsis thaliana]

Seq. No.	159265
Seq. ID	LIB3176-108-P1-K1-D11
Method	BLASTX
NCBI GI	g1732570
BLAST score	692
E value	3.0e-73
Match length	138
% identity	96
NCBI Description	(U72153) beta-glucosidase [Arabidopsis thaliana]

Seq. No.	159266
Seq. ID	LIB3176-108-P1-K1-D12
Method	BLASTN
NCBI GI	g4589412
BLAST score	259
E value	1.0e-144
Match length	259
% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: F6N7, complete sequence

Seq. No.	159267
Seq. ID	LIB3176-108-P1-K1-D2
Method	BLASTN
NCBI GI	g4519183
BLAST score	95
E value	4.0e-46
Match length	139
% identity	94
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K15C23, complete sequence

Seq. No.	159268
Seq. ID	LIB3176-108-P1-K1-D3
Method	BLASTX

NCBI GI	g119350
BLAST score	109
E value	8.0e-31
Match length	74
% identity	92
NCBI Description	ENOLASE (2-PHOSPHOGLYCERATE DEHYDRATASE) (2-PHOSPHO-D-GLYCERATE HYDRO-LYASE) >gi_81608_pir__JQ1187 phosphopyruvate hydratase (EC 4.2.1.11) - Arabidopsis thaliana >gi_16271_emb_CAA41114_ (X58107) enolase [Arabidopsis thaliana] >gi_4581151_gb_AAD24635.1_AC006919_13 (AC006919) enolase (2-phospho-D-glycerate hydroylase);identical to P25696 [Arabidopsis thaliana]

Seq. No.	159269
Seq. ID	LIB3176-108-P1-K1-D5
Method	BLASTX
NCBI GI	g3024426
BLAST score	198
E value	7.0e-16
Match length	52
% identity	77
NCBI Description	PYRUVATE,PHOSPHATE DIKINASE PRECURSOR (PYRUVATE,ORTHOPHOSPHATE DIKINASE) >gi_1084302_pir__S55478 pyruvate,orthophosphate dikinase (EC 2.7.9.1) - common ice plant >gi_854265_emb_CAA57872_ (X82489) pyruvate,orthophosphate dikinase [Mesembryanthemum crystallinum]

Seq. No.	159270
Seq. ID	LIB3176-108-P1-K1-D6
Method	BLASTN
NCBI GI	g2252471
BLAST score	147
E value	3.0e-77
Match length	202
% identity	94
NCBI Description	Arabidopsis thaliana mRNA for argininosuccinate lyase

Seq. No.	159271
Seq. ID	LIB3176-108-P1-K1-D7
Method	BLASTN
NCBI GI	g2347177
BLAST score	299
E value	1.0e-168
Match length	303
% identity	100
NCBI Description	Arabidopsis thaliana catalase 3 (CAT3) gene, complete cds

Seq. No.	159272
Seq. ID	LIB3176-108-P1-K1-D9
Method	BLASTX
NCBI GI	g3319350
BLAST score	251
E value	4.0e-22
Match length	52
% identity	94

NCBI Description	(AF077407) No definition line found [Arabidopsis thaliana]
Seq. No.	159273
Seq. ID	LIB3176-108-P1-K1-E1
Method	BLASTX
NCBI GI	g3738338
BLAST score	220
E value	5.0e-18
Match length	76
% identity	59
NCBI Description	(AC005170) putative polygalacturonase [Arabidopsis thaliana]
Seq. No.	159274
Seq. ID	LIB3176-108-P1-K1-E11
Method	BLASTN
NCBI GI	g4371278
BLAST score	95
E value	2.0e-46
Match length	159
% identity	99
NCBI Description	Arabidopsis thaliana chromosome II BAC T2N18 genomic sequence, complete sequence [Arabidopsis thaliana]
Seq. No.	159275
Seq. ID	LIB3176-108-P1-K1-E12
Method	BLASTX
NCBI GI	g1864017
BLAST score	405
E value	5.0e-40
Match length	79
% identity	99
NCBI Description	(D63396) elongation factor-1 alpha [Nicotiana tabacum]
Seq. No.	159276
Seq. ID	LIB3176-108-P1-K1-E2
Method	BLASTN
NCBI GI	g4757409
BLAST score	116
E value	2.0e-58
Match length	433
% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MVC8, complete sequence
Seq. No.	159277
Seq. ID	LIB3176-108-P1-K1-E3
Method	BLASTN
NCBI GI	g3859590
BLAST score	33
E value	9.0e-10
Match length	53
% identity	91
NCBI Description	Arabidopsis thaliana BAC T15B16
Seq. No.	159278
Seq. ID	LIB3176-108-P1-K1-E4

Method	BLASTX
NCBI GI	g3033384
BLAST score	298
E value	1.0e-27
Match length	75
% identity	75
NCBI Description	(AC004238) putative CTP synthase [Arabidopsis thaliana]

Seq. No.	159279
Seq. ID	LIB3176-108-P1-K1-E5
Method	BLASTX
NCBI GI	g417381
BLAST score	404
E value	1.0e-39
Match length	80
% identity	100
NCBI Description	NITRILASE 1 >gi_99738_pir__S22398 nitrilase (EC 3.5.5.1) - Arabidopsis thaliana >gi_16400_emb_CAA45041_ (X63445) nitrilase I [Arabidopsis thaliana]

Seq. No.	159280
Seq. ID	LIB3176-108-P1-K1-E6
Method	BLASTN
NCBI GI	g4220627
BLAST score	213
E value	1.0e-116
Match length	368
% identity	6
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K20J1, complete sequence [Arabidopsis thaliana]

Seq. No.	159281
Seq. ID	LIB3176-108-P1-K1-E7
Method	BLASTX
NCBI GI	g115783
BLAST score	517
E value	8.0e-53
Match length	97
% identity	99
NCBI Description	CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR (CAB-140) (LHCP) >gi_16376_emb_CAA27543_ (X03909) chlorophyll a/b binding protein (LHCP AB 140) [Arabidopsis thaliana]

Seq. No.	159282
Seq. ID	LIB3176-108-P1-K1-E8
Method	BLASTN
NCBI GI	g4587641
BLAST score	155
E value	6.0e-82
Match length	202
% identity	98
NCBI Description	Arabidopsis thaliana chromosome I BAC F20D21 genomic sequence, complete sequence

Seq. No.	159283
Seq. ID	LIB3176-108-P1-K1-F1

Method	BLASTN
NCBI GI	g4455321
BLAST score	97
E value	1.0e-47
Match length	131
% identity	94
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F4I10 (ESSAII project)

Seq. No.	159284
Seq. ID	LIB3176-108-P1-K1-F10
Method	BLASTX
NCBI GI	g4263783
BLAST score	381
E value	3.0e-37
Match length	78
% identity	99
NCBI Description	(AC006068) putative DNAJ protein [Arabidopsis thaliana]

Seq. No.	159285
Seq. ID	LIB3176-108-P1-K1-F11
Method	BLASTX
NCBI GI	g3176676
BLAST score	488
E value	2.0e-49
Match length	106
% identity	93
NCBI Description	(AC003671) Similar to carbonic anhydrase gb_L19255 from Nicotiana tabacum. ESTs gb_AA597643, gb_T45390, gb_T43963 and gb_AA597734 come from this gene. [Arabidopsis thaliana]

Seq. No.	159286
Seq. ID	LIB3176-108-P1-K1-F12
Method	BLASTX
NCBI GI	g3341723
BLAST score	149
E value	9.0e-10
Match length	57
% identity	30
NCBI Description	(AF052690) CONSTANS-like 1 protein [Raphanus sativus]

Seq. No.	159287
Seq. ID	LIB3176-108-P1-K1-F3
Method	BLASTN
NCBI GI	g4581084
BLAST score	84
E value	1.0e-39
Match length	84
% identity	100
NCBI Description	Arabidopsis thaliana chromosome I BAC T30F21 genomic sequence, complete sequence

Seq. No.	159288
Seq. ID	LIB3176-108-P1-K1-F5
Method	BLASTN
NCBI GI	g2924729
BLAST score	342

E value	0.0e+00
Match length	346
% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MNA5, complete sequence [Arabidopsis thaliana]

Seq. No.	159289
Seq. ID	LIB3176-108-P1-K1-F6
Method	BLASTX
NCBI GI	g1076445
BLAST score	174
E value	2.0e-12
Match length	90
% identity	50
NCBI Description	cyclin - rape >gi_562190 (L25406) cyclin [Brassica napus]

Seq. No.	159290
Seq. ID	LIB3176-108-P1-K1-F7
Method	BLASTX
NCBI GI	g267073
BLAST score	489
E value	2.0e-49
Match length	98
% identity	93
NCBI Description	TUBULIN BETA-2/BETA-3 CHAIN >gi_320184_pir__JQ1587 tubulin beta chain - Arabidopsis thaliana >gi_166898 (M84700) beta-2 tubulin [Arabidopsis thaliana] >gi_166900 (M84701) beta-3 tubulin [Arabidopsis thaliana]

Seq. No.	159291
Seq. ID	LIB3176-108-P1-K1-F8
Method	BLASTX
NCBI GI	g1732570
BLAST score	686
E value	1.0e-72
Match length	130
% identity	98
NCBI Description	(U72153) beta-glucosidase [Arabidopsis thaliana]

Seq. No.	159292
Seq. ID	LIB3176-108-P1-K1-F9
Method	BLASTN
NCBI GI	g4741928
BLAST score	142
E value	2.0e-74
Match length	154
% identity	98
NCBI Description	Arabidopsis thaliana membrane related protein CP5 mRNA, complete cds

Seq. No.	159293
Seq. ID	LIB3176-108-P1-K1-G1
Method	BLASTX
NCBI GI	g2244798
BLAST score	366
E value	3.0e-35
Match length	79

% identity	92
NCBI Description	(Z97336) hypothetical protein [Arabidopsis thaliana]

Seq. No.	159294
Seq. ID	LIB3176-108-P1-K1-G10
Method	BLASTX
NCBI GI	g4468979
BLAST score	393
E value	4.0e-38
Match length	93
% identity	76
NCBI Description	(AL035605) putative protein [Arabidopsis thaliana]

Seq. No.	159295
Seq. ID	LIB3176-108-P1-K1-G11
Method	BLASTN
NCBI GI	g3449327
BLAST score	160
E value	4.0e-85
Match length	172
% identity	98
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MCA23, complete sequence [Arabidopsis thaliana]

Seq. No.	159296
Seq. ID	LIB3176-108-P1-K1-G12
Method	BLASTX
NCBI GI	g135860
BLAST score	429
E value	2.0e-42
Match length	79
% identity	57
NCBI Description	TONOPLAST INTRINSIC PROTEIN, GAMMA (GAMMA TIP) (AQUAPORIN-TIP) >gi_99761_pir__S22202 tonoplast intrinsic protein gamma - Arabidopsis thaliana >gi_16312_emb_CAA45115_ (X63552) tonoplast intrinsic protein, gamma-TIP(Ara). [Arabidopsis thaliana] >gi_166732 (M84344) tonoplast intrinsic protein [Arabidopsis thaliana] >gi_445129_prf__1908432B tonoplast intrinsic protein gamma [Arabidopsis thaliana]

Seq. No.	159297
Seq. ID	LIB3176-108-P1-K1-G2
Method	BLASTN
NCBI GI	g4220627
BLAST score	325
E value	0.0e+00
Match length	403
% identity	99
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K20J1, complete sequence [Arabidopsis thaliana]

Seq. No.	159298
Seq. ID	LIB3176-108-P1-K1-G4
Method	BLASTX
NCBI GI	g548653
BLAST score	531

E value	2.0e-54
Match length	129
% identity	85
NCBI Description	50S RIBOSOMAL PROTEIN L12-A, CHLOROPLAST PRECURSOR (CL12-A) >gi_541895_pir__A53394 ribosomal protein L12.A, chloroplast - Arabidopsis thaliana >gi_468771_emb_CAA48181_ (X68046) ribosomal protein L12 [Arabidopsis thaliana]

Seq. No.	159299
Seq. ID	LIB3176-108-P1-K1-G5
Method	BLASTX
NCBI GI	g2245093
BLAST score	200
E value	8.0e-16
Match length	55
% identity	82
NCBI Description	(Z97343) membrane channel protein [Arabidopsis thaliana]

Seq. No.	159300
Seq. ID	LIB3176-108-P1-K1-G7
Method	BLASTX
NCBI GI	g1172806
BLAST score	320
E value	4.0e-30
Match length	62
% identity	94
NCBI Description	60S RIBOSOMAL PROTEIN L10 (WILM'S TUMOR SUPPRESSOR PROTEIN HOMOLOG) >gi_478401_pir__JQ2244 ribosomal protein L10.e, cytosolic - Arabidopsis thaliana >gi_17682_emb_CAA78856_ (Z15157) Wilm's tumor suppressor homologue [Arabidopsis thaliana]

Seq. No.	159301
Seq. ID	LIB3176-108-P1-K1-G8
Method	BLASTX
NCBI GI	g4204295
BLAST score	108
E value	2.0e-61
Match length	134
% identity	91
NCBI Description	(AC003027) lcl_prt_seq No definition line found [Arabidopsis thaliana]

Seq. No.	159302
Seq. ID	LIB3176-108-P1-K1-G9
Method	BLASTX
NCBI GI	g1702987
BLAST score	345
E value	1.0e-32
Match length	90
% identity	82
NCBI Description	14-3-3-LIKE PROTEIN GF14 PHI >gi_1493805 (L09111) GF14 protein phi chain [Arabidopsis thaliana] >gi_2232146 (AF001414) 14-3-3-like protein GF14 phi [Arabidopsis thaliana]

Seq. No.	159303

Seq. ID LIB3176-108-P1-K1-H1
Method BLASTX
NCBI GI g322794
BLAST score 309
E value 2.0e-28
Match length 82
% identity 72
NCBI Description UTP--glucose-1-phosphate uridylyltransferase (EC 2.7.7.9) - potato >gi_21599_emb_CAA79357_ (Z18924) UTP--glucose-1-phosphate uridylyltransferase [Solanum tuberosum]

Seq. No. 159304
Seq. ID LIB3176-108-P1-K1-H10
Method BLASTN
NCBI GI g4220643
BLAST score 321
E value 0.0e+00
Match length 361
% identity 98
NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MWD22, complete sequence [Arabidopsis thaliana]

Seq. No. 159305
Seq. ID LIB3176-108-P1-K1-H11
Method BLASTN
NCBI GI g4220627
BLAST score 62
E value 4.0e-26
Match length 298
% identity 9
NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K20J1, complete sequence [Arabidopsis thaliana]

Seq. No. 159306
Seq. ID LIB3176-108-P1-K1-H12
Method BLASTX
NCBI GI g114335
BLAST score 342
E value 1.0e-32
Match length 79
% identity 85
NCBI Description PLASMA MEMBRANE ATPASE 2 (PROTON PUMP) >gi_67973_pir__PXMUP2 H+-transporting ATPase (EC 3.6.1.35) type 2, plasma membrane - Arabidopsis thaliana >gi_166629 (J05570) H+-ATPase [Arabidopsis thaliana]

Seq. No. 159307
Seq. ID LIB3176-108-P1-K1-H2
Method BLASTX
NCBI GI g3123188
BLAST score 570
E value 5.0e-59
Match length 124
% identity 81
NCBI Description CATALASE 3 >gi_2347178 (U43147) catalase 3 [Arabidopsis thaliana] >gi_2511726 (AF021937) catalase 3 [Arabidopsis

thaliana]

Seq. No.	159308
Seq. ID	LIB3176-108-P1-K1-H3
Method	BLASTX
NCBI GI	g1732570
BLAST score	549
E value	1.0e-56
Match length	103
% identity	98
NCBI Description	(U72153) beta-glucosidase [Arabidopsis thaliana]

Seq. No.	159309
Seq. ID	LIB3176-108-P1-K1-H4
Method	BLASTN
NCBI GI	g4490291
BLAST score	57
E value	1.0e-23
Match length	170
% identity	94
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F17M5 (ESSA project)

Seq. No.	159310
Seq. ID	LIB3176-108-P1-K1-H5
Method	BLASTN
NCBI GI	g1402874
BLAST score	93
E value	6.0e-45
Match length	177
% identity	90
NCBI Description	A.thaliana 81kb genomic sequence

Seq. No.	159311
Seq. ID	LIB3176-108-P1-K1-H6
Method	BLASTX
NCBI GI	g1145699
BLAST score	257
E value	8.0e-23
Match length	54
% identity	98
NCBI Description	(U39486) delta tonoplast integral protein [Arabidopsis thaliana]

Seq. No.	159312
Seq. ID	LIB3176-108-P1-K1-H7
Method	BLASTX
NCBI GI	g2244750
BLAST score	276
E value	2.0e-24
Match length	79
% identity	73
NCBI Description	(Z97335) adenosylhomocysteinase [Arabidopsis thaliana] >gi_3088579 (AF059581) S-adenosyl-L-homocysteine hydrolase [Arabidopsis thaliana]

Seq. No.	159313

Seq. ID	LIB3176-108-P1-K1-H8
Method	BLASTX
NCBI GI	g4204300
BLAST score	245
E value	2.0e-26
Match length	73
% identity	88
NCBI Description	(AC003027) Unknown protein [Arabidopsis thaliana]

Seq. No.	159314
Seq. ID	LIB3176-108-P1-K1-H9
Method	BLASTX
NCBI GI	g4337027
BLAST score	201
E value	3.0e-16
Match length	48
% identity	83
NCBI Description	(AF123254) MFP2 [Arabidopsis thaliana]

Seq. No.	159315
Seq. ID	LIB3176-109-P1-K1-A1
Method	BLASTX
NCBI GI	g1619956
BLAST score	372
E value	1.0e-35
Match length	85
% identity	87
NCBI Description	(U72151) voltage-gated chloride channel [Arabidopsis thaliana]

Seq. No.	159316
Seq. ID	LIB3176-109-P1-K1-A12
Method	BLASTX
NCBI GI	g4587542
BLAST score	635
E value	2.0e-66
Match length	136
% identity	91
NCBI Description	(AC006577) Belongs to the PF_00657 Lipase/Acylhydrolase with GDSL-motif family. ESTs gb_T45815, gb_T45130 and gb_Z38046 come from this gene. [Arabidopsis thaliana]

Seq. No.	159317
Seq. ID	LIB3176-109-P1-K1-A2
Method	BLASTX
NCBI GI	g1711507
BLAST score	404
E value	2.0e-39
Match length	104
% identity	69
NCBI Description	SIGNAL RECOGNITION PARTICLE 19 KD PROTEIN (SRP19) >gi_624221 (U19030) signal recognition particle 19 kDa protein subunit SRP19 [Oryza sativa]

Seq. No.	159318
Seq. ID	LIB3176-109-P1-K1-A3
Method	BLASTN

NCBI GI	g3776020
BLAST score	56
E value	6.0e-23
Match length	79
% identity	92
NCBI Description	Arabidopsis thaliana mRNA for DEAD box RNA helicase, RH23

Seq. No.	159319
Seq. ID	LIB3176-109-P1-K1-A4
Method	BLASTX
NCBI GI	g4741940
BLAST score	626
E value	2.0e-65
Match length	118
% identity	68
NCBI Description	(AF134120) Lhca2 protein [Arabidopsis thaliana]

Seq. No.	159320
Seq. ID	LIB3176-109-P1-K1-A5
Method	BLASTX
NCBI GI	g3287693
BLAST score	615
E value	3.0e-64
Match length	129
% identity	88
NCBI Description	(AC003979) Similar to LIM17 gene product gb_1653769 from the genome of Synechocystis sp. gb_D90916. [Arabidopsis thaliana]

Seq. No.	159321
Seq. ID	LIB3176-109-P1-K1-A6
Method	BLASTX
NCBI GI	g4337027
BLAST score	626
E value	2.0e-65
Match length	126
% identity	99
NCBI Description	(AF123254) MFP2 [Arabidopsis thaliana]

Seq. No.	159322
Seq. ID	LIB3176-109-P1-K1-A7
Method	BLASTN
NCBI GI	g4589440
BLAST score	308
E value	1.0e-173
Match length	335
% identity	97
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MSD21, complete sequence

Seq. No.	159323
Seq. ID	LIB3176-109-P1-K1-A8
Method	BLASTN
NCBI GI	g4417264
BLAST score	292
E value	1.0e-163
Match length	395

% identity	100
NCBI Description	Arabidopsis thaliana chromosome II BAC F7D8 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	159324
Seq. ID	LIB3176-109-P1-K1-A9
Method	BLASTX
NCBI GI	g2244750
BLAST score	638
E value	8.0e-67
Match length	136
% identity	88
NCBI Description	(Z97335) adenosylhomocysteinase [Arabidopsis thaliana] >gi_3088579 (AF059581) S-adenosyl-L-homocysteine hydrolase [Arabidopsis thaliana]

Seq. No.	159325
Seq. ID	LIB3176-109-P1-K1-B1
Method	BLASTX
NCBI GI	g4741198
BLAST score	410
E value	3.0e-40
Match length	76
% identity	100
NCBI Description	(AL049746) putative protein [Arabidopsis thaliana]

Seq. No.	159326
Seq. ID	LIB3176-109-P1-K1-B11
Method	BLASTX
NCBI GI	g2146746
BLAST score	561
E value	8.0e-58
Match length	109
% identity	99
NCBI Description	protein kinase (EC 2.7.1.-) - Arabidopsis thaliana >gi_166819 (L05562) protein kinase [Arabidopsis thaliana]

Seq. No.	159327
Seq. ID	LIB3176-109-P1-K1-B12
Method	BLASTX
NCBI GI	g4586265
BLAST score	210
E value	1.0e-16
Match length	80
% identity	50
NCBI Description	(AL049640) putative protein [Arabidopsis thaliana]

Seq. No.	159328
Seq. ID	LIB3176-109-P1-K1-B2
Method	BLASTN
NCBI GI	g4220510
BLAST score	228
E value	1.0e-125
Match length	369
% identity	96
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F22K18 (ESSAII project)

Seq. No.	159329
Seq. ID	LIB3176-109-P1-K1-B3
Method	BLASTN
NCBI GI	g2584827
BLAST score	70
E value	2.0e-31
Match length	124
% identity	93
NCBI Description	Arabidopsis thaliana chromosome 1 BAC F12F1 sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	159330
Seq. ID	LIB3176-109-P1-K1-B5
Method	BLASTX
NCBI GI	g4580920
BLAST score	528
E value	6.0e-54
Match length	141
% identity	72
NCBI Description	(AF113545) vacuole-associated annexin VCaB42 [Nicotiana tabacum]

Seq. No.	159331
Seq. ID	LIB3176-109-P1-K1-B6
Method	BLASTN
NCBI GI	g2160132
BLAST score	349
E value	0.0e+00
Match length	455
% identity	94
NCBI Description	Sequence of BAC F19K23 from Arabidopsis thaliana chromosome 1, complete sequence [Arabidopsis thaliana]

Seq. No.	159332
Seq. ID	LIB3176-109-P1-K1-B7
Method	BLASTX
NCBI GI	g459009
BLAST score	171
E value	3.0e-12
Match length	57
% identity	56
NCBI Description	(U00037) similar to multifunctional aminoacyl-tRNA synthetase, especially to the prolyl-tRNA synthetase region [Caenorhabditis elegans]

Seq. No.	159333
Seq. ID	LIB3176-109-P1-K1-B8
Method	BLASTN
NCBI GI	g4490701
BLAST score	108
E value	3.0e-54
Match length	141
% identity	99
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone T24A18 (ESSA project)

Seq. No.	159334
Seq. ID	LIB3176-109-P1-K1-B9
Method	BLASTX
NCBI GI	g3319349
BLAST score	428
E value	2.0e-42
Match length	88
% identity	94
NCBI Description	(AF077407) No definition line found [Arabidopsis thaliana]

Seq. No.	159335
Seq. ID	LIB3176-109-P1-K1-C1
Method	BLASTX
NCBI GI	g4193388
BLAST score	357
E value	5.0e-34
Match length	95
% identity	73
NCBI Description	(AF091455) translationally controlled tumor protein [Hevea brasiliensis]

Seq. No.	159336
Seq. ID	LIB3176-109-P1-K1-C2
Method	BLASTX
NCBI GI	g3913008
BLAST score	198
E value	9.0e-16
Match length	52
% identity	77
NCBI Description	FRUCTOSE-BISPHOSPHATE ALDOLASE, CYTOPLASMIC ISOZYME >gi_3021338_emb_CAA06308_ (AJ005041) cytosolic fructose-1,6-bisphosphate aldolase [Cicer arietinum]

Seq. No.	159337
Seq. ID	LIB3176-109-P1-K1-C3
Method	BLASTN
NCBI GI	g4455290
BLAST score	106
E value	4.0e-53
Match length	110
% identity	99
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F18A5 (ESSAII project)

Seq. No.	159338
Seq. ID	LIB3176-109-P1-K1-C4
Method	BLASTX
NCBI GI	g282865
BLAST score	237
E value	2.0e-20
Match length	51
% identity	84
NCBI Description	chlorophyll a/b-binding protein - Arabidopsis thaliana >gi_16207_emb_CAA39534_ (X56062) chlorophyll A/B-binding protein [Arabidopsis thaliana] >gi_166644 (M85150) chlorophyll a/b-binding protein [Arabidopsis thaliana] >gi_4678304_emb_CAB41095.1_ (AL049655) chlorophyll

a/b-binding protein [Arabidopsis thaliana]

Seq. No.	159339
Seq. ID	LIB3176-109-P1-K1-C7
Method	BLASTN
NCBI GI	g2924733
BLAST score	45
E value	4.0e-16
Match length	81
% identity	96
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MUF9, complete sequence [Arabidopsis thaliana]

Seq. No.	159340
Seq. ID	LIB3176-109-P1-K1-C8
Method	BLASTX
NCBI GI	g4581146
BLAST score	418
E value	2.0e-41
Match length	92
% identity	91
NCBI Description	(AC006919) putative fructose-bisphosphate aldolase, cytoplasmic [Arabidopsis thaliana]

Seq. No.	159341
Seq. ID	LIB3176-109-P1-K1-D1
Method	BLASTX
NCBI GI	g4427003
BLAST score	208
E value	9.0e-17
Match length	42
% identity	93
NCBI Description	(AF127664) NBD-like protein [Arabidopsis thaliana]

Seq. No.	159342
Seq. ID	LIB3176-109-P1-K1-D11
Method	BLASTX
NCBI GI	g512400
BLAST score	574
E value	2.0e-59
Match length	153
% identity	73
NCBI Description	(X74947) annexin [Medicago sativa]

Seq. No.	159343
Seq. ID	LIB3176-109-P1-K1-D12
Method	BLASTN
NCBI GI	g3869075
BLAST score	72
E value	3.0e-32
Match length	199
% identity	87
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MXK3, complete sequence [Arabidopsis thaliana]

Seq. No.	159344
Seq. ID	LIB3176-109-P1-K1-D2

Method	BLASTN
NCBI GI	g4584339
BLAST score	109
E value	2.0e-54
Match length	113
% identity	99
NCBI Description	Arabidopsis thaliana chromosome II BAC T23A1 genomic sequence, complete sequence

Seq. No.	159345
Seq. ID	LIB3176-109-P1-K1-D6
Method	BLASTN
NCBI GI	g4757409
BLAST score	39
E value	1.0e-12
Match length	47
% identity	98
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MVC8, complete sequence

Seq. No.	159346
Seq. ID	LIB3176-109-P1-K1-D7
Method	BLASTX
NCBI GI	g4427003
BLAST score	553
E value	6.0e-57
Match length	135
% identity	81
NCBI Description	(AF127664) NBD-like protein [Arabidopsis thaliana]

Seq. No.	159347
Seq. ID	LIB3176-109-P1-K1-D8
Method	BLASTN
NCBI GI	g4757410
BLAST score	157
E value	3.0e-83
Match length	169
% identity	98
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MVE11, complete sequence

Seq. No.	159348
Seq. ID	LIB3176-109-P1-K1-D9
Method	BLASTX
NCBI GI	g1170505
BLAST score	174
E value	6.0e-13
Match length	37
% identity	92
NCBI Description	EUKARYOTIC INITIATION FACTOR 4A-2 (EIF-4A-2) >gi_322504_pir__JC1453 translation initiation factor eIF-4A2 - Arabidopsis thaliana >gi_16556_emb_CAA46189_ (X65053) eukaryotic translation initiation factor 4A-2 [Arabidopsis thaliana] >gi_4585969_gb_AAD25605.1_AC005287_7 (AC005287) Eukaryotic Initiation Factor 4A-2 [Arabidopsis thaliana]

Seq. No.	159349
Seq. ID	LIB3176-109-P1-K1-E1
Method	BLASTN
NCBI GI	g2980787
BLAST score	234
E value	1.0e-129
Match length	453
% identity	99
NCBI Description	Arabidopsis thaliana DNA chromosome 4, P1 clone M7J2 (ESSAII project)

Seq. No.	159350
Seq. ID	LIB3176-109-P1-K1-E11
Method	BLASTX
NCBI GI	g3738287
BLAST score	140
E value	6.0e-09
Match length	29
% identity	97
NCBI Description	(AC005309) glutathione s-transferase, GST6 [Arabidopsis thaliana]

Seq. No.	159351
Seq. ID	LIB3176-109-P1-K1-E12
Method	BLASTX
NCBI GI	g1350768
BLAST score	422
E value	1.0e-41
Match length	100
% identity	84
NCBI Description	60S RIBOSOMAL PROTEIN L7A

Seq. No.	159352
Seq. ID	LIB3176-109-P1-K1-E5
Method	BLASTN
NCBI GI	g2828182
BLAST score	82
E value	2.0e-38
Match length	206
% identity	83
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MOJ9, complete sequence [Arabidopsis thaliana]

Seq. No.	159353
Seq. ID	LIB3176-109-P1-K1-E7
Method	BLASTN
NCBI GI	g166816
BLAST score	141
E value	1.0e-73
Match length	183
% identity	96
NCBI Description	Arabidopsis thaliana protein kinase mRNA, complete cds

Seq. No.	159354
Seq. ID	LIB3176-109-P1-K1-E8
Method	BLASTN
NCBI GI	g4512646

BLAST score	62
E value	1.0e-26
Match length	137
% identity	96
NCBI Description	Arabidopsis thaliana chromosome II BAC F23N11 genomic sequence, complete sequence

Seq. No.	159355
Seq. ID	LIB3176-109-P1-K1-E9
Method	BLASTX
NCBI GI	g4581146
BLAST score	274
E value	2.0e-24
Match length	75
% identity	80
NCBI Description	(AC006919) putative fructose-bisphosphate aldolase, cytoplasmic [Arabidopsis thaliana]

Seq. No.	159356
Seq. ID	LIB3176-109-P1-K1-F1
Method	BLASTX
NCBI GI	g2199574
BLAST score	220
E value	5.0e-18
Match length	39
% identity	100
NCBI Description	(AF004293) aquaporin [Brassica rapa]

Seq. No.	159357
Seq. ID	LIB3176-109-P1-K1-F10
Method	BLASTN
NCBI GI	g4757395
BLAST score	119
E value	2.0e-60
Match length	221
% identity	99
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K21L13, complete sequence

Seq. No.	159358
Seq. ID	LIB3176-109-P1-K1-F12
Method	BLASTX
NCBI GI	g1702987
BLAST score	631
E value	2.0e-68
Match length	150
% identity	90
NCBI Description	14-3-3-LIKE PROTEIN GF14 PHI >gi_1493805 (L09111) GF14 protein phi chain [Arabidopsis thaliana] >gi_2232146 (AF001414) 14-3-3-like protein GF14 phi [Arabidopsis thaliana]

Seq. No.	159359
Seq. ID	LIB3176-109-P1-K1-F2
Method	BLASTN
NCBI GI	g2980787
BLAST score	81

E value	2.0e-38
Match length	81
% identity	100
NCBI Description	Arabidopsis thaliana DNA chromosome 4, P1 clone M7J2 (ESSAII project)

Seq. No.	159360
Seq. ID	LIB3176-109-P1-K1-F4
Method	BLASTX
NCBI GI	g3024022
BLAST score	578
E value	7.0e-60
Match length	126
% identity	86
NCBI Description	INITIATION FACTOR 5A-5 (EIF-5A) (EIF-4D) >gi_2225885_dbj_BAA20879_ (AB004826) eukaryotic initiation factor 5A5 [Solanum tuberosum]

Seq. No.	159361
Seq. ID	LIB3176-109-P1-K1-F5
Method	BLASTX
NCBI GI	g124224
BLAST score	173
E value	2.0e-12
Match length	75
% identity	55
NCBI Description	INITIATION FACTOR 5A-1 (EIF-5A) (EIF-4D) >gi_100345_pir__S21060 translation initiation factor eIF-5A - common tobacco >gi_19887_emb_CAA45105_ (X63543) eukaryotic initiatin factor 5A (3) [Nicotiana tabacum]

Seq. No.	159362
Seq. ID	LIB3176-109-P1-K1-F7
Method	BLASTN
NCBI GI	g2351061
BLAST score	75
E value	3.0e-34
Match length	193
% identity	98
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MAF19, complete sequence [Arabidopsis thaliana]

Seq. No.	159363
Seq. ID	LIB3176-109-P1-K1-F8
Method	BLASTX
NCBI GI	g3850573
BLAST score	242
E value	5.0e-45
Match length	92
% identity	99
NCBI Description	(AC005278) Similar to gi_1652733 glycogen operon protein GlgX from Synechocystis sp. genome gb_D90908. ESTs gb_H36690, gb_AA712462, gb_AA651230 and gb_N95932 come from this gene. [Arabidopsis thaliana]

Seq. No.	159364
Seq. ID	LIB3176-109-P1-K1-G10

Method	BLASTN
NCBI GI	g4512656
BLAST score	58
E value	8.0e-25
Match length	62
% identity	98
NCBI Description	Arabidopsis thaliana chromosome II BAC F7D19 genomic sequence, complete sequence

Seq. No.	159365
Seq. ID	LIB3176-109-P1-K1-G11
Method	BLASTX
NCBI GI	g4650842
BLAST score	137
E value	1.0e-08
Match length	29
% identity	90
NCBI Description	(AB026185) elongation factor 2 [Lithospermum erythrorhizon]

Seq. No.	159366
Seq. ID	LIB3176-109-P1-K1-G12
Method	BLASTX
NCBI GI	g3759184
BLAST score	310
E value	2.0e-28
Match length	124
% identity	58
NCBI Description	(AB018441) phi-1 [Nicotiana tabacum]

Seq. No.	159367
Seq. ID	LIB3176-109-P1-K1-G4
Method	BLASTX
NCBI GI	g2246621
BLAST score	471
E value	1.0e-47
Match length	95
% identity	100
NCBI Description	(AF004393) salt-stress induced tonoplast intrinsic protein [Arabidopsis thaliana]

Seq. No.	159368
Seq. ID	LIB3176-109-P1-K1-G7
Method	BLASTN
NCBI GI	g2921157
BLAST score	46
E value	7.0e-17
Match length	78
% identity	88
NCBI Description	Arabidopsis thaliana ClpC mRNA, nuclear gene encoding chloroplast protein, complete cds

Seq. No.	159369
Seq. ID	LIB3176-109-P1-K1-G9
Method	BLASTN
NCBI GI	g4220635
BLAST score	216
E value	1.0e-118

Match length	236
% identity	98
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MDB19, complete sequence [Arabidopsis thaliana]

Seq. No.	159370
Seq. ID	LIB3176-109-P1-K1-H1
Method	BLASTX
NCBI GI	g2961343
BLAST score	382
E value	2.0e-37
Match length	77
% identity	99
NCBI Description	(AL022140) symbiosis-related like protein [Arabidopsis thaliana]

Seq. No.	159371
Seq. ID	LIB3176-109-P1-K1-H10
Method	BLASTX
NCBI GI	g1350680
BLAST score	230
E value	2.0e-19
Match length	44
% identity	100
NCBI Description	60S RIBOSOMAL PROTEIN L1

Seq. No.	159372
Seq. ID	LIB3176-109-P1-K1-H12
Method	BLASTX
NCBI GI	g135406
BLAST score	743
E value	4.0e-79
Match length	139
% identity	100
NCBI Description	TUBULIN ALPHA-3/ALPHA-5 CHAIN >gi_99768_pir__A32712 tubulin alpha-5 chain - Arabidopsis thaliana >gi_166912 (M17189) alpha-tubulin [Arabidopsis thaliana] >gi_166918 (M84698) alpha-5 tubulin [Arabidopsis thaliana]

Seq. No.	159373
Seq. ID	LIB3176-109-P1-K1-H2
Method	BLASTX
NCBI GI	g3738287
BLAST score	316
E value	1.0e-29
Match length	65
% identity	95
NCBI Description	(AC005309) glutathione s-transferase, GST6 [Arabidopsis thaliana]

Seq. No.	159374
Seq. ID	LIB3176-109-P1-K1-H4
Method	BLASTN
NCBI GI	g2924768
BLAST score	36
E value	1.0e-11
Match length	64

% identity	89
NCBI Description	Arabidopsis thaliana chromosome II BAC F25I18 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	159375
Seq. ID	LIB3176-109-P1-K1-H6
Method	BLASTN
NCBI GI	g166911
BLAST score	56
E value	7.0e-23
Match length	56
% identity	100
NCBI Description	A.thaliana alpha-tubulin gene, complete cds

Seq. No.	159376
Seq. ID	LIB3176-109-P1-K1-H7
Method	BLASTX
NCBI GI	g1363489
BLAST score	178
E value	3.0e-13
Match length	35
% identity	97
NCBI Description	thioglucosidase (EC 3.2.3.1) 3D precursor - Arabidopsis thaliana >gi_984052_emb_CAA61592_ (X89413) thioglucoside glucohydrolase [Arabidopsis thaliana]

Seq. No.	159377
Seq. ID	LIB3176-109-P1-K1-H8
Method	BLASTX
NCBI GI	g1527172
BLAST score	233
E value	5.0e-20
Match length	43
% identity	86
NCBI Description	(U67676) alpha-2 tubulin [Hirudo medicinalis] >gi_1532193_gb_AAB07891_ (U67678) alpha-2 tubulin [Hirudo medicinalis]

Seq. No.	159378
Seq. ID	LIB3176-109-P1-K1-H9
Method	BLASTX
NCBI GI	g2369714
BLAST score	708
E value	5.0e-75
Match length	148
% identity	92
NCBI Description	(Z97178) elongation factor 2 [Beta vulgaris]

Seq. No.	159379
Seq. ID	LIB3176-110-P1-K1-A10
Method	BLASTX
NCBI GI	g1854386
BLAST score	321
E value	1.0e-29
Match length	120
% identity	50
NCBI Description	(AB001375) similar to soluble NSF attachment protein [Vitis

vinifera]

Seq. No.	159380
Seq. ID	LIB3176-110-P1-K1-A12
Method	BLASTX
NCBI GI	g1781299
BLAST score	263
E value	7.0e-23
Match length	76
% identity	67
NCBI Description	(Y09506) transformer-SR ribonucleoprotein [Nicotiana tabacum]

Seq. No.	159381
Seq. ID	LIB3176-110-P1-K1-A3
Method	BLASTN
NCBI GI	g3047088
BLAST score	103
E value	3.0e-51
Match length	123
% identity	100
NCBI Description	Arabidopsis thaliana BAC T26D22

Seq. No.	159382
Seq. ID	LIB3176-110-P1-K1-A4
Method	BLASTN
NCBI GI	g3335331
BLAST score	98
E value	2.0e-48
Match length	102
% identity	99
NCBI Description	Arabidopsis thaliana chromosome 1 BAC T8F5 sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	159383
Seq. ID	LIB3176-110-P1-K1-A5
Method	BLASTN
NCBI GI	g2341023
BLAST score	70
E value	1.0e-31
Match length	115
% identity	92
NCBI Description	Sequence of BAC F19P19 from Arabidopsis thaliana chromosome 1, complete sequence [Arabidopsis thaliana]

Seq. No.	159384
Seq. ID	LIB3176-110-P1-K1-A6
Method	BLASTX
NCBI GI	g1172806
BLAST score	224
E value	3.0e-18
Match length	60
% identity	75
NCBI Description	60S RIBOSOMAL PROTEIN L10 (WILM'S TUMOR SUPPRESSOR PROTEIN HOMOLOG) >gi_478401_pir__JQ2244 ribosomal protein L10.e, cytosolic - Arabidopsis thaliana >gi_17682_emb_CAA78856_ (Z15157) Wilm's tumor suppressor homologue [Arabidopsis

thaliana]

Seq. No.	159385
Seq. ID	LIB3176-110-P1-K1-A7
Method	BLASTX
NCBI GI	g4262180
BLAST score	149
E value	9.0e-10
Match length	29
% identity	90
NCBI Description	(AC005508) 29621 [Arabidopsis thaliana]

Seq. No.	159386
Seq. ID	LIB3176-110-P1-K1-A8
Method	BLASTN
NCBI GI	g4455168
BLAST score	75
E value	3.0e-34
Match length	235
% identity	97
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F10M10 (ESSAII project)

Seq. No.	159387
Seq. ID	LIB3176-110-P1-K1-A9
Method	BLASTN
NCBI GI	g3869074
BLAST score	310
E value	1.0e-174
Match length	318
% identity	99
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MMI9, complete sequence [Arabidopsis thaliana]

Seq. No.	159388
Seq. ID	LIB3176-110-P1-K1-B1
Method	BLASTN
NCBI GI	g2618602
BLAST score	316
E value	1.0e-178
Match length	406
% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MSJ1, complete sequence [Arabidopsis thaliana]

Seq. No.	159389
Seq. ID	LIB3176-110-P1-K1-B11
Method	BLASTX
NCBI GI	g4582441
BLAST score	160
E value	8.0e-11
Match length	73
% identity	56
NCBI Description	(AC007142) unknown protein [Arabidopsis thaliana]

Seq. No.	159390
Seq. ID	LIB3176-110-P1-K1-B12

Method	BLASTN
NCBI GI	g2351068
BLAST score	242
E value	1.0e-133
Match length	438
% identity	98
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MRH10, complete sequence [Arabidopsis thaliana]

Seq. No.	159391
Seq. ID	LIB3176-110-P1-K1-B3
Method	BLASTX
NCBI GI	g4185599
BLAST score	196
E value	5.0e-15
Match length	129
% identity	36
NCBI Description	(AB010708) Anthocyanin 5-aromatic acyltransferase [Gentiana triflora]

Seq. No.	159392
Seq. ID	LIB3176-110-P1-K1-B4
Method	BLASTN
NCBI GI	g2576360
BLAST score	64
E value	1.0e-27
Match length	88
% identity	95
NCBI Description	Arabidopsis thaliana lysine and histidine specific transporter mRNA, complete cds

Seq. No.	159393
Seq. ID	LIB3176-110-P1-K1-B6
Method	BLASTN
NCBI GI	g2351068
BLAST score	114
E value	3.0e-57
Match length	261
% identity	94
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MRH10, complete sequence [Arabidopsis thaliana]

Seq. No.	159394
Seq. ID	LIB3176-110-P1-K1-B8
Method	BLASTN
NCBI GI	g2980757
BLAST score	107
E value	1.0e-53
Match length	123
% identity	98
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F6I18 (ESSAII project)

Seq. No.	159395
Seq. ID	LIB3176-110-P1-K1-B9
Method	BLASTN
NCBI GI	g2062153

BLAST score	54
E value	4.0e-22
Match length	70
% identity	32
NCBI Description	Arabidopsis thaliana chromosome III BAC T02O04 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	159396
Seq. ID	LIB3176-110-P1-K1-C1
Method	BLASTN
NCBI GI	g2995991
BLAST score	104
E value	1.0e-51
Match length	197
% identity	97
NCBI Description	Arabidopsis thaliana dormancy-associated protein (DRM1) gene, complete cds

Seq. No.	159397
Seq. ID	LIB3176-110-P1-K1-C10
Method	BLASTN
NCBI GI	g2264312
BLAST score	146
E value	1.0e-76
Match length	146
% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MOK16, complete sequence [Arabidopsis thaliana]

Seq. No.	159398
Seq. ID	LIB3176-110-P1-K1-C11
Method	BLASTN
NCBI GI	g4454447
BLAST score	47
E value	3.0e-18
Match length	63
% identity	94
NCBI Description	Arabidopsis thaliana chromosome II BAC F5H14 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	159399
Seq. ID	LIB3176-110-P1-K1-C3
Method	BLASTN
NCBI GI	g3738313
BLAST score	49
E value	2.0e-19
Match length	61
% identity	95
NCBI Description	Arabidopsis thaliana chromosome II BAC T29E15 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	159400
Seq. ID	LIB3176-110-P1-K1-C6
Method	BLASTN
NCBI GI	g1490552
BLAST score	109
E value	8.0e-55

Match length	112
% identity	99
NCBI Description	Arabidopsis thaliana S-adenosylmethionine decarboxylase (SAMdc) mRNA, complete cds

Seq. No.	159401
Seq. ID	LIB3176-110-P1-K1-C8
Method	BLASTN
NCBI GI	g4191771
BLAST score	65
E value	3.0e-28
Match length	69
% identity	99
NCBI Description	Arabidopsis thaliana chromosome II BAC F3P11 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	159402
Seq. ID	LIB3176-110-P1-K1-D1
Method	BLASTX
NCBI GI	g399298
BLAST score	212
E value	6.0e-17
Match length	65
% identity	69
NCBI Description	STRESS-INDUCED KIN2 PROTEIN (COLD-INDUCED COR6.6 PROTEIN) >gi_1084343_pir__S22529 cold-regulated protein kin2 - Arabidopsis thaliana >gi_16230_emb_CAA38894_ (X55053) cold regulated [Arabidopsis thaliana]

Seq. No.	159403
Seq. ID	LIB3176-110-P1-K1-D10
Method	BLASTX
NCBI GI	g1350783
BLAST score	107
E value	1.0e-04
Match length	136
% identity	5
NCBI Description	RECEPTOR-LIKE PROTEIN KINASE 5 PRECURSOR >gi_282883_pir__S27756 receptor-like protein kinase precursor - Arabidopsis thaliana >gi_166850 (M84660) receptor-like protein kinase [Arabidopsis thaliana] >gi_2842492_emb_CAA16889_ (AL021749) receptor-like protein kinase 5 precursor (RLK5) [Arabidopsis thaliana]

Seq. No.	159404
Seq. ID	LIB3176-110-P1-K1-D11
Method	BLASTN
NCBI GI	g2494110
BLAST score	158
E value	6.0e-84
Match length	170
% identity	98
NCBI Description	Sequence of BAC T1G11 from Arabidopsis thaliana chromosome 1, complete sequence [Arabidopsis thaliana]

Seq. No.	159405
Seq. ID	LIB3176-110-P1-K1-D12

Method	BLASTN
NCBI GI	g4309683
BLAST score	109
E value	1.0e-54
Match length	157
% identity	92
NCBI Description	Arabidopsis thaliana chromosome 1 BAC T31J12 sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	159406
Seq. ID	LIB3176-110-P1-K1-D3
Method	BLASTN
NCBI GI	g4589419
BLAST score	101
E value	8.0e-50
Match length	198
% identity	50
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K2I5, complete sequence

Seq. No.	159407
Seq. ID	LIB3176-110-P1-K1-D4
Method	BLASTN
NCBI GI	g3702722
BLAST score	132
E value	2.0e-68
Match length	136
% identity	99
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K12B20, complete sequence [Arabidopsis thaliana]

Seq. No.	159408
Seq. ID	LIB3176-110-P1-K1-D6
Method	BLASTX
NCBI GI	g1061040
BLAST score	235
E value	3.0e-20
Match length	57
% identity	82
NCBI Description	(X89867) sterol-C-methyltransferase [Arabidopsis thaliana] >gi_1587694_prf__2207220A sterol C-methyltransferase [Arabidopsis thaliana]

Seq. No.	159409
Seq. ID	LIB3176-110-P1-K1-D7
Method	BLASTN
NCBI GI	g968976
BLAST score	61
E value	1.0e-25
Match length	96
% identity	93
NCBI Description	Arabidopsis thaliana light-dependent NADPH:protochlorophyllide oxidoreductase B (PorB) mRNA, nuclear gene encoding chloroplast protein, complete cds

Seq. No.	159410
Seq. ID	LIB3176-110-P1-K1-D8

Method	BLASTX
NCBI GI	g3286693
BLAST score	481
E value	1.0e-48
Match length	99
% identity	95
NCBI Description	(Y15433) 33 kDa polypeptide of oxygen-evolving complex (OEC) in photosystem II [Arabidopsis thaliana]

Seq. No.	159411
Seq. ID	LIB3176-110-P1-K1-D9
Method	BLASTN
NCBI GI	g2073547
BLAST score	55
E value	1.0e-22
Match length	108
% identity	98
NCBI Description	Arabidopsis thaliana polyubiquitin (ubq4) gene, complete cds

Seq. No.	159412
Seq. ID	LIB3176-110-P1-K1-E10
Method	BLASTN
NCBI GI	g4519195
BLAST score	83
E value	6.0e-39
Match length	274
% identity	99
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MQC12, complete sequence

Seq. No.	159413
Seq. ID	LIB3176-110-P1-K1-E11
Method	BLASTN
NCBI GI	g16562
BLAST score	58
E value	4.0e-24
Match length	62
% identity	98
NCBI Description	A.thaliana gene for tRNA-Phe (P-2-S)

Seq. No.	159414
Seq. ID	LIB3176-110-P1-K1-E2
Method	BLASTX
NCBI GI	g464707
BLAST score	230
E value	5.0e-19
Match length	49
% identity	96
NCBI Description	40S RIBOSOMAL PROTEIN S18 >gi_480908_pir__S37496 ribosomal protein S18.A - Arabidopsis thaliana >gi_405613_emb_CAA80684_ (Z23165) ribosomal protein S18A [Arabidopsis thaliana] >gi_434343_emb_CAA82273_ (Z28701) S18 ribosomal protein [Arabidopsis thaliana] >gi_434345_emb_CAA82274_ (Z28702) S18 ribosomal protein [Arabidopsis thaliana] >gi_434906_emb_CAA82275_ (Z28962) S18 ribosomal protein [Arabidopsis thaliana]

	>gi_2505871_emb_CAA72909_ (Y12227) ribosomal protein S18A [Arabidopsis thaliana] >gi_3287678 (AC003979) Match to ribosomal S18 gene mRNA gb_Z28701, DNA gb_Z23165 from A. thaliana. ESTs gb_T21121, gb_Z17755, gb_R64776 and gb_R30430 come from this gene. [Arabidopsis thaliana] >gi_4538910_emb_CAB39647.1_ (AL049482) S18.A ribosomal protein [Arabidopsis thaliana]
Seq. No.	159415
Seq. ID	LIB3176-110-P1-K1-E3
Method	BLASTN
NCBI GI	g16562
BLAST score	63
E value	2.0e-27
Match length	63
% identity	100
NCBI Description	A.thaliana gene for tRNA-Phe (P-2-S)
Seq. No.	159416
Seq. ID	LIB3176-110-P1-K1-E4
Method	BLASTN
NCBI GI	g4538895
BLAST score	80
E value	2.0e-37
Match length	147
% identity	97
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F17A8 (ESSA project)
Seq. No.	159417
Seq. ID	LIB3176-110-P1-K1-E6
Method	BLASTX
NCBI GI	g4371298
BLAST score	170
E value	3.0e-12
Match length	53
% identity	64
NCBI Description	(AC006260) putative RNA-binding protein [Arabidopsis thaliana]
Seq. No.	159418
Seq. ID	LIB3176-110-P1-K1-E8
Method	BLASTN
NCBI GI	g166787
BLAST score	114
E value	2.0e-57
Match length	159
% identity	92
NCBI Description	A.thaliana chloroplast ATP synthase gamma subunit (atpC2) gene, complete cds
Seq. No.	159419
Seq. ID	LIB3176-110-P1-K1-E9
Method	BLASTN
NCBI GI	g4376087
BLAST score	105
E value	3.0e-52

Match length	125
% identity	97
NCBI Description	Arabidopsis thaliana DNA chromosome 4, ESSA I AP2 contig fragment No

Seq. No.	159420
Seq. ID	LIB3176-110-P1-K1-F10
Method	BLASTN
NCBI GI	g3702732
BLAST score	87
E value	2.0e-41
Match length	264
% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MGF10, complete sequence [Arabidopsis thaliana]

Seq. No.	159421
Seq. ID	LIB3176-110-P1-K1-F11
Method	BLASTX
NCBI GI	g1363489
BLAST score	195
E value	1.0e-15
Match length	41
% identity	90
NCBI Description	thioglucosidase (EC 3.2.3.1) 3D precursor - Arabidopsis thaliana >gi_984052_emb_CAA61592_ (X89413) thioglucoside glucohydrolase [Arabidopsis thaliana]

Seq. No.	159422
Seq. ID	LIB3176-110-P1-K1-F12
Method	BLASTX
NCBI GI	g2119927
BLAST score	498
E value	1.0e-50
Match length	106
% identity	92
NCBI Description	translation elongation factor G, chloroplast - soybean

Seq. No.	159423
Seq. ID	LIB3176-110-P1-K1-F2
Method	BLASTN
NCBI GI	g1617273
BLAST score	170
E value	8.0e-91
Match length	258
% identity	91
NCBI Description	B.napus mRNA for AMP-binding protein (2287 bp)

Seq. No.	159424
Seq. ID	LIB3176-110-P1-K1-F5
Method	BLASTN
NCBI GI	g2062153
BLAST score	45
E value	9.0e-17
Match length	45
% identity	54
NCBI Description	Arabidopsis thaliana chromosome III BAC T02O04 genomic

sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	159425
Seq. ID	LIB3176-110-P1-K1-F7
Method	BLASTX
NCBI GI	g3170531
BLAST score	162
E value	2.0e-13
Match length	75
% identity	55
NCBI Description	(AF055635) protein tyrosine phosphatase 1; PTP1; tyrosine-specific protein phosphatase [Arabidopsis thaliana]

Seq. No.	159426
Seq. ID	LIB3176-110-P1-K1-F8
Method	BLASTN
NCBI GI	g3413422
BLAST score	42
E value	2.0e-14
Match length	74
% identity	89
NCBI Description	Arabidopsis thaliana gene encoding protein tyrosine phosphatase, ORF1 and ORF2 genes

Seq. No.	159427
Seq. ID	LIB3176-110-P1-K1-G1
Method	BLASTX
NCBI GI	g133938
BLAST score	591
E value	2.0e-61
Match length	134
% identity	86
NCBI Description	CHLOROPLAST 30S RIBOSOMAL PROTEIN S3 >gi_70866_pir__R3SP3 ribosomal protein S3 - spinach chloroplast >gi_12310_emb_CAA31715_ (X13336) ribosomal protein S3 [Spinacia oleracea]

Seq. No.	159428
Seq. ID	LIB3176-110-P1-K1-G10
Method	BLASTX
NCBI GI	g132863
BLAST score	244
E value	3.0e-21
Match length	49
% identity	96
NCBI Description	CHLOROPLAST 50S RIBOSOMAL PROTEIN L2 >gi_12214_emb_CAA46568_ (X65615) ribosomal protein L2 [Sinapis alba]

Seq. No.	159429
Seq. ID	LIB3176-110-P1-K1-G11
Method	BLASTN
NCBI GI	g16470
BLAST score	101
E value	1.0e-49
Match length	137

% identity	93
NCBI Description	Arabidopsis thaliana mRNA for rubisco activase
Seq. No.	159430
Seq. ID	LIB3176-110-P1-K1-G12
Method	BLASTN
NCBI GI	g16255
BLAST score	64
E value	4.0e-28
Match length	84
% identity	47
NCBI Description	A.thaliana A2 and A3 genes encoding elongation factor 1-alpha
Seq. No.	159431
Seq. ID	LIB3176-110-P1-K1-G2
Method	BLASTN
NCBI GI	g4314374
BLAST score	81
E value	7.0e-38
Match length	137
% identity	94
NCBI Description	Arabidopsis thaliana chromosome II BAC F10A12 genomic sequence, complete sequence [Arabidopsis thaliana]
Seq. No.	159432
Seq. ID	LIB3176-110-P1-K1-G5
Method	BLASTN
NCBI GI	g2760167
BLAST score	65
E value	1.0e-28
Match length	77
% identity	96
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MCO15, complete sequence [Arabidopsis thaliana]
Seq. No.	159433
Seq. ID	LIB3176-110-P1-K1-G6
Method	BLASTX
NCBI GI	g3193319
BLAST score	214
E value	9.0e-18
Match length	46
% identity	93
NCBI Description	(AF069299) contains similarity to mouse brain protein E46 (GB:X61506) [Arabidopsis thaliana]
Seq. No.	159434
Seq. ID	LIB3176-110-P1-K1-G8
Method	BLASTX
NCBI GI	g2894574
BLAST score	311
E value	8.0e-29
Match length	69
% identity	87
NCBI Description	(AL021890) peroxidase prxr1 [Arabidopsis thaliana] >gi_2961341_emb_CAA18099.1_ (AL022140) peroxidase prxr1

[Arabidopsis thaliana]

Seq. No.	159435
Seq. ID	LIB3176-110-P1-K1-H1
Method	BLASTN
NCBI GI	g2815519
BLAST score	208
E value	1.0e-113
Match length	224
% identity	99
NCBI Description	Arabidopsis thaliana BAC T5J8 from chromosome IV, top arm, complete sequence [Arabidopsis thaliana]

Seq. No.	159436
Seq. ID	LIB3176-110-P1-K1-H10
Method	BLASTX
NCBI GI	g2062161
BLAST score	173
E value	6.0e-13
Match length	32
% identity	100
NCBI Description	(AC001645) jasmonate inducible protein isolog [Arabidopsis thaliana]

Seq. No.	159437
Seq. ID	LIB3176-110-P1-K1-H11
Method	BLASTX
NCBI GI	g1170089
BLAST score	469
E value	3.0e-48
Match length	105
% identity	96
NCBI Description	GLUTATHIONE S-TRANSFERASE ERD13 (CLASS PHI) >gi_481822_pir__S39542 probable glutathione transferase (EC 2.5.1.18) (clone ERD13) - Arabidopsis thaliana >gi_497789_dbj_BAA04554_ (D17673) glutathione S-transferase [Arabidopsis thaliana] >gi_3201614 (AC004669) glutathione S-transferase [Arabidopsis thaliana]

Seq. No.	159438
Seq. ID	LIB3176-110-P1-K1-H12
Method	BLASTX
NCBI GI	g2495179
BLAST score	571
E value	5.0e-59
Match length	116
% identity	100
NCBI Description	PORPHOBILINOGEN DEAMINASE PRECURSOR (PBG) (HYDROXYMETHYLBILANE SYNTHASE) (HMBS) (PRE-UROPORPHYRINOGEN SYNTHASE) >gi_1084340_pir__S50762 hydroxymethylbilane synthase (EC 4.3.1.8) precursor - Arabidopsis thaliana >gi_313150_emb_CAA51941_ (X73535) hydroxymethylbilane synthase [Arabidopsis thaliana] >gi_313838_emb_CAA52061_ (X73839) hydroxymethylbilane synthase [Arabidopsis thaliana]

Seq. No.	159439

Seq. ID	LIB3176-110-P1-K1-H2
Method	BLASTX
NCBI GI	g3451071
BLAST score	184
E value	3.0e-14
Match length	70
% identity	61
NCBI Description	(AL031326) beta adaptin - like protein [Arabidopsis thaliana]

Seq. No.	159440
Seq. ID	LIB3176-110-P1-K1-H3
Method	BLASTN
NCBI GI	g2564050
BLAST score	322
E value	0.0e+00
Match length	322
% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MUA22, complete sequence [Arabidopsis thaliana]

Seq. No.	159441
Seq. ID	LIB3176-110-P1-K1-H4
Method	BLASTN
NCBI GI	g16375
BLAST score	135
E value	3.0e-70
Match length	159
% identity	97
NCBI Description	A.thaliana gene (LHCP AB 140) for chlorophyll a/b binding protein

Seq. No.	159442
Seq. ID	LIB3176-110-P1-K1-H5
Method	BLASTX
NCBI GI	g1170089
BLAST score	99
E value	5.0e-24
Match length	75
% identity	87
NCBI Description	GLUTATHIONE S-TRANSFERASE ERD13 (CLASS PHI) >gi_481822_pir__S39542 probable glutathione transferase (EC 2.5.1.18) (clone ERD13) - Arabidopsis thaliana >gi_497789_dbj_BAA04554_ (D17673) glutathione S-transferase [Arabidopsis thaliana] >gi_3201614 (AC004669) glutathione S-transferase [Arabidopsis thaliana]

Seq. No.	159443
Seq. ID	LIB3176-111-P1-K1-A1
Method	BLASTN
NCBI GI	g2702261
BLAST score	77
E value	3.0e-35
Match length	77
% identity	100
NCBI Description	Arabidopsis thaliana chromosome II BAC T21L14 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	159444
Seq. ID	LIB3176-111-P1-K1-A10
Method	BLASTN
NCBI GI	g3510343
BLAST score	217
E value	1.0e-119
Match length	225
% identity	99
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MJC20, complete sequence [Arabidopsis thaliana]

Seq. No.	159445
Seq. ID	LIB3176-111-P1-K1-A11
Method	BLASTN
NCBI GI	g4678219
BLAST score	49
E value	6.0e-19
Match length	93
% identity	96
NCBI Description	Arabidopsis thaliana chromosome II BAC F9C22 genomic sequence, complete sequence

Seq. No.	159446
Seq. ID	LIB3176-111-P1-K1-A12
Method	BLASTX
NCBI GI	g2462929
BLAST score	482
E value	9.0e-49
Match length	99
% identity	95
NCBI Description	(Y12295) glutathione transferase [Arabidopsis thaliana]

Seq. No.	159447
Seq. ID	LIB3176-111-P1-K1-A3
Method	BLASTN
NCBI GI	g2815519
BLAST score	105
E value	3.0e-52
Match length	112
% identity	98
NCBI Description	Arabidopsis thaliana BAC T5J8 from chromosome IV, top arm, complete sequence [Arabidopsis thaliana]

Seq. No.	159448
Seq. ID	LIB3176-111-P1-K1-A4
Method	BLASTN
NCBI GI	g2335089
BLAST score	87
E value	3.0e-41
Match length	95
% identity	82
NCBI Description	Arabidopsis thaliana chromosome II BAC T11A7 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	159449
Seq. ID	LIB3176-111-P1-K1-A6

Method	BLASTN
NCBI GI	g4115370
BLAST score	181
E value	2.0e-97
Match length	193
% identity	99
NCBI Description	Arabidopsis thaliana chromosome II BAC F27D4 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	159450
Seq. ID	LIB3176-111-P1-K1-A7
Method	BLASTN
NCBI GI	g16131
BLAST score	68
E value	6.0e-30
Match length	80
% identity	96
NCBI Description	Arabidopsis thaliana genes for 5.8S rRNA and 25S rRNA with 18S rRNA fragment

Seq. No.	159451
Seq. ID	LIB3176-111-P1-K1-A8
Method	BLASTN
NCBI GI	g1769904
BLAST score	161
E value	1.0e-85
Match length	165
% identity	99
NCBI Description	A.thaliana psbP gene

Seq. No.	159452
Seq. ID	LIB3176-111-P1-K1-B10
Method	BLASTN
NCBI GI	g2191126
BLAST score	33
E value	5.0e-10
Match length	33
% identity	100
NCBI Description	Arabidopsis thaliana BAC IG002N01

Seq. No.	159453
Seq. ID	LIB3176-111-P1-K1-B11
Method	BLASTX
NCBI GI	g4454037
BLAST score	451
E value	2.0e-45
Match length	83
% identity	99
NCBI Description	(AL035394) putative major latex protein [Arabidopsis thaliana]

Seq. No.	159454
Seq. ID	LIB3176-111-P1-K1-B12
Method	BLASTX
NCBI GI	g2499811
BLAST score	270
E value	4.0e-24

Match length	50
% identity	100
NCBI Description	PROFILIN 2 >gi_1353766 (U43323) profilin 2 [Arabidopsis thaliana] >gi_1353772 (U43326) profilin 2 [Arabidopsis thaliana]

Seq. No.	159455
Seq. ID	LIB3176-111-P1-K1-B2
Method	BLASTX
NCBI GI	g3413707
BLAST score	295
E value	4.0e-27
Match length	63
% identity	40
NCBI Description	(AC004747) hypothetical protein [Arabidopsis thaliana]

Seq. No.	159456
Seq. ID	LIB3176-111-P1-K1-B3
Method	BLASTN
NCBI GI	g4512656
BLAST score	305
E value	1.0e-171
Match length	392
% identity	91
NCBI Description	Arabidopsis thaliana chromosome II BAC F7D19 genomic sequence, complete sequence

Seq. No.	159457
Seq. ID	LIB3176-111-P1-K1-B5
Method	BLASTN
NCBI GI	g2656029
BLAST score	126
E value	7.0e-65
Match length	165
% identity	97
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MQB2

Seq. No.	159458
Seq. ID	LIB3176-111-P1-K1-B7
Method	BLASTX
NCBI GI	g3023848
BLAST score	386
E value	1.0e-37
Match length	82
% identity	36
NCBI Description	GUANINE NUCLEOTIDE-BINDING PROTEIN BETA SUBUNIT-LIKE PROTEIN (WD-40 REPEAT AUXIN-DEPENDENT PROTEIN ARCA) >gi_2289095 (U77381) WD-40 repeat protein [Arabidopsis thaliana]

Seq. No.	159459
Seq. ID	LIB3176-111-P1-K1-B8
Method	BLASTX
NCBI GI	g4490746
BLAST score	436
E value	1.0e-43

Match length	86
% identity	97
NCBI Description	(AL035708) cytochrome P450-like protein [Arabidopsis thaliana]

Seq. No.	159460
Seq. ID	LIB3176-111-P1-K1-B9
Method	BLASTN
NCBI GI	g2827513
BLAST score	107
E value	3.0e-53
Match length	139
% identity	94
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F8F16 (ESSAII project)

Seq. No.	159461
Seq. ID	LIB3176-111-P1-K1-C10
Method	BLASTN
NCBI GI	g2459406
BLAST score	122
E value	2.0e-62
Match length	188
% identity	99
NCBI Description	Arabidopsis thaliana chromosome II BAC F4P9 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	159462
Seq. ID	LIB3176-111-P1-K1-C11
Method	BLASTN
NCBI GI	g4584531
BLAST score	35
E value	6.0e-11
Match length	63
% identity	98
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone T9E8 (ESSA project)

Seq. No.	159463
Seq. ID	LIB3176-111-P1-K1-C2
Method	BLASTN
NCBI GI	g2191126
BLAST score	250
E value	1.0e-138
Match length	254
% identity	100
NCBI Description	Arabidopsis thaliana BAC IG002N01

Seq. No.	159464
Seq. ID	LIB3176-111-P1-K1-C3
Method	BLASTN
NCBI GI	g2828186
BLAST score	202
E value	1.0e-110
Match length	214
% identity	99
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:

K18I23, complete sequence [Arabidopsis thaliana]

Seq. No.	159465
Seq. ID	LIB3176-111-P1-K1-C4
Method	BLASTN
NCBI GI	g2924651
BLAST score	124
E value	2.0e-63
Match length	240
% identity	96
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K2A18, complete sequence [Arabidopsis thaliana]

Seq. No.	159466
Seq. ID	LIB3176-111-P1-K1-C6
Method	BLASTX
NCBI GI	g1363489
BLAST score	413
E value	1.0e-40
Match length	78
% identity	96
NCBI Description	thioglucosidase (EC 3.2.3.1) 3D precursor - Arabidopsis thaliana >gi_984052_emb_CAA61592_ (X89413) thioglucoside glucohydrolase [Arabidopsis thaliana]

Seq. No.	159467
Seq. ID	LIB3176-111-P1-K1-C7
Method	BLASTN
NCBI GI	g3241922
BLAST score	203
E value	1.0e-110
Match length	203
% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MLM24, complete sequence [Arabidopsis thaliana]

Seq. No.	159468
Seq. ID	LIB3176-111-P1-K1-C8
Method	BLASTX
NCBI GI	g4325343
BLAST score	380
E value	6.0e-37
Match length	79
% identity	96
NCBI Description	(AF128393) contains similarity to homeobox domains (Pfam: PF00046, Score,36.5, E=6.9e-08, N=1) [Arabidopsis thaliana]

Seq. No.	159469
Seq. ID	LIB3176-111-P1-K1-C9
Method	BLASTN
NCBI GI	g2584827
BLAST score	135
E value	5.0e-70
Match length	143
% identity	99
NCBI Description	Arabidopsis thaliana chromosome 1 BAC F12F1 sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	159470
Seq. ID	LIB3176-111-P1-K1-D10
Method	BLASTN
NCBI GI	g4159706
BLAST score	86
E value	4.0e-41
Match length	114
% identity	95
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MGL6, complete sequence

Seq. No.	159471
Seq. ID	LIB3176-111-P1-K1-D11
Method	BLASTN
NCBI GI	g4757403
BLAST score	62
E value	2.0e-26
Match length	62
% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MJL12, complete sequence

Seq. No.	159472
Seq. ID	LIB3176-111-P1-K1-D12
Method	BLASTN
NCBI GI	g429107
BLAST score	45
E value	1.0e-16
Match length	77
% identity	90
NCBI Description	L.esculentum S-adenosyl-L-methionine synthetase mRNA, complete CDS

Seq. No.	159473
Seq. ID	LIB3176-111-P1-K1-D4
Method	BLASTX
NCBI GI	g1353121
BLAST score	174
E value	9.0e-13
Match length	96
% identity	40
NCBI Description	PUTATIVE ATP-DEPENDENT RNA HELICASE ZK512.2 IN CHROMOSOME III >gi_3881691_emb_CAA80151_ (Z22177) similar to RNA binding proteins (helicase etc.); cDNA EST EMBL:D74667 comes from this gene; cDNA EST EMBL:D71919 comes from this gene; cDNA EST yk496b4.3 comes from this gene; cDNA EST yk231f3.3 comes from this gene; c

Seq. No.	159474
Seq. ID	LIB3176-111-P1-K1-D5
Method	BLASTX
NCBI GI	g3249099
BLAST score	364
E value	4.0e-35
Match length	71
% identity	99

NCBI Description	(AC003114) EST gb_T21244 comes from this gene. [Arabidopsis thaliana] >gi_4220616_dbj_BAA74591_ (AB021936) nicotianamine synthase [Arabidopsis thaliana]
Seq. No.	159475
Seq. ID	LIB3176-111-P1-K1-D6
Method	BLASTN
NCBI GI	g2244870
BLAST score	288
E value	1.0e-161
Match length	288
% identity	93
NCBI Description	Arabidopsis thaliana DNA chromosome 4, ESSA I contig fragment No
Seq. No.	159476
Seq. ID	LIB3176-111-P1-K1-D7
Method	BLASTX
NCBI GI	g3269284
BLAST score	497
E value	3.0e-50
Match length	131
% identity	78
NCBI Description	(AL030978) histone H2A- like protein [Arabidopsis thaliana]
Seq. No.	159477
Seq. ID	LIB3176-111-P1-K1-D8
Method	BLASTX
NCBI GI	g2117612
BLAST score	307
E value	1.0e-28
Match length	58
% identity	100
NCBI Description	catalase (EC 1.11.1.6) 3 - Arabidopsis thaliana
Seq. No.	159478
Seq. ID	LIB3176-111-P1-K1-D9
Method	BLASTN
NCBI GI	g402903
BLAST score	102
E value	1.0e-50
Match length	114
% identity	98
NCBI Description	Arabidopsis thaliana Columbia laminin receptor-like protein mRNA, complete cds
Seq. No.	159479
Seq. ID	LIB3176-111-P1-K1-E1
Method	BLASTX
NCBI GI	g2454182
BLAST score	281
E value	2.0e-25
Match length	58
% identity	95
NCBI Description	(U80185) pyruvate dehydrogenase E1 alpha subunit [Arabidopsis thaliana]

Seq. No.	159480
Seq. ID	LIB3176-111-P1-K1-E10
Method	BLASTN
NCBI GI	g2827887
BLAST score	317
E value	1.0e-178
Match length	337
% identity	99
NCBI Description	Arabidopsis thaliana ATP-dependent Clp protease proteolytic subunit (clpP) mRNA, nuclear gene encoding chloroplast protein, complete cds

Seq. No.	159481
Seq. ID	LIB3176-111-P1-K1-E12
Method	BLASTX
NCBI GI	g113024
BLAST score	584
E value	1.0e-60
Match length	137
% identity	88
NCBI Description	ISOCITRATE LYASE (ISOCITRASE) (ISOCITRATASE) (ICL) >gi_553043 (M83534) isocitrate lyase [Arabidopsis thaliana]

Seq. No.	159482
Seq. ID	LIB3176-111-P1-K1-E4
Method	BLASTN
NCBI GI	g472876
BLAST score	119
E value	2.0e-60
Match length	139
% identity	96
NCBI Description	A.thaliana mRNA for plasma membrane intrinsic protein 2a

Seq. No.	159483
Seq. ID	LIB3176-111-P1-K1-E5
Method	BLASTX
NCBI GI	g1170089
BLAST score	736
E value	3.0e-78
Match length	146
% identity	100
NCBI Description	GLUTATHIONE S-TRANSFERASE ERD13 (CLASS PHI) >gi_481822_pir__S39542 probable glutathione transferase (EC 2.5.1.18) (clone ERD13) - Arabidopsis thaliana >gi_497789_dbj_BAA04554_ (D17673) glutathione S-transferase [Arabidopsis thaliana] >gi_3201614 (AC004669) glutathione S-transferase [Arabidopsis thaliana]

Seq. No.	159484
Seq. ID	LIB3176-111-P1-K1-E6
Method	BLASTN
NCBI GI	g3873174
BLAST score	111
E value	5.0e-56
Match length	119
% identity	98
NCBI Description	Genomic sequence for Arabidopsis thaliana BAC F14N23,

complete sequence [Arabidopsis thaliana]

Seq. No.	159485
Seq. ID	LIB3176-111-P1-K1-E7
Method	BLASTX
NCBI GI	g1170089
BLAST score	241
E value	4.0e-23
Match length	77
% identity	80
NCBI Description	GLUTATHIONE S-TRANSFERASE ERD13 (CLASS PHI) >gi_481822_pir__S39542 probable glutathione transferase (EC 2.5.1.18) (clone ERD13) - Arabidopsis thaliana >gi_497789_dbj_BAA04554_ (D17673) glutathione S-transferase [Arabidopsis thaliana] >gi_3201614 (AC004669) glutathione S-transferase [Arabidopsis thaliana]

Seq. No.	159486
Seq. ID	LIB3176-111-P1-K1-E8
Method	BLASTN
NCBI GI	g3128166
BLAST score	84
E value	9.0e-40
Match length	96
% identity	97
NCBI Description	Arabidopsis thaliana chromosome II BAC F4I1 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	159487
Seq. ID	LIB3176-111-P1-K1-E9
Method	BLASTX
NCBI GI	g1076678
BLAST score	331
E value	2.0e-31
Match length	71
% identity	94
NCBI Description	ubiquitin / ribosomal protein S27a - potato (fragment)

Seq. No.	159488
Seq. ID	LIB3176-111-P1-K1-F10
Method	BLASTX
NCBI GI	g166765
BLAST score	432
E value	6.0e-43
Match length	84
% identity	98
NCBI Description	(M23106) heat shock protein HSP70-1 [Arabidopsis thaliana]

Seq. No.	159489
Seq. ID	LIB3176-111-P1-K1-F11
Method	BLASTX
NCBI GI	g2655420
BLAST score	207
E value	2.0e-16
Match length	67
% identity	66
NCBI Description	(AF035414) heat shock cognate protein HSC70 [Brassica

napus]

Seq. No.	159490
Seq. ID	LIB3176-111-P1-K1-F12
Method	BLASTX
NCBI GI	g4585966
BLAST score	322
E value	9.0e-30
Match length	153
% identity	51
NCBI Description	(AC005287) Putative dihyrdolipoamide acetyltransferase [Arabidopsis thaliana]

Seq. No.	159491
Seq. ID	LIB3176-111-P1-K1-F4
Method	BLASTX
NCBI GI	g2341034
BLAST score	530
E value	3.0e-54
Match length	109
% identity	98
NCBI Description	(AC000104) F19P19.13 [Arabidopsis thaliana]

Seq. No.	159492
Seq. ID	LIB3176-111-P1-K1-F5
Method	BLASTX
NCBI GI	g2833388
BLAST score	147
E value	9.0e-10
Match length	59
% identity	54
NCBI Description	GRANULE-BOUND GLYCOGEN (STARCH) SYNTHASE PRECURSOR >gi_629660_pir__S43341 ADPglucose--starch glucosyltransferase (EC 2.4.1.21) precursor - cassava >gi_437042_emb_CAA52273_ (X74160) starch (bacterial glycogen) synthase [Manihot esculenta]

Seq. No.	159493
Seq. ID	LIB3176-111-P1-K1-F6
Method	BLASTN
NCBI GI	g1655479
BLAST score	150
E value	4.0e-79
Match length	178
% identity	96
NCBI Description	Arabidopsis thaliana mRNA for gamma subunit of mitochondrial F1-ATPase, complete cds

Seq. No.	159494
Seq. ID	LIB3176-111-P1-K1-F7
Method	BLASTN
NCBI GI	g4586241
BLAST score	210
E value	1.0e-115
Match length	261
% identity	98
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone T20K18

(ESSA project)

Seq. No.	159495
Seq. ID	LIB3176-111-P1-K1-F9
Method	BLASTN
NCBI GI	g2760170
BLAST score	259
E value	1.0e-144
Match length	317
% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MIO24, complete sequence [Arabidopsis thaliana]

Seq. No.	159496
Seq. ID	LIB3176-111-P1-K1-G1
Method	BLASTX
NCBI GI	g4006883
BLAST score	402
E value	3.0e-39
Match length	86
% identity	88
NCBI Description	(Z99707) cysteine proteinase [Arabidopsis thaliana]

Seq. No.	159497
Seq. ID	LIB3176-111-P1-K1-G10
Method	BLASTN
NCBI GI	g166705
BLAST score	174
E value	2.0e-93
Match length	194
% identity	98
NCBI Description	Arabidopsis thaliana glyceraldehyde-3-phosphate dehydrogenase C subunit (GapC) gene, complete cds

Seq. No.	159498
Seq. ID	LIB3176-111-P1-K1-G11
Method	BLASTX
NCBI GI	g3334142
BLAST score	254
E value	2.0e-22
Match length	70
% identity	76
NCBI Description	CENTROMERE/MICROTUBULE BINDING PROTEIN CBF5 (CENTROMERE-BINDING FACTOR 5) (NUCLEOLAR PROTEIN CBF5) >gi_2737892 (U59150) nucleolar protein AfCbf5p [Sartorya fumigata]

Seq. No.	159499
Seq. ID	LIB3176-111-P1-K1-G12
Method	BLASTN
NCBI GI	g2924651
BLAST score	228
E value	1.0e-125
Match length	257
% identity	96
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K2A18, complete sequence [Arabidopsis thaliana]

Seq. No.	159500
Seq. ID	LIB3176-111-P1-K1-G2
Method	BLASTN
NCBI GI	g4376087
BLAST score	145
E value	8.0e-76
Match length	208
% identity	93
NCBI Description	Arabidopsis thaliana DNA chromosome 4, ESSA I AP2 contig fragment No

Seq. No.	159501
Seq. ID	LIB3176-111-P1-K1-G4
Method	BLASTX
NCBI GI	g2440029
BLAST score	209
E value	3.0e-17
Match length	41
% identity	98
NCBI Description	(Y14851) DAL1 protein [Arabidopsis thaliana] >gi_2440031_emb_CAA75115_ (Y14850) DAL1 protein [Arabidopsis thaliana]

Seq. No.	159502
Seq. ID	LIB3176-111-P1-K1-G5
Method	BLASTN
NCBI GI	g4756963
BLAST score	100
E value	3.0e-49
Match length	129
% identity	93
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F10M23 (ESSA project)

Seq. No.	159503
Seq. ID	LIB3176-111-P1-K1-G9
Method	BLASTX
NCBI GI	g3334409
BLAST score	238
E value	2.0e-20
Match length	59
% identity	85
NCBI Description	VACUOLAR ATP SYNTHASE SUBUNIT E (V-ATPASE E SUBUNIT) >gi_2129765_pir__S71261 V-type proton-ATPase - Arabidopsis thaliana >gi_1143394_emb_CAA63086_ (X92117) V-type proton-ATPase [Arabidopsis thaliana]

Seq. No.	159504
Seq. ID	LIB3176-111-P1-K1-H12
Method	BLASTN
NCBI GI	g3763944
BLAST score	297
E value	1.0e-166
Match length	321
% identity	98
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F28A23

(ESSAII project)

Seq. No.	159505
Seq. ID	LIB3176-111-P1-K1-H3
Method	BLASTX
NCBI GI	g3242720
BLAST score	53
E value	2.0e-22
Match length	124
% identity	45
NCBI Description	(AC003040) putative acetone-cyanohydrin lyase [Arabidopsis thaliana]

Seq. No.	159506
Seq. ID	LIB3176-111-P1-K1-H4
Method	BLASTN
NCBI GI	g498913
BLAST score	89
E value	5.0e-43
Match length	97
% identity	99
NCBI Description	Arabidopsis thaliana Columbia glutamate-1-semialdehyde aminotransferase (gsa2) gene, complete cds

Seq. No.	159507
Seq. ID	LIB3176-111-P1-K1-H5
Method	BLASTN
NCBI GI	g4582444
BLAST score	140
E value	6.0e-73
Match length	263
% identity	98
NCBI Description	Arabidopsis thaliana chromosome II BAC T9H9 genomic sequence, complete sequence

Seq. No.	159508
Seq. ID	LIB3176-111-P1-K1-H7
Method	BLASTN
NCBI GI	g4235150
BLAST score	170
E value	1.0e-90
Match length	190
% identity	97
NCBI Description	Arabidopsis thaliana chromosome I BAC T25B24 genomic sequence, complete sequence

Seq. No.	159509
Seq. ID	LIB3176-111-P1-K1-H8
Method	BLASTX
NCBI GI	g1710394
BLAST score	265
E value	1.0e-23
Match length	50
% identity	96
NCBI Description	RIBONUCLEOSIDE-DIPHOSPHATE REDUCTASE SMALL CHAIN (RIBONUCLEOTIDE REDUCTASE) (R2 SUBUNIT) >gi_840719_emb_CAA54549_ (X77336) ribonucleotide reductase

R2 [Arabidopsis thaliana]

Seq. No.	159510
Seq. ID	LIB3176-112-P1-K1-A1
Method	BLASTN
NCBI GI	g4199934
BLAST score	152
E value	3.0e-80
Match length	181
% identity	97
NCBI Description	Genomic sequence for Arabidopsis thaliana BAC T3P18, complete sequence [Arabidopsis thaliana]

Seq. No.	159511
Seq. ID	LIB3176-112-P1-K1-A12
Method	BLASTX
NCBI GI	g3979665
BLAST score	138
E value	8.0e-09
Match length	43
% identity	63
NCBI Description	(X66482) orf [Arabidopsis thaliana]

Seq. No.	159512
Seq. ID	LIB3176-112-P1-K1-A2
Method	BLASTX
NCBI GI	g1709970
BLAST score	240
E value	8.0e-21
Match length	61
% identity	80
NCBI Description	60S RIBOSOMAL PROTEIN L10A

Seq. No.	159513
Seq. ID	LIB3176-112-P1-K1-A3
Method	BLASTN
NCBI GI	g4757411
BLAST score	144
E value	2.0e-75
Match length	168
% identity	88
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MXC7, complete sequence

Seq. No.	159514
Seq. ID	LIB3176-112-P1-K1-A4
Method	BLASTX
NCBI GI	g3738285
BLAST score	512
E value	3.0e-52
Match length	101
% identity	99
NCBI Description	(AC005309) unknown protein [Arabidopsis thaliana]

Seq. No.	159515
Seq. ID	LIB3176-112-P1-K1-A5
Method	BLASTN

NCBI GI	g2924733
BLAST score	47
E value	4.0e-18
Match length	67
% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MUF9, complete sequence [Arabidopsis thaliana]

Seq. No.	159516
Seq. ID	LIB3176-112-P1-K1-A6
Method	BLASTN
NCBI GI	g3676295
BLAST score	33
E value	7.0e-10
Match length	61
% identity	90
NCBI Description	Nicotiana sylvestris ATPase beta subunit (nsatp2.2.1) mRNA, nuclear gene encoding mitochondrial protein, complete cds

Seq. No.	159517
Seq. ID	LIB3176-112-P1-K1-A8
Method	BLASTN
NCBI GI	g3766106
BLAST score	32
E value	4.0e-09
Match length	40
% identity	95
NCBI Description	Arabidopsis thaliana chromosome 1 BAC F9K20 sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	159518
Seq. ID	LIB3176-112-P1-K1-A9
Method	BLASTN
NCBI GI	g4544435
BLAST score	88
E value	3.0e-42
Match length	124
% identity	94
NCBI Description	Arabidopsis thaliana chromosome II BAC F14M13 genomic sequence, complete sequence

Seq. No.	159519
Seq. ID	LIB3176-112-P1-K1-B1
Method	BLASTN
NCBI GI	g4468103
BLAST score	189
E value	1.0e-102
Match length	197
% identity	99
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone M3E9 (ESSA project)

Seq. No.	159520
Seq. ID	LIB3176-112-P1-K1-B10
Method	BLASTX
NCBI GI	g3249100
BLAST score	421

E value	7.0e-42
Match length	80
% identity	97
NCBI Description	(AC003114) Match to calreticulin (AtCRTL) mRNA gb_U27698 and DNA gb_U66344. ESTs gb_T45719, gb_T22451, gb_H36323 and gb_AA042519 come from this gene. [Arabidopsis thaliana]

Seq. No.	159521
Seq. ID	LIB3176-112-P1-K1-B5
Method	BLASTN
NCBI GI	g2245073
BLAST score	39
E value	2.0e-13
Match length	43
% identity	98
NCBI Description	Arabidopsis thaliana DNA chromosome 4, ESSA I contig fragment No

Seq. No.	159522
Seq. ID	LIB3176-112-P1-K1-B6
Method	BLASTX
NCBI GI	g2443878
BLAST score	166
E value	4.0e-12
Match length	35
% identity	91
NCBI Description	(AC002294) Unknown protein [Arabidopsis thaliana]

Seq. No.	159523
Seq. ID	LIB3176-112-P1-K1-B9
Method	BLASTX
NCBI GI	g2623881
BLAST score	212
E value	3.0e-17
Match length	62
% identity	66
NCBI Description	(AF031318) catalase [Raphanus sativus]

Seq. No.	159524
Seq. ID	LIB3176-112-P1-K1-C1
Method	BLASTX
NCBI GI	g2924519
BLAST score	514
E value	3.0e-75
Match length	137
% identity	92
NCBI Description	(AL022023) catalase [Arabidopsis thaliana]

Seq. No.	159525
Seq. ID	LIB3176-112-P1-K1-C11
Method	BLASTN
NCBI GI	g16172
BLAST score	94
E value	6.0e-46
Match length	94
% identity	100
NCBI Description	A.thaliana mRNA for ascorbate peroxidase

Seq. No.	159526
Seq. ID	LIB3176-112-P1-K1-C12
Method	BLASTN
NCBI GI	g3492855
BLAST score	69
E value	7.0e-31
Match length	128
% identity	95
NCBI Description	Genomic sequence for Arabidopsis thaliana BAC F20N2, complete sequence [Arabidopsis thaliana]

Seq. No.	159527
Seq. ID	LIB3176-112-P1-K1-C2
Method	BLASTN
NCBI GI	g3510339
BLAST score	96
E value	5.0e-47
Match length	124
% identity	94
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K3K7, complete sequence [Arabidopsis thaliana]

Seq. No.	159528
Seq. ID	LIB3176-112-P1-K1-C3
Method	BLASTN
NCBI GI	g4371278
BLAST score	52
E value	4.0e-20
Match length	80
% identity	91
NCBI Description	Arabidopsis thaliana chromosome II BAC T2N18 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	159529
Seq. ID	LIB3176-112-P1-K1-C4
Method	BLASTN
NCBI GI	g4581138
BLAST score	91
E value	4.0e-44
Match length	98
% identity	98
NCBI Description	Arabidopsis thaliana chromosome II BAC F1O11 genomic sequence, complete sequence

Seq. No.	159530
Seq. ID	LIB3176-112-P1-K1-C6
Method	BLASTX
NCBI GI	g3550519
BLAST score	328
E value	8.0e-31
Match length	93
% identity	65
NCBI Description	(AJ007630) oxygenase [Nicotiana tabacum]

Seq. No.	159531
Seq. ID	LIB3176-112-P1-K1-C7

Method	BLASTX
NCBI GI	g3024126
BLAST score	283
E value	1.0e-25
Match length	54
% identity	98
NCBI Description	S-ADENOSYLMETHIONINE SYNTHETASE 1 (METHIONINE ADENOSYLTRANSFERASE 1) (ADOMET SYNTHETASE 1) >gi_1655576_emb_CAA95856_ (Z71271) S-adenosyl-L-methionine synthetase 1 [Catharanthus roseus]

Seq. No.	159532
Seq. ID	LIB3176-112-P1-K1-C8
Method	BLASTN
NCBI GI	g4512656
BLAST score	131
E value	1.0e-67
Match length	202
% identity	85
NCBI Description	Arabidopsis thaliana chromosome II BAC F7D19 genomic sequence, complete sequence

Seq. No.	159533
Seq. ID	LIB3176-112-P1-K1-C9
Method	BLASTN
NCBI GI	g3164125
BLAST score	58
E value	2.0e-24
Match length	78
% identity	95
NCBI Description	Arabidopsis thaliana mRNA for cytochrome P450 monooxygenase, complete cds, clone P450-2

Seq. No.	159534
Seq. ID	LIB3176-112-P1-K1-D1
Method	BLASTN
NCBI GI	g3367500
BLAST score	103
E value	1.0e-50
Match length	428
% identity	100
NCBI Description	REVERSE-COMPLEMENT OF: F23J3.GCG.SEQ CHECK: 2754 FROM: 1 TO: 93489, complete sequence [Arabidopsis thaliana]

Seq. No.	159535
Seq. ID	LIB3176-112-P1-K1-D10
Method	BLASTN
NCBI GI	g4159705
BLAST score	63
E value	2.0e-27
Match length	67
% identity	99
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MGD8, complete sequence

Seq. No.	159536
Seq. ID	LIB3176-112-P1-K1-D12

Method	BLASTN
NCBI GI	g3449320
BLAST score	35
E value	4.0e-10
Match length	66
% identity	88
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MRB17, complete sequence [Arabidopsis thaliana]

Seq. No.	159537
Seq. ID	LIB3176-112-P1-K1-D2
Method	BLASTN
NCBI GI	g1546691
BLAST score	67
E value	1.0e-29
Match length	99
% identity	92
NCBI Description	A.thaliana mRNA for peroxidase ATP19a

Seq. No.	159538
Seq. ID	LIB3176-112-P1-K1-D3
Method	BLASTN
NCBI GI	g2924257
BLAST score	56
E value	3.0e-23
Match length	84
% identity	46
NCBI Description	Tobacco chloroplast genome DNA

Seq. No.	159539
Seq. ID	LIB3176-112-P1-K1-D4
Method	BLASTX
NCBI GI	g1170505
BLAST score	202
E value	3.0e-16
Match length	38
% identity	100
NCBI Description	EUKARYOTIC INITIATION FACTOR 4A-2 (EIF-4A-2) >gi_322504_pir__JC1453 translation initiation factor eIF-4A2 - Arabidopsis thaliana >gi_16556_emb_CAA46189_ (X65053) eukaryotic translation initiation factor 4A-2 [Arabidopsis thaliana] >gi_4585969_gb_AAD25605.1_AC005287_7 (AC005287) Eukaryotic Initiation Factor 4A-2 [Arabidopsis thaliana]

Seq. No.	159540
Seq. ID	LIB3176-112-P1-K1-D5
Method	BLASTN
NCBI GI	g3882354
BLAST score	101
E value	2.0e-49
Match length	121
% identity	96
NCBI Description	Arabidopsis thaliana 12-oxophytodienoate reductase OPR1 and 12-oxophytodienoate reductase OPR2 genes, complete cds

Seq. No.	159541

Seq. ID	LIB3176-112-P1-K1-D6
Method	BLASTX
NCBI GI	g4455307
BLAST score	252
E value	3.0e-22
Match length	53
% identity	96
NCBI Description	(AL035528) methionyl-tRNA synthetase-like protein [Arabidopsis thaliana]

Seq. No.	159542
Seq. ID	LIB3176-112-P1-K1-E1
Method	BLASTX
NCBI GI	g3348077
BLAST score	553
E value	7.0e-57
Match length	129
% identity	85
NCBI Description	(AF078080) isochorismate synthase [Arabidopsis thaliana]

Seq. No.	159543
Seq. ID	LIB3176-112-P1-K1-E10
Method	BLASTN
NCBI GI	g681901
BLAST score	99
E value	8.0e-49
Match length	139
% identity	93
NCBI Description	Arabidopsis thaliana gene for chloroplast RNA-binding protein cp29, complete cds (exon1, exon2, exon3, exon4)

Seq. No.	159544
Seq. ID	LIB3176-112-P1-K1-E11
Method	BLASTX
NCBI GI	g1076366
BLAST score	248
E value	9.0e-22
Match length	59
% identity	83
NCBI Description	peptidylprolyl isomerase (EC 5.2.1.8) - Arabidopsis thaliana >gi_460968 (U07276) peptidyl-prolyl cis-trans isomerase [Arabidopsis thaliana] >gi_992643 (U32186) cyclophilin [Arabidopsis thaliana] >gi_1091580_prf__2021266A peptidyl-Pro cis-trans isomerase [Arabidopsis thaliana]

Seq. No.	159545
Seq. ID	LIB3176-112-P1-K1-E12
Method	BLASTX
NCBI GI	g4220446
BLAST score	281
E value	2.0e-25
Match length	89
% identity	63
NCBI Description	(AC006216) Strong similarity to gi_2062155 T02O04.2 mitochondrial processing peptidase alpha subunit precusor isolog from Arabidopsis thaliana BAC gb_AC001645. ESTs

	gb_Z18504 and gb_AA395715 come from this gene. [Arabidopsis thaliana]
Seq. No.	159546
Seq. ID	LIB3176-112-P1-K1-E2
Method	BLASTX
NCBI GI	g3738287
BLAST score	168
E value	2.0e-12
Match length	36
% identity	94
NCBI Description	(AC005309) glutathione s-transferase, GST6 [Arabidopsis thaliana]
Seq. No.	159547
Seq. ID	LIB3176-112-P1-K1-E4
Method	BLASTN
NCBI GI	g619752
BLAST score	92
E value	1.0e-44
Match length	153
% identity	90
NCBI Description	Arabidopsis thaliana tryptophan synthase alpha chain (TSA1) gene, complete cds
Seq. No.	159548
Seq. ID	LIB3176-112-P1-K1-E5
Method	BLASTX
NCBI GI	g3319349
BLAST score	351
E value	1.0e-33
Match length	78
% identity	92
NCBI Description	(AF077407) No definition line found [Arabidopsis thaliana]
Seq. No.	159549
Seq. ID	LIB3176-112-P1-K1-E6
Method	BLASTX
NCBI GI	g121080
BLAST score	256
E value	2.0e-22
Match length	75
% identity	68
NCBI Description	GLYCINE CLEAVAGE SYSTEM H PROTEIN PRECURSOR >gi_1070638_pir__GCPMH glycine cleavage system protein H precursor - garden pea >gi_20737_emb_CAA45978_ (X64726) H protein [Pisum sativum] >gi_169093 (J05164) H-protein of glycine decarboxylase precursor (EC 2.1.2.10) [Pisum sativum] >gi_287815_emb_CAA37704_ (X53656) H-protein [Pisum sativum]
Seq. No.	159550
Seq. ID	LIB3176-112-P1-K1-E7
Method	BLASTX
NCBI GI	g3913791
BLAST score	203
E value	8.0e-16

Match length	52
% identity	79
NCBI Description	GLUTAMATE--CYSTEINE LIGASE PRECURSOR (GAMMA-GLUTAMYLCYSTEINE SYNTHETASE) (GAMMA-ECS) (GCS) >gi_2407615 (AF017983) gamma-glutamylcysteine synthetase [Lycopersicon esculentum]
Seq. No.	159551
Seq. ID	LIB3176-112-P1-K1-E8
Method	BLASTN
NCBI GI	g1303694
BLAST score	64
E value	1.0e-27
Match length	76
% identity	96
NCBI Description	Arabidopsis thaliana mRNA for luminal binding protein (BiP), complete cds
Seq. No.	159552
Seq. ID	LIB3176-112-P1-K1-F1
Method	BLASTN
NCBI GI	g1009711
BLAST score	71
E value	1.0e-31
Match length	115
% identity	93
NCBI Description	Arabidopsis thaliana calreticulin (AtCRTL) mRNA, partial cds
Seq. No.	159553
Seq. ID	LIB3176-112-P1-K1-F10
Method	BLASTX
NCBI GI	g2959767
BLAST score	638
E value	6.0e-67
Match length	127
% identity	97
NCBI Description	(AJ002584) AtMRP4 [Arabidopsis thaliana] >gi_3738292 (AC005309) glutathione-conjugate transporter AtMRP4 [Arabidopsis thaliana]
Seq. No.	159554
Seq. ID	LIB3176-112-P1-K1-F11
Method	BLASTX
NCBI GI	g3249100
BLAST score	761
E value	3.0e-81
Match length	141
% identity	100
NCBI Description	(AC003114) Match to calreticulin (AtCRTL) mRNA gb_U27698 and DNA gb_U66344. ESTs gb_T45719, gb_T22451, gb_H36323 and gb_AA042519 come from this gene. [Arabidopsis thaliana]
Seq. No.	159555
Seq. ID	LIB3176-112-P1-K1-F12
Method	BLASTN
NCBI GI	g3080352

BLAST score	73
E value	6.0e-33
Match length	263
% identity	97
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone T5K18 (ESSAII project)

Seq. No.	159556
Seq. ID	LIB3176-112-P1-K1-F2
Method	BLASTN
NCBI GI	g3282170
BLAST score	194
E value	1.0e-105
Match length	226
% identity	96
NCBI Description	Arabidopsis thaliana chromosome 1 BAC F8K4 sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	159557
Seq. ID	LIB3176-112-P1-K1-F4
Method	BLASTN
NCBI GI	g397481
BLAST score	73
E value	3.0e-33
Match length	93
% identity	95
NCBI Description	A.thaliana hsc70 mRNA for heat shock cognate protein

Seq. No.	159558
Seq. ID	LIB3176-112-P1-K1-F5
Method	BLASTN
NCBI GI	g3063690
BLAST score	103
E value	3.0e-51
Match length	130
% identity	95
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F4D11 (ESSAII project)

Seq. No.	159559
Seq. ID	LIB3176-112-P1-K1-F6
Method	BLASTN
NCBI GI	g2098816
BLAST score	67
E value	3.0e-29
Match length	74
% identity	97
NCBI Description	Arabidopsis thaliana BAC F19G10, complete sequence

Seq. No.	159560
Seq. ID	LIB3176-112-P1-K1-F7
Method	BLASTN
NCBI GI	g3719208
BLAST score	140
E value	3.0e-73
Match length	163
% identity	98

NCBI Description	Arabidopsis thaliana UFO binding protein UIP1 mRNA, complete cds
Seq. No.	159561
Seq. ID	LIB3176-112-P1-K1-F8
Method	BLASTX
NCBI GI	g2791896
BLAST score	251
E value	4.0e-22
Match length	58
% identity	86
NCBI Description	(Y08997) 146kDa nuclear protein [Xenopus laevis]
Seq. No.	159562
Seq. ID	LIB3176-112-P1-K1-G1
Method	BLASTX
NCBI GI	g541954
BLAST score	340
E value	3.0e-32
Match length	93
% identity	77
NCBI Description	ubiquitin extension protein - white lupine >gi_438111_emb_CAA80334_ (Z22613) ubiquitin extension protein [Lupinus albus]
Seq. No.	159563
Seq. ID	LIB3176-112-P1-K1-G2
Method	BLASTN
NCBI GI	g4539290
BLAST score	157
E value	3.0e-83
Match length	177
% identity	97
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F14M19 (ESSA project)
Seq. No.	159564
Seq. ID	LIB3176-112-P1-K1-G3
Method	BLASTN
NCBI GI	g2245377
BLAST score	50
E value	5.0e-20
Match length	62
% identity	95
NCBI Description	Arabidopsis thaliana auxin response factor 1 (ARF1) mRNA, complete cds
Seq. No.	159565
Seq. ID	LIB3176-112-P1-K1-G6
Method	BLASTX
NCBI GI	g3738091
BLAST score	299
E value	5.0e-27
Match length	84
% identity	76
NCBI Description	(AC005617) similar to symbiotic ammonium transporter, SAT1 [Arabidopsis thaliana]

Seq. No.	159566
Seq. ID	LIB3176-112-P1-K1-G7
Method	BLASTX
NCBI GI	g3395436
BLAST score	291
E value	8.0e-27
Match length	64
% identity	92
NCBI Description	(AC004683) unknown protein [Arabidopsis thaliana]

Seq. No.	159567
Seq. ID	LIB3176-112-P1-K1-G9
Method	BLASTN
NCBI GI	g4589445
BLAST score	198
E value	1.0e-107
Match length	241
% identity	95
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MWL2, complete sequence

Seq. No.	159568
Seq. ID	LIB3176-112-P1-K1-H1
Method	BLASTX
NCBI GI	g3402487
BLAST score	469
E value	3.0e-47
Match length	100
% identity	91
NCBI Description	(AB015138) Vacuolar proton pyrophosphatase [Arabidopsis thaliana]

Seq. No.	159569
Seq. ID	LIB3176-112-P1-K1-H12
Method	BLASTX
NCBI GI	g4759160
BLAST score	169
E value	8.0e-12
Match length	64
% identity	50
NCBI Description	small nuclear ribonucleoprotein D3 polypeptide (18kD) >gi_1173456_sp_P43331_SMD3_HUMAN SMALL NUCLEAR RIBONUCLEOPROTEIN SM D3 (SNRNP CORE PROTEIN D3) (SM-D3) >gi_600750 (U15009) Sm D3 [Homo sapiens]

Seq. No.	159570
Seq. ID	LIB3176-112-P1-K1-H2
Method	BLASTN
NCBI GI	g3367500
BLAST score	208
E value	1.0e-113
Match length	208
% identity	100
NCBI Description	REVERSE-COMPLEMENT OF: F23J3.GCG.SEQ CHECK: 2754 FROM: 1 TO: 93489, complete sequence [Arabidopsis thaliana]

Seq. No.	159571
Seq. ID	LIB3176-112-P1-K1-H5
Method	BLASTX
NCBI GI	g3063472
BLAST score	438
E value	1.0e-43
Match length	86
% identity	95
NCBI Description	(AC003981) F22O13.34 [Arabidopsis thaliana]

Seq. No.	159572
Seq. ID	LIB3176-112-P1-K1-H6
Method	BLASTX
NCBI GI	g231683
BLAST score	506
E value	1.0e-51
Match length	94
% identity	97
NCBI Description	CALNEXIN HOMOLOG PRECURSOR >gi_421825_pir__JN0597 calnexin-like protein - Arabidopsis thaliana >gi_16211_emb_CAA79144_ (Z18242) calnexin homolog [Arabidopsis thaliana]

Seq. No.	159573
Seq. ID	LIB3176-113-P2-K1-A11
Method	BLASTN
NCBI GI	g4263694
BLAST score	132
E value	1.0e-68
Match length	132
% identity	100
NCBI Description	Arabidopsis thaliana chromosome II BAC F22D22 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	159574
Seq. ID	LIB3176-113-P2-K1-A12
Method	BLASTX
NCBI GI	g1621268
BLAST score	240
E value	2.0e-20
Match length	77
% identity	60
NCBI Description	(Z81012) unknown [Ricinus communis]

Seq. No.	159575
Seq. ID	LIB3176-113-P2-K1-A2
Method	BLASTX
NCBI GI	g2062161
BLAST score	375
E value	2.0e-36
Match length	78
% identity	46
NCBI Description	(AC001645) jasmonate inducible protein isolog [Arabidopsis thaliana]

Seq. No.	159576
Seq. ID	LIB3176-113-P2-K1-A5

Method	BLASTX
NCBI GI	g1170505
BLAST score	243
E value	1.0e-20
Match length	51
% identity	96
NCBI Description	EUKARYOTIC INITIATION FACTOR 4A-2 (EIF-4A-2) >gi_322504_pir__JC1453 translation initiation factor eIF-4A2 - Arabidopsis thaliana >gi_16556_emb_CAA46189_ (X65053) eukaryotic translation initiation factor 4A-2 [Arabidopsis thaliana] >gi_4585969_gb_AAD25605.1_AC005287_7 (AC005287) Eukaryotic Initiation Factor 4A-2 [Arabidopsis thaliana]

Seq. No.	159577
Seq. ID	LIB3176-113-P2-K1-A6
Method	BLASTN
NCBI GI	g3075383
BLAST score	52
E value	4.0e-21
Match length	60
% identity	97
NCBI Description	Arabidopsis thaliana chromosome II BAC T1D16 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	159578
Seq. ID	LIB3176-113-P2-K1-A7
Method	BLASTN
NCBI GI	g2828182
BLAST score	355
E value	0.0e+00
Match length	399
% identity	97
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MOJ9, complete sequence [Arabidopsis thaliana]

Seq. No.	159579
Seq. ID	LIB3176-113-P2-K1-A9
Method	BLASTX
NCBI GI	g2760839
BLAST score	226
E value	1.0e-18
Match length	109
% identity	45
NCBI Description	(AC003105) putative receptor kinase [Arabidopsis thaliana]

Seq. No.	159580
Seq. ID	LIB3176-113-P2-K1-B10
Method	BLASTX
NCBI GI	g1076366
BLAST score	664
E value	6.0e-70
Match length	125
% identity	99
NCBI Description	peptidylprolyl isomerase (EC 5.2.1.8) - Arabidopsis thaliana >gi_460968 (U07276) peptidyl-prolyl cis-trans isomerase [Arabidopsis thaliana] >gi_992643 (U32186)

cyclophilin [Arabidopsis thaliana]
>gi_1091580_prf__2021266A peptidyl-Pro cis-trans isomerase [Arabidopsis thaliana]

Seq. No.	159581
Seq. ID	LIB3176-113-P2-K1-B12
Method	BLASTN
NCBI GI	g2459406
BLAST score	123
E value	5.0e-63
Match length	166
% identity	93
NCBI Description	Arabidopsis thaliana chromosome II BAC F4P9 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	159582
Seq. ID	LIB3176-113-P2-K1-B2
Method	BLASTX
NCBI GI	g1769905
BLAST score	244
E value	6.0e-21
Match length	101
% identity	50
NCBI Description	(X98108) 23 kDa polypeptide of oxygen-evolving comlex (OEC) [Arabidopsis thaliana]

Seq. No.	159583
Seq. ID	LIB3176-113-P2-K1-B3
Method	BLASTN
NCBI GI	g4580744
BLAST score	76
E value	3.0e-35
Match length	92
% identity	49
NCBI Description	Sequence of BAC F15I1 from Arabidopsis thaliana chromosome 1, complete sequence

Seq. No.	159584
Seq. ID	LIB3176-113-P2-K1-B6
Method	BLASTN
NCBI GI	g2252823
BLAST score	120
E value	3.0e-61
Match length	162
% identity	98
NCBI Description	Arabidopsis thaliana BAC IG005I10

Seq. No.	159585
Seq. ID	LIB3176-113-P2-K1-B7
Method	BLASTX
NCBI GI	g2738248
BLAST score	261
E value	3.0e-23
Match length	57
% identity	93
NCBI Description	(U97200) cobalamin-independent methionine synthase [Arabidopsis thaliana]

Seq. No.	159586
Seq. ID	LIB3176-113-P2-K1-B8
Method	BLASTN
NCBI GI	g166767
BLAST score	54
E value	3.0e-22
Match length	80
% identity	91
NCBI Description	A.thaliana heat shock protein HSP70-3 gene, exon 1 (partial)

Seq. No.	159587
Seq. ID	LIB3176-113-P2-K1-B9
Method	BLASTX
NCBI GI	g2253291
BLAST score	166
E value	9.0e-12
Match length	33
% identity	97
NCBI Description	(AF006067) catalase-1 [Nicotiana glutinosa]

Seq. No.	159588
Seq. ID	LIB3176-113-P2-K1-C1
Method	BLASTX
NCBI GI	g3915037
BLAST score	320
E value	1.0e-33
Match length	97
% identity	76
NCBI Description	SUCROSE SYNTHASE 2 (SUCROSE-UDP GLUCOSYLTRANSFERASE 2) >gi_2570067_emb_CAA04512_ (AJ001071) second sucrose synthase [Pisum sativum]

Seq. No.	159589
Seq. ID	LIB3176-113-P2-K1-C10
Method	BLASTX
NCBI GI	g4539327
BLAST score	428
E value	2.0e-42
Match length	87
% identity	95
NCBI Description	(AL035679) putative proton pump [Arabidopsis thaliana]

Seq. No.	159590
Seq. ID	LIB3176-113-P2-K1-C11
Method	BLASTX
NCBI GI	g2829899
BLAST score	194
E value	8.0e-15
Match length	66
% identity	58
NCBI Description	(AC002311) similar to ripening-induced protein, gp_AJ001449_2465015 and major#latex protein, gp_X91961_1107495 [Arabidopsis thaliana]

Seq. No.	159591

Seq. ID	LIB3176-113-P2-K1-C12
Method	BLASTX
NCBI GI	g2961346
BLAST score	641
E value	3.0e-67
Match length	137
% identity	92
NCBI Description	(AL022140) pectinesterase like protein [Arabidopsis thaliana]

Seq. No.	159592
Seq. ID	LIB3176-113-P2-K1-C2
Method	BLASTX
NCBI GI	g2956760
BLAST score	225
E value	6.0e-19
Match length	74
% identity	35
NCBI Description	(AL022104) probable atp-dependent transporter [Schizosaccharomyces pombe]

Seq. No.	159593
Seq. ID	LIB3176-113-P2-K1-C4
Method	BLASTN
NCBI GI	g4432811
BLAST score	141
E value	7.0e-74
Match length	145
% identity	99
NCBI Description	Arabidopsis thaliana chromosome II BAC F16D14 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	159594
Seq. ID	LIB3176-113-P2-K1-C5
Method	BLASTX
NCBI GI	g131754
BLAST score	260
E value	1.0e-22
Match length	92
% identity	60
NCBI Description	PPLZ02 PROTEIN >gi_99973_pir__S11881 hypothetical protein (clone pPLZ2) - large-leaved lupine >gi_19507_emb_CAA36069_ (X51767) put. pPLZ2 product (AA 1-164) [Lupinus polyphyllus]

Seq. No.	159595
Seq. ID	LIB3176-113-P2-K1-C7
Method	BLASTX
NCBI GI	g4539327
BLAST score	814
E value	2.0e-87
Match length	157
% identity	99
NCBI Description	(AL035679) putative proton pump [Arabidopsis thaliana]

Seq. No.	159596
Seq. ID	LIB3176-113-P2-K1-C8

Method	BLASTX
NCBI GI	g2262165
BLAST score	413
E value	6.0e-46
Match length	104
% identity	92
NCBI Description	(AC002329) predicted protein of unknown function [Arabidopsis thaliana]

Seq. No.	159597
Seq. ID	LIB3176-113-P2-K1-C9
Method	BLASTX
NCBI GI	g4755193
BLAST score	545
E value	5.0e-56
Match length	113
% identity	96
NCBI Description	(AC007018) putative ribosomal protein S17 [Arabidopsis thaliana]

Seq. No.	159598
Seq. ID	LIB3176-113-P2-K1-D1
Method	BLASTX
NCBI GI	g115783
BLAST score	617
E value	2.0e-64
Match length	118
% identity	98
NCBI Description	CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR (CAB-140) (LHCP) >gi_16376_emb_CAA27543_ (X03909) chlorophyll a/b binding protein (LHCP AB 140) [Arabidopsis thaliana]

Seq. No.	159599
Seq. ID	LIB3176-113-P2-K1-D10
Method	BLASTN
NCBI GI	g3985931
BLAST score	127
E value	2.0e-65
Match length	151
% identity	97
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K21H1, complete sequence [Arabidopsis thaliana]

Seq. No.	159600
Seq. ID	LIB3176-113-P2-K1-D12
Method	BLASTX
NCBI GI	g4583546
BLAST score	470
E value	2.0e-47
Match length	98
% identity	97
NCBI Description	(AJ010819) GrpE protein [Arabidopsis thaliana]

Seq. No.	159601
Seq. ID	LIB3176-113-P2-K1-D4
Method	BLASTN

NCBI GI	g3236234
BLAST score	82
E value	2.0e-38
Match length	185
% identity	93
NCBI Description	Arabidopsis thaliana chromosome II BAC F13M22 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	159602
Seq. ID	LIB3176-113-P2-K1-D6
Method	BLASTX
NCBI GI	g3047125
BLAST score	459
E value	5.0e-46
Match length	92
% identity	95
NCBI Description	(AF058919) No definition line found [Arabidopsis thaliana]

Seq. No.	159603
Seq. ID	LIB3176-113-P2-K1-D8
Method	BLASTX
NCBI GI	g4406816
BLAST score	214
E value	9.0e-18
Match length	43
% identity	95
NCBI Description	(AC006201) 60S ribosomal protein L2 [Arabidopsis thaliana]

Seq. No.	159604
Seq. ID	LIB3176-113-P2-K1-D9
Method	BLASTX
NCBI GI	g625977
BLAST score	187
E value	1.0e-14
Match length	39
% identity	95
NCBI Description	p40 protein homolog - Arabidopsis thaliana >gi_402904 (U01955) laminin receptor-like protein [Arabidopsis thaliana]

Seq. No.	159605
Seq. ID	LIB3176-113-P2-K1-E11
Method	BLASTX
NCBI GI	g131381
BLAST score	330
E value	2.0e-31
Match length	66
% identity	98
NCBI Description	OXYGEN-EVOLVING ENHANCER PROTEIN 1 PRECURSOR (OEE1) (33 KD SUBUNIT OF OXYGEN EVOLVING SYSTEM OF PHOTOSYSTEM II) (33 KD THYLAKOID MEMBRANE PROTEIN) >gi_99745_pir__S11852 photosystem II oxygen-evolving complex protein 1 precursor - Arabidopsis thaliana >gi_22571_emb_CAA36675_ (X52428) 33 kDa oxygen-evolving protein [Arabidopsis thaliana]

Seq. No.	159606
Seq. ID	LIB3176-113-P2-K1-E2

Method	BLASTN
NCBI GI	g4835223
BLAST score	194
E value	1.0e-105
Match length	348
% identity	100
NCBI Description	Arabidopsis thaliana DNA chromosome 3, BAC clone F18B3 (ESSA project)

Seq. No.	159607
Seq. ID	LIB3176-113-P2-K1-E4
Method	BLASTN
NCBI GI	g4582444
BLAST score	45
E value	8.0e-17
Match length	73
% identity	90
NCBI Description	Arabidopsis thaliana chromosome II BAC T9H9 genomic sequence, complete sequence

Seq. No.	159608
Seq. ID	LIB3176-113-P2-K1-E5
Method	BLASTX
NCBI GI	g1871199
BLAST score	236
E value	1.0e-19
Match length	115
% identity	38
NCBI Description	(U91318) pM5 (3' partial) [Homo sapiens]

Seq. No.	159609
Seq. ID	LIB3176-113-P2-K1-E8
Method	BLASTX
NCBI GI	g232031
BLAST score	43
E value	5.0e-21
Match length	98
% identity	53
NCBI Description	ELONGATION FACTOR 1 BETA' >gi_322851_pir__S29224 translation elongation factor eEF-1 beta' chain - rice >gi_218161_dbj_BAA02253_ (D12821) elongation factor 1 beta' [Oryza sativa]

Seq. No.	159610
Seq. ID	LIB3176-113-P2-K1-F1
Method	BLASTN
NCBI GI	g3702731
BLAST score	295
E value	1.0e-165
Match length	299
% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MFC19, complete sequence [Arabidopsis thaliana]

Seq. No.	159611
Seq. ID	LIB3176-113-P2-K1-F10
Method	BLASTX

NCBI GI	g2224699
BLAST score	100
E value	9.0e-04
Match length	127
% identity	4
NCBI Description	(AB002377) KIAA0379 [Homo sapiens]

Seq. No.	159612
Seq. ID	LIB3176-113-P2-K1-F2
Method	BLASTX
NCBI GI	g266463
BLAST score	235
E value	3.0e-20
Match length	51
% identity	90
NCBI Description	3-ISOPROPYLMALATE DEHYDROGENASE PRECURSOR (BETA-IPM DEHYDROGENASE) (IMDH) (3-IPM-DH) >gi_82259_pir__S25670 3-isopropylmalate dehydrogenase (EC 1.1.1.85) precursor - potato >gi_22643_emb_CAA47720_ (X67310) 3-isopropylmalate dehydrogenase [Solanum tuberosum] >gi_445064_prf__1908380A beta isopropylmalate dehydrogenase [Solanum tuberosum]

Seq. No.	159613
Seq. ID	LIB3176-113-P2-K1-F7
Method	BLASTX
NCBI GI	g114421
BLAST score	527
E value	5.0e-54
Match length	108
% identity	97
NCBI Description	ATP SYNTHASE BETA CHAIN, MITOCHONDRIAL PRECURSOR >gi_82133_pir__A24355 H+-transporting ATP synthase (EC 3.6.1.34) beta-1 chain, mitochondrial - curled-leaved tobacco >gi_19685_emb_CAA26620_ (X02868) ATP synthase beta subunit [Nicotiana plumbaginifolia]

Seq. No.	159614
Seq. ID	LIB3176-113-P2-K1-F8
Method	BLASTN
NCBI GI	g4220627
BLAST score	37
E value	2.0e-11
Match length	148
% identity	4
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K20J1, complete sequence [Arabidopsis thaliana]

Seq. No.	159615
Seq. ID	LIB3176-113-P2-K1-G1
Method	BLASTN
NCBI GI	g2760167
BLAST score	61
E value	6.0e-26
Match length	121
% identity	95
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MCO15, complete sequence [Arabidopsis thaliana]

Seq. No.	159616
Seq. ID	LIB3176-113-P2-K1-G10
Method	BLASTX
NCBI GI	g4572674
BLAST score	736
E value	2.0e-78
Match length	132
% identity	100
NCBI Description	(AC006954) unknown protein [Arabidopsis thaliana]

Seq. No.	159617
Seq. ID	LIB3176-113-P2-K1-G11
Method	BLASTX
NCBI GI	g4056469
BLAST score	436
E value	3.0e-43
Match length	88
% identity	97
NCBI Description	(AC005990) Strong similarity to gb_M95166 ADP-ribosylation factor from Arabidopsis thaliana. ESTs gb_Z25826, gb_R90191, gb_N65697, gb_AA713150, gb_T46332, gb_AA040967, gb_AA712956, gb_T46403, gb_T46050, gb_AI100391 and gb_Z25043 come from t

Seq. No.	159618
Seq. ID	LIB3176-113-P2-K1-G2
Method	BLASTN
NCBI GI	g16316
BLAST score	178
E value	8.0e-96
Match length	190
% identity	98
NCBI Description	A.thaliana gene for histone H1-1

Seq. No.	159619
Seq. ID	LIB3176-113-P2-K1-G3
Method	BLASTX
NCBI GI	g131381
BLAST score	746
E value	2.0e-79
Match length	153
% identity	96
NCBI Description	OXYGEN-EVOLVING ENHANCER PROTEIN 1 PRECURSOR (OEE1) (33 KD SUBUNIT OF OXYGEN EVOLVING SYSTEM OF PHOTOSYSTEM II) (33 KD THYLAKOID MEMBRANE PROTEIN) >gi_99745_pir__S11852 photosystem II oxygen-evolving complex protein 1 precursor - Arabidopsis thaliana >gi_22571_emb_CAA36675_ (X52428) 33 kDa oxygen-evolving protein [Arabidopsis thaliana]

Seq. No.	159620
Seq. ID	LIB3176-113-P2-K1-G4
Method	BLASTX
NCBI GI	g2492952
BLAST score	259
E value	2.0e-22
Match length	56

% identity	89
NCBI Description	CHORISMATE SYNTHASE 1 PRECURSOR (5-ENOLPYRUVYLSHIKIMATE-3-PHOSPHATE PHOSPHOLYASE 1) >gi_542026_pir__S40410 chorismate synthase (EC 4.6.1.4) 1 precursor - tomato >gi_410482_emb_CAA79859_ (Z21796) chorismate synthase 1 [Lycopersicon esculentum]

Seq. No.	159621
Seq. ID	LIB3176-113-P2-K1-G5
Method	BLASTX
NCBI GI	g2492952
BLAST score	180
E value	9.0e-14
Match length	49
% identity	78
NCBI Description	CHORISMATE SYNTHASE 1 PRECURSOR (5-ENOLPYRUVYLSHIKIMATE-3-PHOSPHATE PHOSPHOLYASE 1) >gi_542026_pir__S40410 chorismate synthase (EC 4.6.1.4) 1 precursor - tomato >gi_410482_emb_CAA79859_ (Z21796) chorismate synthase 1 [Lycopersicon esculentum]

Seq. No.	159622
Seq. ID	LIB3176-113-P2-K1-G9
Method	BLASTX
NCBI GI	g3169185
BLAST score	289
E value	6.0e-26
Match length	70
% identity	79
NCBI Description	(AC004401) unknown protein [Arabidopsis thaliana]

Seq. No.	159623
Seq. ID	LIB3176-113-P2-K1-H10
Method	BLASTX
NCBI GI	g2911057
BLAST score	238
E value	1.0e-20
Match length	59
% identity	83
NCBI Description	(AL021961) caffeoyl-CoA O-methyltransferase - like protein [Arabidopsis thaliana]

Seq. No.	159624
Seq. ID	LIB3176-113-P2-K1-H11
Method	BLASTN
NCBI GI	g2760172
BLAST score	355
E value	0.0e+00
Match length	355
% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MUB3, complete sequence [Arabidopsis thaliana]

Seq. No.	159625
Seq. ID	LIB3176-113-P2-K1-H12
Method	BLASTX
NCBI GI	g2062163

BLAST score	220
E value	2.0e-18
Match length	46
% identity	89
NCBI Description	(AC001645) jasmonate inducible protein isolog [Arabidopsis thaliana]

Seq. No.	159626
Seq. ID	LIB3176-113-P2-K1-H2
Method	BLASTX
NCBI GI	g2924779
BLAST score	279
E value	2.0e-25
Match length	65
% identity	85
NCBI Description	(AC002334) putative 3-ketoacyl-CoA thiolase [Arabidopsis thaliana] >gi_2981616_dbj_BAA25248_ (AB008854) 3-ketoacyl-CoA thiolase [Arabidopsis thaliana] >gi_2981618_dbj_BAA25249_ (AB008855) 3-ketoacyl-CoA thiolase [Arabidopsis thaliana]

Seq. No.	159627
Seq. ID	LIB3176-113-P2-K1-H4
Method	BLASTX
NCBI GI	g3249100
BLAST score	602
E value	9.0e-63
Match length	114
% identity	98
NCBI Description	(AC003114) Match to calreticulin (AtCRTL) mRNA gb_U27698 and DNA gb_U66344. ESTs gb_T45719, gb_T22451, gb_H36323 and gb_AA042519 come from this gene. [Arabidopsis thaliana]

Seq. No.	159628
Seq. ID	LIB3176-113-P2-K1-H6
Method	BLASTX
NCBI GI	g2062163
BLAST score	216
E value	1.0e-17
Match length	43
% identity	93
NCBI Description	(AC001645) jasmonate inducible protein isolog [Arabidopsis thaliana]

Seq. No.	159629
Seq. ID	LIB3176-113-P2-K1-H7
Method	BLASTX
NCBI GI	g2129629
BLAST score	151
E value	2.0e-10
Match length	34
% identity	94
NCBI Description	L-ascorbate peroxidase (EC 1.11.1.11) - Arabidopsis thaliana >gi_1332439_emb_CAA66640_ (X98003) ascorbate peroxidase [Arabidopsis thaliana] >gi_1523791_emb_CAA66926_ (X98276) L-ascorbate peroxidase [Arabidopsis thaliana] >gi_2444019 (U69138) ascorbate peroxidase 3 [Arabidopsis

thaliana] >gi_2924511_emb_CAA17765.1_ (AL022023) L-ascorbate peroxidase [Arabidopsis thaliana]

Seq. No.	159630
Seq. ID	LIB3176-113-P2-K1-H8
Method	BLASTX
NCBI GI	g1669389
BLAST score	493
E value	4.0e-50
Match length	101
% identity	96
NCBI Description	(U42007) actin 8 [Arabidopsis thaliana]

Seq. No.	159631
Seq. ID	LIB3176-113-P2-K1-H9
Method	BLASTX
NCBI GI	g3236242
BLAST score	370
E value	2.0e-35
Match length	87
% identity	87
NCBI Description	(AC004684) putative ribosomal protein L36 [Arabidopsis thaliana]

Seq. No.	159632
Seq. ID	LIB3176-114-P2-K1-A1
Method	BLASTX
NCBI GI	g1175011
BLAST score	708
E value	5.0e-75
Match length	135
% identity	100
NCBI Description	PLASMA MEMBRANE INTRINSIC PROTEIN 1B (TRANSMEMBRANE PROTEIN A) (TMP-A) >gi_296085_emb_CAA48356_ (X68293) transmembrane protein [Arabidopsis thaliana] >gi_3386599 (AC004665) plasma membrane intrinsic protein 1B [Arabidopsis thaliana]

Seq. No.	159633
Seq. ID	LIB3176-114-P2-K1-A10
Method	BLASTX
NCBI GI	g4371282
BLAST score	604
E value	7.0e-63
Match length	121
% identity	100
NCBI Description	(AC006260) putative 60S ribosomal protein L12 [Arabidopsis thaliana]

Seq. No.	159634
Seq. ID	LIB3176-114-P2-K1-A11
Method	BLASTX
NCBI GI	g3983125
BLAST score	579
E value	6.0e-60
Match length	138
% identity	82
NCBI Description	(AF097648) phosphate/triose-phosphate translocator

precursor [Arabidopsis thaliana]

Seq. No.	159635
Seq. ID	LIB3176-114-P2-K1-A2
Method	BLASTX
NCBI GI	g120667
BLAST score	122
E value	3.0e-39
Match length	109
% identity	79
NCBI Description	GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE, CYTOSOLIC >gi_81622_pir__JQ1287 glyceraldehyde-3-phosphate dehydrogenase (EC 1.2.1.12), cytosolic - Arabidopsis thaliana >gi_166706 (M64116) cystolic glyceraldehyde-3-phosphate dehydrogenase [Arabidopsis thaliana] >gi_166710 (M64119) glyceraldehyde-3-phosphate dehydrogenase [Arabidopsis thaliana]

Seq. No.	159636
Seq. ID	LIB3176-114-P2-K1-A3
Method	BLASTN
NCBI GI	g2642427
BLAST score	240
E value	1.0e-132
Match length	346
% identity	96
NCBI Description	Arabidopsis thaliana chromosome II BAC T20D16 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	159637
Seq. ID	LIB3176-114-P2-K1-A4
Method	BLASTX
NCBI GI	g166570
BLAST score	197
E value	4.0e-15
Match length	130
% identity	36
NCBI Description	(L04173) glycine rich protein [Arabidopsis thaliana]

Seq. No.	159638
Seq. ID	LIB3176-114-P2-K1-A5
Method	BLASTN
NCBI GI	g2351068
BLAST score	294
E value	1.0e-164
Match length	420
% identity	99
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MRH10, complete sequence [Arabidopsis thaliana]

Seq. No.	159639
Seq. ID	LIB3176-114-P2-K1-A6
Method	BLASTX
NCBI GI	g4689316
BLAST score	593
E value	1.0e-61
Match length	119

% identity	43
NCBI Description	(AF130973) peroxisomal targeting signal type 2 receptor [Arabidopsis thaliana]

Seq. No.	159640
Seq. ID	LIB3176-114-P2-K1-A8
Method	BLASTX
NCBI GI	g1363489
BLAST score	617
E value	2.0e-64
Match length	123
% identity	93
NCBI Description	thioglucosidase (EC 3.2.3.1) 3D precursor - Arabidopsis thaliana >gi_984052_emb_CAA61592_ (X89413) thioglucoside glucohydrolase [Arabidopsis thaliana]

Seq. No.	159641
Seq. ID	LIB3176-114-P2-K1-A9
Method	BLASTX
NCBI GI	g4544399
BLAST score	272
E value	4.0e-24
Match length	103
% identity	51
NCBI Description	(AC007047) putative beta-ketoacyl-CoA synthase [Arabidopsis thaliana]

Seq. No.	159642
Seq. ID	LIB3176-114-P2-K1-B1
Method	BLASTX
NCBI GI	g1419388
BLAST score	353
E value	1.0e-33
Match length	120
% identity	60
NCBI Description	(X98925) stromal ascorbate peroxidase [Arabidopsis thaliana]

Seq. No.	159643
Seq. ID	LIB3176-114-P2-K1-B10
Method	BLASTX
NCBI GI	g3372671
BLAST score	42
E value	2.0e-18
Match length	83
% identity	72
NCBI Description	(AF061286) gamma-adaptin 1 [Arabidopsis thaliana] >gi_4704741_gb_AAD28247.1_AF124524_1 (AF124524) gamma-adaptin 1 [Arabidopsis thaliana]

Seq. No.	159644
Seq. ID	LIB3176-114-P2-K1-B11
Method	BLASTX
NCBI GI	g3273743
BLAST score	281
E value	2.0e-25
Match length	66

% identity	82
NCBI Description	(AF057357) lipid transfer protein 2 precursor [Arabidopsis thaliana] >gi_3786019 (AC005499) unknown protein [Arabidopsis thaliana]

Seq. No.	159645
Seq. ID	LIB3176-114-P2-K1-B12
Method	BLASTN
NCBI GI	g1657620
BLAST score	400
E value	0.0e+00
Match length	412
% identity	100
NCBI Description	Arabidopsis thaliana putative acyl-coA dehydrogenase G6p (AtG6) mRNA, complete cds

Seq. No.	159646
Seq. ID	LIB3176-114-P2-K1-B3
Method	BLASTX
NCBI GI	g99751
BLAST score	426
E value	5.0e-42
Match length	83
% identity	100
NCBI Description	phosphoprotein phosphatase (EC 3.1.3.16) 1A catalytic chain - Arabidopsis thaliana >gi_16433_emb_CAA78153_ (Z12163) protein phosphatase 1A [Arabidopsis thaliana]

Seq. No.	159647
Seq. ID	LIB3176-114-P2-K1-B4
Method	BLASTX
NCBI GI	g2494174
BLAST score	653
E value	1.0e-68
Match length	127
% identity	100
NCBI Description	GLUTAMATE DECARBOXYLASE 1 (GAD 1) >gi_497979 (U10034) glutamate decarboxylase [Arabidopsis thaliana]

Seq. No.	159648
Seq. ID	LIB3176-114-P2-K1-B5
Method	BLASTX
NCBI GI	g3273743
BLAST score	43
E value	1.0e-28
Match length	92
% identity	80
NCBI Description	(AF057357) lipid transfer protein 2 precursor [Arabidopsis thaliana] >gi_3786019 (AC005499) unknown protein [Arabidopsis thaliana]

Seq. No.	159649
Seq. ID	LIB3176-114-P2-K1-B6
Method	BLASTN
NCBI GI	g4263694
BLAST score	113
E value	1.0e-56

Match length	451
% identity	98
NCBI Description	Arabidopsis thaliana chromosome II BAC F22D22 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	159650
Seq. ID	LIB3176-114-P2-K1-B7
Method	BLASTN
NCBI GI	g2245073
BLAST score	366
E value	0.0e+00
Match length	370
% identity	100
NCBI Description	Arabidopsis thaliana DNA chromosome 4, ESSA I contig fragment No

Seq. No.	159651
Seq. ID	LIB3176-114-P2-K1-B8
Method	BLASTX
NCBI GI	g4049354
BLAST score	629
E value	8.0e-66
Match length	143
% identity	86
NCBI Description	(AL034567) glycine hydroxymethyltransferase (EC 2.1.2.1)-like protein [Arabidopsis thaliana]

Seq. No.	159652
Seq. ID	LIB3176-114-P2-K1-C1
Method	BLASTX
NCBI GI	g1363488
BLAST score	501
E value	9.0e-51
Match length	98
% identity	100
NCBI Description	IAA8 protein - Arabidopsis thaliana >gi_972919 (U18410) IAA8 [Arabidopsis thaliana] >gi_4314364_gb_AAD15575_ (AC006340) auxin-induced IAA8 protein [Arabidopsis thaliana]

Seq. No.	159653
Seq. ID	LIB3176-114-P2-K1-C10
Method	BLASTX
NCBI GI	g4490323
BLAST score	377
E value	3.0e-36
Match length	114
% identity	68
NCBI Description	(AJ131464) nitrate transporter [Arabidopsis thaliana]

Seq. No.	159654
Seq. ID	LIB3176-114-P2-K1-C11
Method	BLASTX
NCBI GI	g3421077
BLAST score	544
E value	7.0e-56
Match length	109

% identity	100
NCBI Description	(AF043521) 20S proteasome subunit PAC1 [Arabidopsis thaliana]

Seq. No.	159655
Seq. ID	LIB3176-114-P2-K1-C12
Method	BLASTN
NCBI GI	g4519190
BLAST score	222
E value	1.0e-121
Match length	449
% identity	98
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K6A12, complete sequence

Seq. No.	159656
Seq. ID	LIB3176-114-P2-K1-C2
Method	BLASTX
NCBI GI	g3978578
BLAST score	543
E value	1.0e-55
Match length	145
% identity	40
NCBI Description	(AB020528) Polygalacturonase inhibitor [Poncirus trifoliata]

Seq. No.	159657
Seq. ID	LIB3176-114-P2-K1-C3
Method	BLASTX
NCBI GI	g3269290
BLAST score	764
E value	1.0e-81
Match length	148
% identity	100
NCBI Description	(AL030978) putative receptor like kinase [Arabidopsis thaliana]

Seq. No.	159658
Seq. ID	LIB3176-114-P2-K1-C4
Method	BLASTX
NCBI GI	g1778095
BLAST score	419
E value	3.0e-41
Match length	123
% identity	69
NCBI Description	(U64903) putative sugar transporter; member of major facilitative superfamily; integral membrane protein [Beta vulgaris]

Seq. No.	159659
Seq. ID	LIB3176-114-P2-K1-C6
Method	BLASTX
NCBI GI	g3550519
BLAST score	528
E value	5.0e-54
Match length	141
% identity	68

NCBI Description	(AJ007630) oxygenase [Nicotiana tabacum]
Seq. No.	159660
Seq. ID	LIB3176-114-P2-K1-C7
Method	BLASTX
NCBI GI	g1550738
BLAST score	371
E value	1.0e-35
Match length	107
% identity	73
NCBI Description	(Y08061) endomembrane-associated protein [Arabidopsis thaliana] >gi_2982443_emb_CAA18251_ (AL022224) endomembrane-associated protein [Arabidopsis thaliana]
Seq. No.	159661
Seq. ID	LIB3176-114-P2-K1-C8
Method	BLASTX
NCBI GI	g4454468
BLAST score	481
E value	2.0e-48
Match length	145
% identity	65
NCBI Description	(AC006234) putative NADH dehydrogenase [Arabidopsis thaliana]
Seq. No.	159662
Seq. ID	LIB3176-114-P2-K1-C9
Method	BLASTN
NCBI GI	g2623294
BLAST score	145
E value	9.0e-76
Match length	383
% identity	97
NCBI Description	Arabidopsis thaliana chromosome II BAC T20B5 genomic sequence, complete sequence [Arabidopsis thaliana]
Seq. No.	159663
Seq. ID	LIB3176-114-P2-K1-D10
Method	BLASTX
NCBI GI	g99771
BLAST score	622
E value	6.0e-65
Match length	147
% identity	84
NCBI Description	ubiquitin 81-aa extension protein 1 - Arabidopsis thaliana >gi_166934 (J05539) ubiquitin extension protein (UBQ5) [Arabidopsis thaliana]
Seq. No.	159664
Seq. ID	LIB3176-114-P2-K1-D11
Method	BLASTX
NCBI GI	g132110
BLAST score	731
E value	9.0e-78
Match length	139
% identity	99
NCBI Description	RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN 3B PRECURSOR

	(RUBISCO SMALL SUBUNIT 3B) >gi_68060_pir__RKMUB3 ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain B3 precursor - Arabidopsis thaliana >gi_16195_emb_CAA32702_ (X14564) ribulose bisphosphate carboxylase [Arabidopsis thaliana]
Seq. No.	159665
Seq. ID	LIB3176-114-P2-K1-D12
Method	BLASTX
NCBI GI	g4006883
BLAST score	390
E value	5.0e-38
Match length	88
% identity	84
NCBI Description	(Z99707) cysteine proteinase [Arabidopsis thaliana]
Seq. No.	159666
Seq. ID	LIB3176-114-P2-K1-D2
Method	BLASTX
NCBI GI	g2191155
BLAST score	166
E value	2.0e-11
Match length	124
% identity	35
NCBI Description	(AF007269) contains weak similarity with bacterial SECA proteins. [Arabidopsis thaliana]
Seq. No.	159667
Seq. ID	LIB3176-114-P2-K1-D3
Method	BLASTN
NCBI GI	g3805755
BLAST score	223
E value	1.0e-122
Match length	259
% identity	97
NCBI Description	Arabidopsis thaliana chromosome II BAC T25N22 genomic sequence, complete sequence [Arabidopsis thaliana]
Seq. No.	159668
Seq. ID	LIB3176-114-P2-K1-D4
Method	BLASTX
NCBI GI	g3212877
BLAST score	678
E value	2.0e-71
Match length	149
% identity	91
NCBI Description	(AC004005) Lea-like protein [Arabidopsis thaliana]
Seq. No.	159669
Seq. ID	LIB3176-114-P2-K1-D5
Method	BLASTX
NCBI GI	g2924779
BLAST score	650
E value	3.0e-68
Match length	128
% identity	100
NCBI Description	(AC002334) putative 3-ketoacyl-CoA thiolase [Arabidopsis

thaliana] >gi_2981616_dbj_BAA25248_ (AB008854) 3-ketoacyl-CoA thiolase [Arabidopsis thaliana] >gi_2981618_dbj_BAA25249_ (AB008855) 3-ketoacyl-CoA thiolase [Arabidopsis thaliana]

Seq. No.	159670
Seq. ID	LIB3176-114-P2-K1-D6
Method	BLASTX
NCBI GI	g267069
BLAST score	664
E value	7.0e-70
Match length	123
% identity	100
NCBI Description	TUBULIN ALPHA-2/ALPHA-4 CHAIN >gi_320183_pir__JQ1594 tubulin alpha chain - Arabidopsis thaliana >gi_166914 (M84696) apha-2 tubulin [Arabidopsis thaliana] >gi_166916 (M84697) alpha-4 tubulin [Arabidopsis thaliana]

Seq. No.	159671
Seq. ID	LIB3176-114-P2-K1-D8
Method	BLASTX
NCBI GI	g1814424
BLAST score	409
E value	4.0e-40
Match length	117
% identity	67
NCBI Description	(U85254) homeodomain protein AHDP [Arabidopsis thaliana]

Seq. No.	159672
Seq. ID	LIB3176-114-P2-K1-D9
Method	BLASTX
NCBI GI	g4454039
BLAST score	458
E value	9.0e-46
Match length	146
% identity	60
NCBI Description	(AL035394) putative Na+/H+-exchanging protein [Arabidopsis thaliana]

Seq. No.	159673
Seq. ID	LIB3176-114-P2-K1-E1
Method	BLASTX
NCBI GI	g3242075
BLAST score	535
E value	9.0e-55
Match length	105
% identity	99
NCBI Description	(Z97059) S-adenosyl-L-homocysteine hydrolase [Arabidopsis thaliana]

Seq. No.	159674
Seq. ID	LIB3176-114-P2-K1-E10
Method	BLASTX
NCBI GI	g2062161
BLAST score	283
E value	9.0e-26
Match length	60

% identity	92
NCBI Description	(AC001645) jasmonate inducible protein isolog [Arabidopsis thaliana]
Seq. No.	159675
Seq. ID	LIB3176-114-P2-K1-E12
Method	BLASTX
NCBI GI	g4262236
BLAST score	231
E value	3.0e-19
Match length	86
% identity	58
NCBI Description	(AC006200) putative ribose 5-phosphate isomerase [Arabidopsis thaliana]
Seq. No.	159676
Seq. ID	LIB3176-114-P2-K1-E2
Method	BLASTX
NCBI GI	g2446981
BLAST score	729
E value	2.0e-77
Match length	142
% identity	99
NCBI Description	(AB005560) AtGDI2 [Arabidopsis thaliana] >gi_2569936_emb_CAA04727_ (AJ001397) GDI2 [Arabidopsis thaliana]
Seq. No.	159677
Seq. ID	LIB3176-114-P2-K1-E3
Method	BLASTN
NCBI GI	g3869075
BLAST score	275
E value	1.0e-153
Match length	451
% identity	98
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MXK3, complete sequence [Arabidopsis thaliana]
Seq. No.	159678
Seq. ID	LIB3176-114-P2-K1-E4
Method	BLASTX
NCBI GI	g4512707
BLAST score	535
E value	9.0e-55
Match length	117
% identity	89
NCBI Description	(AC006569) hypothetical protein [Arabidopsis thaliana]
Seq. No.	159679
Seq. ID	LIB3176-114-P2-K1-E5
Method	BLASTN
NCBI GI	g3420043
BLAST score	363
E value	0.0e+00
Match length	411
% identity	96
NCBI Description	Arabidopsis thaliana chromosome II BAC F23F1 genomic

sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	159680
Seq. ID	LIB3176-114-P2-K1-E6
Method	BLASTX
NCBI GI	g3953473
BLAST score	611
E value	1.0e-63
Match length	128
% identity	96
NCBI Description	(AC002328) F22O2.18 [Arabidopsis thaliana]

Seq. No.	159681
Seq. ID	LIB3176-114-P2-K1-E8
Method	BLASTX
NCBI GI	g3176676
BLAST score	53
E value	4.0e-40
Match length	85
% identity	100
NCBI Description	(AC003671) Similar to carbonic anhydrase gb_L19255 from Nicotiana tabacum. ESTs gb_AA597643, gb_T45390, gb_T43963 and gb_AA597734 come from this gene. [Arabidopsis thaliana]

Seq. No.	159682
Seq. ID	LIB3176-114-P2-K1-F1
Method	BLASTX
NCBI GI	g2605761
BLAST score	717
E value	4.0e-76
Match length	150
% identity	92
NCBI Description	(AF027284) NADH dehydrogenase [Tectona grandis]

Seq. No.	159683
Seq. ID	LIB3176-114-P2-K1-F10
Method	BLASTN
NCBI GI	g2564050
BLAST score	353
E value	0.0e+00
Match length	365
% identity	99
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MUA22, complete sequence [Arabidopsis thaliana]

Seq. No.	159684
Seq. ID	LIB3176-114-P2-K1-F11
Method	BLASTN
NCBI GI	g2689438
BLAST score	69
E value	1.0e-30
Match length	134
% identity	91
NCBI Description	Arabidopsis thaliana BAC F24O1 chromosome 1, complete sequence [Arabidopsis thaliana]

Seq. No.	159685

Seq. ID	LIB3176-114-P2-K1-F12
Method	BLASTX
NCBI GI	g132102
BLAST score	700
E value	4.0e-74
Match length	132
% identity	98
NCBI Description	RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN 2B PRECURSOR (RUBISCO SMALL SUBUNIT 2B) >gi_68061_pir__RKMUB2 ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain B2 precursor - Arabidopsis thaliana >gi_16194_emb_CAA32701_ (X14564) ribulose bisphosphate carboxylase [Arabidopsis thaliana]

Seq. No.	159686
Seq. ID	LIB3176-114-P2-K1-F2
Method	BLASTX
NCBI GI	g4581108
BLAST score	298
E value	3.0e-27
Match length	142
% identity	49
NCBI Description	(AC005825) putative chloroplast outer membrane protein 86,also very similar to GTP-inding protein from pea (GB:L36857) [Arabidopsis thaliana]

Seq. No.	159687
Seq. ID	LIB3176-114-P2-K1-F4
Method	BLASTN
NCBI GI	g4376087
BLAST score	245
E value	1.0e-135
Match length	320
% identity	95
NCBI Description	Arabidopsis thaliana DNA chromosome 4, ESSA I AP2 contig fragment No

Seq. No.	159688
Seq. ID	LIB3176-114-P2-K1-F5
Method	BLASTX
NCBI GI	g2246456
BLAST score	720
E value	2.0e-76
Match length	138
% identity	99
NCBI Description	(U71400) S-adenosyl-methionine-sterol-C-methyltransferase [Arabidopsis thaliana]

Seq. No.	159689
Seq. ID	LIB3176-114-P2-K1-F6
Method	BLASTX
NCBI GI	g113171
BLAST score	383
E value	4.0e-37
Match length	89
% identity	92
NCBI Description	ACYL CARRIER PROTEIN 1 PRECURSOR (ACP)

>gi_81596_pir__S03267 acyl carrier protein precursor - Arabidopsis thaliana >gi_16152_emb_CAA31991_ (X13708) acyl carrier protein [Arabidopsis thaliana]

Seq. No.	159690
Seq. ID	LIB3176-114-P2-K1-F8
Method	BLASTN
NCBI GI	g4206764
BLAST score	432
E value	0.0e+00
Match length	436
% identity	100
NCBI Description	Arabidopsis thaliana putative type 1 membrane protein (PMP) mRNA, complete cds

Seq. No.	159691
Seq. ID	LIB3176-114-P2-K1-F9
Method	BLASTX
NCBI GI	g2191155
BLAST score	179
E value	5.0e-13
Match length	97
% identity	44
NCBI Description	(AF007269) contains weak similarity with bacterial SECA proteins. [Arabidopsis thaliana]

Seq. No.	159692
Seq. ID	LIB3176-114-P2-K1-G1
Method	BLASTX
NCBI GI	g1766046
BLAST score	490
E value	3.0e-54
Match length	114
% identity	99
NCBI Description	(U81993) NAD+ dependent isocitrate dehydrogenase subunit 1 [Arabidopsis thaliana]

Seq. No.	159693
Seq. ID	LIB3176-114-P2-K1-G10
Method	BLASTX
NCBI GI	g4741954
BLAST score	470
E value	2.0e-47
Match length	102
% identity	88
NCBI Description	(AF134127) Lhcb4.2 protein [Arabidopsis thaliana]

Seq. No.	159694
Seq. ID	LIB3176-114-P2-K1-G11
Method	BLASTX
NCBI GI	g3122724
BLAST score	347
E value	5.0e-33
Match length	69
% identity	99
NCBI Description	60S RIBOSOMAL PROTEIN L38 >gi_2289009 (AC002335) ribosomal protein L38 isolog [Arabidopsis thaliana]

Seq. No.	159695
Seq. ID	LIB3176-114-P2-K1-G12
Method	BLASTX
NCBI GI	g231660
BLAST score	69
E value	4.0e-16
Match length	92
% identity	60
NCBI Description	HYPOTHETICAL 226 KD PROTEIN (ORF 1901)

Seq. No.	159696
Seq. ID	LIB3176-114-P2-K1-G2
Method	BLASTX
NCBI GI	g2160142
BLAST score	493
E value	8.0e-50
Match length	122
% identity	83
NCBI Description	(AC000375) Strong similarity to Arabidopsis APR2 (gb_U56921). [Arabidopsis thaliana] >gi_2738758 (AF016283) 5'-adenylylsulfate reductase [Arabidopsis thaliana]

Seq. No.	159697
Seq. ID	LIB3176-114-P2-K1-G3
Method	BLASTN
NCBI GI	g3980374
BLAST score	192
E value	1.0e-104
Match length	355
% identity	100
NCBI Description	Arabidopsis thaliana chromosome II BAC F16P2 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	159698
Seq. ID	LIB3176-114-P2-K1-G4
Method	BLASTN
NCBI GI	g3980374
BLAST score	134
E value	3.0e-69
Match length	230
% identity	90
NCBI Description	Arabidopsis thaliana chromosome II BAC F16P2 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	159699
Seq. ID	LIB3176-114-P2-K1-G5
Method	BLASTX
NCBI GI	g729102
BLAST score	606
E value	3.0e-63
Match length	120
% identity	99
NCBI Description	CHALCONE--FLAVONONE ISOMERASE >gi_320138_pir__JQ1687 chalcone isomerase (EC 5.5.1.6) - Arabidopsis thaliana >gi_166660_gb_AAA32766.1_ (M86358) chalcone isomerase [Arabidopsis thaliana]

Seq. No.	159700
Seq. ID	LIB3176-114-P2-K1-G6
Method	BLASTX
NCBI GI	g1363489
BLAST score	693
E value	3.0e-73
Match length	129
% identity	98
NCBI Description	thioglucosidase (EC 3.2.3.1) 3D precursor - Arabidopsis thaliana >gi_984052_emb_CAA61592_ (X89413) thioglucoside glucohydrolase [Arabidopsis thaliana]

Seq. No.	159701
Seq. ID	LIB3176-114-P2-K1-G7
Method	BLASTX
NCBI GI	g2160142
BLAST score	469
E value	5.0e-47
Match length	94
% identity	100
NCBI Description	(AC000375) Strong similarity to Arabidopsis APR2 (gb_U56921). [Arabidopsis thaliana] >gi_2738758 (AF016283) 5'-adenylylsulfate reductase [Arabidopsis thaliana]

Seq. No.	159702
Seq. ID	LIB3176-114-P2-K1-G8
Method	BLASTN
NCBI GI	g4220635
BLAST score	48
E value	8.0e-19
Match length	59
% identity	97
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MDB19, complete sequence [Arabidopsis thaliana]

Seq. No.	159703
Seq. ID	LIB3176-114-P2-K1-G9
Method	BLASTX
NCBI GI	g1916290
BLAST score	149
E value	2.0e-09
Match length	68
% identity	50
NCBI Description	(U89876) ALY [Mus musculus]

Seq. No.	159704
Seq. ID	LIB3176-114-P2-K1-H11
Method	BLASTX
NCBI GI	g4103987
BLAST score	565
E value	3.0e-58
Match length	136
% identity	79
NCBI Description	(AF030516) 5,10-methylenetetrahydrofolate dehydrogenase-5,10-methenyltetrahydrofolate cyclohydrolase [Pisum sativum]

Seq. No.	159705
Seq. ID	LIB3176-114-P2-K1-H12
Method	BLASTX
NCBI GI	g3377797
BLAST score	571
E value	6.0e-59
Match length	140
% identity	80
NCBI Description	(AF075597) Similar to 60S ribosome protein L19; coded for by A. thaliana cDNA T04719; coded for by A. thaliana cDNA H36046; coded for by A. thaliana cDNA T44067; coded for by A. thaliana cDNA T14056; coded for by A. thaliana cDNA R90691 [Ara

Seq. No.	159706
Seq. ID	LIB3176-114-P2-K1-H2
Method	BLASTN
NCBI GI	g1732569
BLAST score	38
E value	7.0e-12
Match length	98
% identity	90
NCBI Description	Arabidopsis thaliana beta-glucosidase (psr3.1) mRNA, complete cds

Seq. No.	159707
Seq. ID	LIB3176-114-P2-K1-H3
Method	BLASTX
NCBI GI	g2088662
BLAST score	597
E value	4.0e-62
Match length	138
% identity	85
NCBI Description	(AF002109) unknown protein [Arabidopsis thaliana]

Seq. No.	159708
Seq. ID	LIB3176-114-P2-K1-H4
Method	BLASTX
NCBI GI	g832876
BLAST score	386
E value	2.0e-37
Match length	122
% identity	64
NCBI Description	(L41345) ascorbate free radical reductase [Solanum lycopersicum] >gi_1097368_prf__2113407A ascorbate free radical reductase [Lycopersicon esculentum]

Seq. No.	159709
Seq. ID	LIB3176-114-P2-K1-H5
Method	BLASTN
NCBI GI	g4733953
BLAST score	341
E value	0.0e+00
Match length	426
% identity	99
NCBI Description	Arabidopsis thaliana chromosome I BAC F13O11 genomic

sequence, complete sequence

Seq. No.	159710
Seq. ID	LIB3176-114-P2-K1-H6
Method	BLASTX
NCBI GI	g1172568
BLAST score	228
E value	1.0e-18
Match length	86
% identity	55
NCBI Description	LOW MOLECULAR WEIGHT PHOSPHOTYROSINE PROTEIN PHOSPHATASE (LOW MOLECULAR WEIGHT CYTOSOLIC ACID PHOSPHATASE) (PTPASE) (SMALL TYROSINE PHOSPHATASE) >gi_1076916_pir__A55446 protein-tyrosine-phosphatase (EC 3.1.3.48), low molecular weight - fission yeast (Schizosaccharomyces pombe) >gi_602992 (L33929) low Mr protein tyrosine phosphatase [Schizosaccharomyces pombe]

Seq. No.	159711
Seq. ID	LIB3176-114-P2-K1-H7
Method	BLASTX
NCBI GI	g4580394
BLAST score	273
E value	1.0e-24
Match length	75
% identity	72
NCBI Description	(AC007171) putative fatty acid elongase [Arabidopsis thaliana]

Seq. No.	159712
Seq. ID	LIB3176-114-P2-K1-H8
Method	BLASTN
NCBI GI	g4589436
BLAST score	47
E value	3.0e-17
Match length	247
% identity	85
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MPA22, complete sequence

Seq. No.	159713
Seq. ID	LIB3176-114-P2-K1-H9
Method	BLASTN
NCBI GI	g4589436
BLAST score	43
E value	7.0e-15
Match length	103
% identity	85
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MPA22, complete sequence

Seq. No.	159714
Seq. ID	LIB3176-115-P2-K1-A1
Method	BLASTX
NCBI GI	g115783
BLAST score	625
E value	2.0e-65

Match length	119
% identity	100
NCBI Description	CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR (CAB-140) (LHCP) >gi_16376_emb_CAA27543_ (X03909) chlorophyll a/b binding protein (LHCP AB 140) [Arabidopsis thaliana]

Seq. No.	159715
Seq. ID	LIB3176-115-P2-K1-A11
Method	BLASTX
NCBI GI	g1173187
BLAST score	607
E value	3.0e-63
Match length	124
% identity	94
NCBI Description	40S RIBOSOMAL PROTEIN S23 (S12) >gi_1362041_pir__S56673 ribosomal protein S23.e, cytosolic (clone RJ3) - garden strawberry >gi_643074 (U19940) putative 40S ribosomal protein s12 [Fragaria x ananassa]

Seq. No.	159716
Seq. ID	LIB3176-115-P2-K1-A12
Method	BLASTX
NCBI GI	g3785989
BLAST score	642
E value	3.0e-67
Match length	134
% identity	89
NCBI Description	(AC005560) unknown protein [Arabidopsis thaliana]

Seq. No.	159717
Seq. ID	LIB3176-115-P2-K1-A3
Method	BLASTX
NCBI GI	g2982463
BLAST score	669
E value	2.0e-70
Match length	141
% identity	87
NCBI Description	(AL022223) putative protein [Arabidopsis thaliana]

Seq. No.	159718
Seq. ID	LIB3176-115-P2-K1-A4
Method	BLASTX
NCBI GI	g113024
BLAST score	543
E value	8.0e-56
Match length	125
% identity	90
NCBI Description	ISOCITRATE LYASE (ISOCITRASE) (ISOCITRATASE) (ICL) >gi_553043 (M83534) isocitrate lyase [Arabidopsis thaliana]

Seq. No.	159719
Seq. ID	LIB3176-115-P2-K1-A5
Method	BLASTN
NCBI GI	g3241925
BLAST score	444
E value	0.0e+00

Match length	456
% identity	99
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MOK9, complete sequence [Arabidopsis thaliana]

Seq. No.	159720
Seq. ID	LIB3176-115-P2-K1-A6
Method	BLASTX
NCBI GI	g1363489
BLAST score	708
E value	5.0e-75
Match length	147
% identity	90
NCBI Description	thioglucosidase (EC 3.2.3.1) 3D precursor - Arabidopsis thaliana >gi_984052_emb_CAA61592_ (X89413) thioglucoside glucohydrolase [Arabidopsis thaliana]

Seq. No.	159721
Seq. ID	LIB3176-115-P2-K1-A7
Method	BLASTN
NCBI GI	g3869072
BLAST score	51
E value	5.0e-20
Match length	79
% identity	91
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MJB24, complete sequence [Arabidopsis thaliana]

Seq. No.	159722
Seq. ID	LIB3176-115-P2-K1-B10
Method	BLASTX
NCBI GI	g2827559
BLAST score	265
E value	5.0e-23
Match length	67
% identity	79
NCBI Description	(AL021635) predicted protein [Arabidopsis thaliana] >gi_3292808_emb_CAA19798_ (AL031018) putative protein [Arabidopsis thaliana]

Seq. No.	159723
Seq. ID	LIB3176-115-P2-K1-B2
Method	BLASTX
NCBI GI	g3023848
BLAST score	635
E value	2.0e-66
Match length	136
% identity	32
NCBI Description	GUANINE NUCLEOTIDE-BINDING PROTEIN BETA SUBUNIT-LIKE PROTEIN (WD-40 REPEAT AUXIN-DEPENDENT PROTEIN ARCA) >gi_2289095 (U77381) WD-40 repeat protein [Arabidopsis thaliana]

Seq. No.	159724
Seq. ID	LIB3176-115-P2-K1-B3
Method	BLASTX
NCBI GI	g115783

BLAST score	254
E value	3.0e-22
Match length	61
% identity	85
NCBI Description	CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR (CAB-140) (LHCP) >gi_16376_emb_CAA27543_ (X03909) chlorophyll a/b binding protein (LHCP AB 140) [Arabidopsis thaliana]

Seq. No.	159725
Seq. ID	LIB3176-115-P2-K1-B4
Method	BLASTX
NCBI GI	g2119846
BLAST score	631
E value	4.0e-66
Match length	119
% identity	100
NCBI Description	chlorophyll a/b-binding protein type I precursor Lhb1B2 - Arabidopsis thaliana >gi_16364_emb_CAA45790_ (X64460) photosystem II type I chlorophyll a /b binding protein [Arabidopsis thaliana] >gi_3128230 (AC004077) photosystem II type I chlorophyll a/b binding protein [Arabidopsis thaliana] >gi_3337371 (AC004481) photosystem II type I chlorophyll a/b binding protein [Arabidopsis thaliana]

Seq. No.	159726
Seq. ID	LIB3176-115-P2-K1-B5
Method	BLASTX
NCBI GI	g2529665
BLAST score	606
E value	5.0e-63
Match length	145
% identity	84
NCBI Description	(AC002535) putative ribosomal protein L7A [Arabidopsis thaliana]

Seq. No.	159727
Seq. ID	LIB3176-115-P2-K1-B6
Method	BLASTX
NCBI GI	g1170939
BLAST score	489
E value	2.0e-49
Match length	102
% identity	91
NCBI Description	S-ADENOSYLMETHIONINE SYNTHETASE 3 (METHIONINE ADENOSYLTRANSFERASE 3) (ADOMET SYNTHETASE 3) >gi_1084408_pir__S46540 methionine adenosyltransferase (EC 2.5.1.6) - tomato >gi_429108_emb_CAA80867_ (Z24743) S-adenosyl-L-methionine synthetase [Lycopersicon esculentum]

Seq. No.	159728
Seq. ID	LIB3176-115-P2-K1-B7
Method	BLASTX
NCBI GI	g730645
BLAST score	595
E value	8.0e-62

Match length	130
% identity	92
NCBI Description	40S RIBOSOMAL PROTEIN S15 >gi_629556_pir__S43412 ribosomal protein S15 - Arabidopsis thaliana >gi_313152_emb_CAA80679_ (Z23161) ribosomal protein S15 [Arabidopsis thaliana] >gi_313188_emb_CAA80681_ (Z23162) ribosomal protein S15 [Arabidopsis thaliana] >gi_1903366_gb_AAB70449_ (AC000104) Strong similarity to Oryza 40S ribosomal protein S15. ESTs gb_R29788,gb_ATTS0365 come from this gene. [Arabidopsis thaliana]

Seq. No.	159729
Seq. ID	LIB3176-115-P2-K1-B8
Method	BLASTX
NCBI GI	g4741966
BLAST score	414
E value	2.0e-40
Match length	131
% identity	66
NCBI Description	(AF134133) Lil3 protein [Arabidopsis thaliana]

Seq. No.	159730
Seq. ID	LIB3176-115-P2-K1-B9
Method	BLASTX
NCBI GI	g3004560
BLAST score	586
E value	1.0e-60
Match length	149
% identity	81
NCBI Description	(AC003673) putative ATP binding protein [Arabidopsis thaliana]

Seq. No.	159731
Seq. ID	LIB3176-115-P2-K1-C1
Method	BLASTX
NCBI GI	g4544434
BLAST score	641
E value	4.0e-67
Match length	126
% identity	99
NCBI Description	(AC006955) putative DNA-directed RNA polymerase II [Arabidopsis thaliana]

Seq. No.	159732
Seq. ID	LIB3176-115-P2-K1-C10
Method	BLASTX
NCBI GI	g3377797
BLAST score	595
E value	8.0e-62
Match length	144
% identity	81
NCBI Description	(AF075597) Similar to 60S ribosome protein L19; coded for by A. thaliana cDNA T04719; coded for by A. thaliana cDNA H36046; coded for by A. thaliana cDNA T44067; coded for by A. thaliana cDNA T14056; coded for by A. thaliana cDNA R90691 [Ara

Seq. No.	159733
Seq. ID	LIB3176-115-P2-K1-C12
Method	BLASTN
NCBI GI	g3650026
BLAST score	215
E value	1.0e-117
Match length	355
% identity	99
NCBI Description	Arabidopsis thaliana chromosome II BAC T26I20 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	159734
Seq. ID	LIB3176-115-P2-K1-C4
Method	BLASTN
NCBI GI	g3241923
BLAST score	194
E value	1.0e-105
Match length	225
% identity	97
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MMN10, complete sequence [Arabidopsis thaliana]

Seq. No.	159735
Seq. ID	LIB3176-115-P2-K1-C5
Method	BLASTX
NCBI GI	g1561730
BLAST score	153
E value	6.0e-10
Match length	58
% identity	47
NCBI Description	(U65491) Dreg-3 protein [Drosophila melanogaster]

Seq. No.	159736
Seq. ID	LIB3176-115-P2-K1-C7
Method	BLASTX
NCBI GI	g1922242
BLAST score	339
E value	9.0e-32
Match length	68
% identity	100
NCBI Description	(Y10084) hypothetical protein [Arabidopsis thaliana]

Seq. No.	159737
Seq. ID	LIB3176-115-P2-K1-C8
Method	BLASTN
NCBI GI	g4159706
BLAST score	457
E value	0.0e+00
Match length	477
% identity	99
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MGL6, complete sequence

Seq. No.	159738
Seq. ID	LIB3176-115-P2-K1-C9
Method	BLASTN
NCBI GI	g4159706

BLAST score	140
E value	1.0e-72
Match length	216
% identity	94
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MGL6, complete sequence

Seq. No.	159739
Seq. ID	LIB3176-115-P2-K1-D1
Method	BLASTX
NCBI GI	g3024022
BLAST score	625
E value	3.0e-65
Match length	142
% identity	83
NCBI Description	INITIATION FACTOR 5A-5 (EIF-5A) (EIF-4D) >gi_2225885_dbj_BAA20879_ (AB004826) eukaryotic initiation factor 5A5 [Solanum tuberosum]

Seq. No.	159740
Seq. ID	LIB3176-115-P2-K1-D11
Method	BLASTX
NCBI GI	g3334124
BLAST score	626
E value	2.0e-65
Match length	127
% identity	99
NCBI Description	ATP SYNTHASE DELTA CHAIN, MITOCHONDRIAL PRECURSOR (OLIGOMYCIN SENSITIVITY CONFERRAL PROTEIN) (OSCP) >gi_1655482_dbj_BAA13600_ (D88375) delta subunit of mitochondrial F1-ATPase [Arabidopsis thaliana]

Seq. No.	159741
Seq. ID	LIB3176-115-P2-K1-D12
Method	BLASTN
NCBI GI	g4662609
BLAST score	251
E value	1.0e-139
Match length	467
% identity	99
NCBI Description	Genomic sequence for Arabidopsis thaliana BAC F10A5, complete sequence

Seq. No.	159742
Seq. ID	LIB3176-115-P2-K1-D2
Method	BLASTX
NCBI GI	g1546692
BLAST score	812
E value	4.0e-87
Match length	160
% identity	98
NCBI Description	(X98805) peroxidase ATP19a [Arabidopsis thaliana]

Seq. No.	159743
Seq. ID	LIB3176-115-P2-K1-D3
Method	BLASTN
NCBI GI	g2656031

BLAST score	164
E value	5.0e-87
Match length	332
% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MXC20

Seq. No.	159744
Seq. ID	LIB3176-115-P2-K1-D4
Method	BLASTX
NCBI GI	g3334404
BLAST score	775
E value	7.0e-83
Match length	155
% identity	99
NCBI Description	VACUOLAR ATP SYNTHASE CATALYTIC SUBUNIT A (V-ATPASE 69 KD SUBUNIT) >gi_2266990 (U65638) vacuolar type ATPase subunit A [Arabidopsis thaliana] >gi_3834305 (AC005679) Identical to gb_U65638 Arabidopsis thaliana vacuolar type ATPase subunit A mRNA. ESTs gb_N96435, gb_N96106, gb_N96189, gb_N96091, gb_AA042286, gb_F14324, gb_W43643, gb_N96027, gb_N96299, gb_R29943, gb_T43460, gb_T43544, gb_T22472

Seq. No.	159745
Seq. ID	LIB3176-115-P2-K1-D5
Method	BLASTX
NCBI GI	g3309086
BLAST score	420
E value	3.0e-41
Match length	83
% identity	99
NCBI Description	(AF076253) calcineurin B-like protein 3 [Arabidopsis thaliana]

Seq. No.	159746
Seq. ID	LIB3176-115-P2-K1-D6
Method	BLASTX
NCBI GI	g4544369
BLAST score	243
E value	2.0e-20
Match length	154
% identity	39
NCBI Description	(AC006920) hypothetical protein [Arabidopsis thaliana]

Seq. No.	159747
Seq. ID	LIB3176-115-P2-K1-D8
Method	BLASTX
NCBI GI	g2642429
BLAST score	453
E value	4.0e-45
Match length	103
% identity	29
NCBI Description	(AC002391) putative poly(A)-binding protein [Arabidopsis thaliana]

Seq. No.	159748
Seq. ID	LIB3176-115-P2-K1-D9

Method	BLASTX
NCBI GI	g1498053
BLAST score	570
E value	8.0e-59
Match length	159
% identity	72
NCBI Description	(U64436) ribosomal protein S8 [Zea mays]

Seq. No.	159749
Seq. ID	LIB3176-115-P2-K1-E1
Method	BLASTX
NCBI GI	g3122038
BLAST score	273
E value	5.0e-24
Match length	112
% identity	50
NCBI Description	DIHYDROPYRIMIDINASE RELATED PROTEIN-3 (DRP-3) (COLLAPSIN RESPONSE MEDIATOR PROTEIN 4) (CRMP-4) >gi_1399542 (U52104) rCRMP-4 [Rattus norvegicus]

Seq. No.	159750
Seq. ID	LIB3176-115-P2-K1-E2
Method	BLASTX
NCBI GI	g4539458
BLAST score	177
E value	1.0e-12
Match length	169
% identity	30
NCBI Description	(AL049500) hypothetical protein [Arabidopsis thaliana]

Seq. No.	159751
Seq. ID	LIB3176-115-P2-K1-E3
Method	BLASTN
NCBI GI	g2828182
BLAST score	82
E value	4.0e-38
Match length	324
% identity	95
NCBI Description	Arabidopsis thaliana genomic DNA; chromosome 5, P1 clone: MOJ9, complete sequence [Arabidopsis thaliana]

Seq. No.	159752
Seq. ID	LIB3176-115-P2-K1-E4
Method	BLASTX
NCBI GI	g2961343
BLAST score	470
E value	4.0e-47
Match length	96
% identity	97
NCBI Description	(AL022140) symbiosis-related like protein [Arabidopsis thaliana]

Seq. No.	159753
Seq. ID	LIB3176-115-P2-K1-E5
Method	BLASTX
NCBI GI	g2760843
BLAST score	473

E value	2.0e-47
Match length	98
% identity	54
NCBI Description	(AC003105) unknown protein [Arabidopsis thaliana]

Seq. No.	159754
Seq. ID	LIB3176-115-P2-K1-E6
Method	BLASTX
NCBI GI	g1546696
BLAST score	459
E value	9.0e-46
Match length	90
% identity	98
NCBI Description	(X98807) peroxidase ATP21a [Arabidopsis thaliana]

Seq. No.	159755
Seq. ID	LIB3176-115-P2-K1-E7
Method	BLASTX
NCBI GI	g1175011
BLAST score	643
E value	2.0e-67
Match length	126
% identity	97
NCBI Description	PLASMA MEMBRANE INTRINSIC PROTEIN 1B (TRANSMEMBRANE PROTEIN A) (TMP-A) >gi_296085_emb_CAA48356_ (X68293) transmembrane protein [Arabidopsis thaliana] >gi_3386599 (AC004665) plasma membrane intrinsic protein 1B [Arabidopsis thaliana]

Seq. No.	159756
Seq. ID	LIB3176-115-P2-K1-F1
Method	BLASTX
NCBI GI	g1169476
BLAST score	717
E value	4.0e-76
Match length	137
% identity	100
NCBI Description	ELONGATION FACTOR 1-ALPHA (EF-1-ALPHA) (VITRONECTIN-LIKE ADHESION PROTEIN 1) (PVN1) >gi_439577 (U04632) vitronectin-like adhesion protein [Nicotiana tabacum]

Seq. No.	159757
Seq. ID	LIB3176-115-P2-K1-F10
Method	BLASTN
NCBI GI	g4760369
BLAST score	60
E value	3.0e-25
Match length	112
% identity	88
NCBI Description	Arabidopsis thaliana ATP dependent copper transporter (RAN1) mRNA, complete cds

Seq. No.	159758
Seq. ID	LIB3176-115-P2-K1-F11
Method	BLASTN
NCBI GI	g21142
BLAST score	36
E value	2.0e-11

Match length	52
% identity	92
NCBI Description	Mustard mRNA for cytosolic glyceraldehyde-3-phosphate dehydrogenase (GAPDH, NAD-specific; EC 1.2.1.12)

Seq. No.	159759
Seq. ID	LIB3176-115-P2-K1-F12
Method	BLASTX
NCBI GI	g4510424
BLAST score	203
E value	2.0e-58
Match length	123
% identity	98
NCBI Description	(AC006929) putative carboxypeptidase [Arabidopsis thaliana]

Seq. No.	159760
Seq. ID	LIB3176-115-P2-K1-F2
Method	BLASTX
NCBI GI	g3915847
BLAST score	718
E value	3.0e-76
Match length	149
% identity	93
NCBI Description	40S RIBOSOMAL PROTEIN S2 >gi_2335095 (AC002339) putative 40S ribosomal protein S2 [Arabidopsis thaliana]

Seq. No.	159761
Seq. ID	LIB3176-115-P2-K1-F3
Method	BLASTX
NCBI GI	g3915847
BLAST score	54
E value	1.0e-08
Match length	66
% identity	61
NCBI Description	40S RIBOSOMAL PROTEIN S2 >gi_2335095 (AC002339) putative 40S ribosomal protein S2 [Arabidopsis thaliana]

Seq. No.	159762
Seq. ID	LIB3176-115-P2-K1-F4
Method	BLASTX
NCBI GI	g2443755
BLAST score	679
E value	1.0e-71
Match length	147
% identity	84
NCBI Description	(AF020433) cyclophilin [Arabidopsis thaliana]

Seq. No.	159763
Seq. ID	LIB3176-115-P2-K1-F5
Method	BLASTX
NCBI GI	g2443755
BLAST score	398
E value	5.0e-39
Match length	92
% identity	79
NCBI Description	(AF020433) cyclophilin [Arabidopsis thaliana]

Seq. No.	159764
Seq. ID	LIB3176-115-P2-K1-F7
Method	BLASTX
NCBI GI	g2342687
BLAST score	76
E value	2.0e-16
Match length	73
% identity	58
NCBI Description	(AC000106) Similar to Beta integral membrane protein (gb_U43629). EST gb_W43122 comes from this gene. [Arabidopsis thaliana]

Seq. No.	159765
Seq. ID	LIB3176-115-P2-K1-F9
Method	BLASTX
NCBI GI	g1695717
BLAST score	679
E value	1.0e-71
Match length	138
% identity	98
NCBI Description	(D89341) luminal binding protein [Arabidopsis thaliana]

Seq. No.	159766
Seq. ID	LIB3176-115-P2-K1-G1
Method	BLASTN
NCBI GI	g2351062
BLAST score	278
E value	1.0e-155
Match length	428
% identity	99
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MAH20, complete sequence [Arabidopsis thaliana]

Seq. No.	159767
Seq. ID	LIB3176-115-P2-K1-G11
Method	BLASTX
NCBI GI	g3122673
BLAST score	693
E value	3.0e-73
Match length	151
% identity	89
NCBI Description	60S RIBOSOMAL PROTEIN L15 >gi_2245027_emb_CAB10447_ (Z97341) ribosomal protein [Arabidopsis thaliana]

Seq. No.	159768
Seq. ID	LIB3176-115-P2-K1-G12
Method	BLASTX
NCBI GI	g3128228
BLAST score	817
E value	9.0e-88
Match length	157
% identity	98
NCBI Description	(AC004077) putative ribosomal protein L18A [Arabidopsis thaliana] >gi_3337376 (AC004481) putative ribosomal protein L18A [Arabidopsis thaliana]

Seq. No.	159769

Seq. ID	LIB3176-115-P2-K1-G2
Method	BLASTX
NCBI GI	g1750376
BLAST score	60
E value	4.0e-70
Match length	150
% identity	54
NCBI Description	(U80808) ubiquitin activating enzyme [Arabidopsis thaliana] >gi_3150409 (AC004165) ubiquitin activating enzyme (UBA1) [Arabidopsis thaliana]

Seq. No.	159770
Seq. ID	LIB3176-115-P2-K1-G3
Method	BLASTX
NCBI GI	g4337027
BLAST score	746
E value	2.0e-79
Match length	151
% identity	99
NCBI Description	(AF123254) MFP2 [Arabidopsis thaliana]

Seq. No.	159771
Seq. ID	LIB3176-115-P2-K1-G4
Method	BLASTX
NCBI GI	g3319350
BLAST score	841
E value	2.0e-90
Match length	169
% identity	98
NCBI Description	(AF077407) No definition line found [Arabidopsis thaliana]

Seq. No.	159772
Seq. ID	LIB3176-115-P2-K1-G5
Method	BLASTX
NCBI GI	g3851636
BLAST score	565
E value	3.0e-58
Match length	140
% identity	75
NCBI Description	(AF098519) unknown [Avicennia marina] >gi_4128206 (AF056316) 40S ribosome protein S7 [Avicennia marina]

Seq. No.	159773
Seq. ID	LIB3176-115-P2-K1-G7
Method	BLASTX
NCBI GI	g2827141
BLAST score	694
E value	2.0e-73
Match length	149
% identity	88
NCBI Description	(AF027173) cellulose synthase catalytic subunit [Arabidopsis thaliana]

Seq. No.	159774
Seq. ID	LIB3176-115-P2-K1-G8
Method	BLASTX
NCBI GI	g2827141

BLAST score	551
E value	1.0e-56
Match length	117
% identity	90
NCBI Description	(AF027173) cellulose synthase catalytic subunit [Arabidopsis thaliana]

Seq. No.	159775
Seq. ID	LIB3176-115-P2-K1-H1
Method	BLASTN
NCBI GI	g3702728
BLAST score	155
E value	1.0e-81
Match length	450
% identity	78
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K19M13, complete sequence [Arabidopsis thaliana]

Seq. No.	159776
Seq. ID	LIB3176-115-P2-K1-H10
Method	BLASTX
NCBI GI	g3738092
BLAST score	93
E value	4.0e-60
Match length	130
% identity	90
NCBI Description	(AC005617) similar to glyoxysomal malate dehydrogenase [Arabidopsis thaliana]

Seq. No.	159777
Seq. ID	LIB3176-115-P2-K1-H11
Method	BLASTN
NCBI GI	g3413696
BLAST score	208
E value	1.0e-113
Match length	288
% identity	77
NCBI Description	Arabidopsis thaliana chromosome II BAC T19L18 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	159778
Seq. ID	LIB3176-115-P2-K1-H2
Method	BLASTX
NCBI GI	g3068704
BLAST score	680
E value	8.0e-72
Match length	136
% identity	98
NCBI Description	(AF049236) unknown [Arabidopsis thaliana]

Seq. No.	159779
Seq. ID	LIB3176-115-P2-K1-H3
Method	BLASTN
NCBI GI	g2245073
BLAST score	316
E value	1.0e-177
Match length	465

% identity	100
NCBI Description	Arabidopsis thaliana DNA chromosome 4, ESSA I contig fragment No

Seq. No.	159780
Seq. ID	LIB3176-115-P2-K1-H4
Method	BLASTX
NCBI GI	g2494299
BLAST score	253
E value	1.0e-21
Match length	129
% identity	47
NCBI Description	EUKARYOTIC TRANSLATION INITIATION FACTOR 2 BETA SUBUNIT (EIF-2-BETA) >gi_1732361 (U80269) translation initiation factor 2 beta [Malus domestica]

Seq. No.	159781
Seq. ID	LIB3176-115-P2-K1-H5
Method	BLASTN
NCBI GI	g3108024
BLAST score	34
E value	1.0e-09
Match length	42
% identity	95
NCBI Description	Arabidopsis thaliana chromosome 1 BAC T1F15 sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	159782
Seq. ID	LIB3176-115-P2-K1-H6
Method	BLASTN
NCBI GI	g2760167
BLAST score	246
E value	1.0e-136
Match length	369
% identity	98
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MCO15, complete sequence [Arabidopsis thaliana]

Seq. No.	159783
Seq. ID	LIB3176-115-P2-K1-H7
Method	BLASTX
NCBI GI	g1916290
BLAST score	188
E value	4.0e-14
Match length	78
% identity	53
NCBI Description	(U89876) ALY [Mus musculus]

Seq. No.	159784
Seq. ID	LIB3176-115-P2-K1-H8
Method	BLASTX
NCBI GI	g1916290
BLAST score	185
E value	1.0e-13
Match length	79
% identity	52
NCBI Description	(U89876) ALY [Mus musculus]

Seq. No.	159785
Seq. ID	LIB3176-115-P2-K1-H9
Method	BLASTX
NCBI GI	g2462748
BLAST score	566
E value	2.0e-58
Match length	110
% identity	100
NCBI Description	(AC002292) putative Clathrin Coat Assembly protein [Arabidopsis thaliana]

Seq. No.	159786
Seq. ID	LIB3176-116-P2-K1-A11
Method	BLASTX
NCBI GI	g1173187
BLAST score	571
E value	4.0e-59
Match length	115
% identity	95
NCBI Description	40S RIBOSOMAL PROTEIN S23 (S12) >gi_1362041_pir__S56673 ribosomal protein S23.e, cytosolic (clone RJ3) - garden strawberry >gi_643074 (U19940) putative 40S ribosomal protein s12 [Fragaria x ananassa]

Seq. No.	159787
Seq. ID	LIB3176-116-P2-K1-A3
Method	BLASTX
NCBI GI	g4056469
BLAST score	569
E value	1.0e-58
Match length	112
% identity	99
NCBI Description	(AC005990) Strong similarity to gb_M95166 ADP-ribosylation factor from Arabidopsis thaliana. ESTs gb_Z25826, gb_R90191, gb_N65697, gb_AA713150, gb_T46332, gb_AA040967, gb_AA712956, gb_T46403, gb_T46050, gb_AI100391 and gb_Z25043 come from t

Seq. No.	159788
Seq. ID	LIB3176-116-P2-K1-A4
Method	BLASTX
NCBI GI	g1363489
BLAST score	688
E value	1.0e-72
Match length	127
% identity	99
NCBI Description	thioglucosidase (EC 3.2.3.1) 3D precursor - Arabidopsis thaliana >gi_984052_emb_CAA61592_ (X89413) thioglucoside glucohydrolase [Arabidopsis thaliana]

Seq. No.	159789
Seq. ID	LIB3176-116-P2-K1-A5
Method	BLASTX
NCBI GI	g2244750
BLAST score	642
E value	2.0e-67

Match length	128
% identity	96
NCBI Description	(Z97335) adenosylhomocysteinase [Arabidopsis thaliana] >gi_3088579 (AF059581) S-adenosyl-L-homocysteine hydrolase [Arabidopsis thaliana]

Seq. No.	159790
Seq. ID	LIB3176-116-P2-K1-A7
Method	BLASTX
NCBI GI	g2160168
BLAST score	311
E value	2.0e-28
Match length	83
% identity	67
NCBI Description	(AC000132) Strong similarity to R. communis phosphoglycerate mutase (gb_X70652). ESTs gb_T41853,gb_T76648 come from this gene. [Arabidopsis thaliana]

Seq. No.	159791
Seq. ID	LIB3176-116-P2-K1-A8
Method	BLASTX
NCBI GI	g2854182
BLAST score	156
E value	3.0e-10
Match length	110
% identity	30
NCBI Description	(AF045644) similar to the ARF family of ATP-binding proteins [Caenorhabditis elegans]

Seq. No.	159792
Seq. ID	LIB3176-116-P2-K1-A9
Method	BLASTX
NCBI GI	g4324967
BLAST score	510
E value	7.0e-52
Match length	109
% identity	91
NCBI Description	(AF114796) ADP-ribosylation factor [Glycine max]

Seq. No.	159793
Seq. ID	LIB3176-116-P2-K1-B1
Method	BLASTX
NCBI GI	g131770
BLAST score	275
E value	2.0e-24
Match length	83
% identity	61
NCBI Description	40S RIBOSOMAL PROTEIN S9 (40S RIBOSOMAL PROTEIN 1024) (VEGETATIVE SPECIFIC PROTEIN V12) >gi_70880_pir__R3DO24 ribosomal protein S9.e - slime mold (Dictyostelium discoideum) >gi_7353_emb_CAA29844_ (X06636) rp1024 protein [Dictyostelium discoideum]

Seq. No.	159794
Seq. ID	LIB3176-116-P2-K1-B11
Method	BLASTX

NCBI GI	g4105262
BLAST score	142
E value	3.0e-09
Match length	28
% identity	96
NCBI Description	(AF044573) actin [Brassica oleracea]

Seq. No.	159795
Seq. ID	LIB3176-116-P2-K1-B12
Method	BLASTX
NCBI GI	g1669389
BLAST score	344
E value	1.0e-32
Match length	74
% identity	88
NCBI Description	(U42007) actin 8 [Arabidopsis thaliana]

Seq. No.	159796
Seq. ID	LIB3176-116-P2-K1-B2
Method	BLASTX
NCBI GI	g4193388
BLAST score	327
E value	2.0e-30
Match length	94
% identity	68
NCBI Description	(AF091455) translationally controlled tumor protein [Hevea brasiliensis]

Seq. No.	159797
Seq. ID	LIB3176-116-P2-K1-B3
Method	BLASTN
NCBI GI	g2924505
BLAST score	223
E value	1.0e-122
Match length	416
% identity	100
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone M4E13 (ESSAII project)

Seq. No.	159798
Seq. ID	LIB3176-116-P2-K1-B5
Method	BLASTX
NCBI GI	g4105262
BLAST score	168
E value	2.0e-12
Match length	33
% identity	97
NCBI Description	(AF044573) actin [Brassica oleracea]

Seq. No.	159799
Seq. ID	LIB3176-116-P2-K1-B6
Method	BLASTN
NCBI GI	g4220640
BLAST score	158
E value	1.0e-83
Match length	348
% identity	100

NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MPE11, complete sequence [Arabidopsis thaliana]
Seq. No.	159800
Seq. ID	LIB3176-116-P2-K1-B7
Method	BLASTN
NCBI GI	g3193282
BLAST score	59
E value	8.0e-25
Match length	171
% identity	81
NCBI Description	Arabidopsis thaliana BAC T14P8
Seq. No.	159801
Seq. ID	LIB3176-116-P2-K1-B8
Method	BLASTX
NCBI GI	g1351014
BLAST score	451
E value	5.0e-45
Match length	107
% identity	83
NCBI Description	40S RIBOSOMAL PROTEIN S8 >gi_968902_dbj_BAA07207_ (D38010) ribosomal protein S8 [Oryza sativa]
Seq. No.	159802
Seq. ID	LIB3176-116-P2-K1-C1
Method	BLASTX
NCBI GI	g4646218
BLAST score	351
E value	4.0e-33
Match length	155
% identity	52
NCBI Description	(AC007290) putative GTP-binding protein [Arabidopsis thaliana]
Seq. No.	159803
Seq. ID	LIB3176-116-P2-K1-C10
Method	BLASTX
NCBI GI	g127045
BLAST score	664
E value	7.0e-70
Match length	125
% identity	100
NCBI Description	S-ADENOSYLMETHIONINE SYNTHETASE 2 (METHIONINE ADENOSYLTRANSFERASE 2) (ADOMET SYNTHETASE 2) >gi_99756_pir__JQ0410 methionine adenosyltransferase (EC 2.5.1.6) 2 - Arabidopsis thaliana >gi_166874 (M33217) S-adenosylmethionine synthetase (sam-2) [Arabidopsis thaliana] >gi_4558554_gb_AAD22647.1_AC007138_11 (AC007138) S-adenosylmethionine synthase 2 [Arabidopsis thaliana]
Seq. No.	159804
Seq. ID	LIB3176-116-P2-K1-C11
Method	BLASTX
NCBI GI	g4544408
BLAST score	561
E value	8.0e-58

Match length	108
% identity	98
NCBI Description	(AC006955) unknown protein [Arabidopsis thaliana]

Seq. No.	159805
Seq. ID	LIB3176-116-P2-K1-C2
Method	BLASTN
NCBI GI	g4757410
BLAST score	470
E value	0.0e+00
Match length	478
% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MVE11, complete sequence

Seq. No.	159806
Seq. ID	LIB3176-116-P2-K1-C3
Method	BLASTX
NCBI GI	g3335340
BLAST score	378
E value	2.0e-36
Match length	88
% identity	81
NCBI Description	(AC004512) Strong similarity to xylglucan endo-transglycolsylase (TCH4) gene gb_U27609, first exon contains strong similarity to meri 5 gene gb_Z17989 from A. thaliana. EST gb_N37583 comes from this gene. [Arabidopsis thaliana]

Seq. No.	159807
Seq. ID	LIB3176-116-P2-K1-C7
Method	BLASTX
NCBI GI	g120675
BLAST score	444
E value	3.0e-44
Match length	91
% identity	92
NCBI Description	GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE, CYTOSOLIC >gi_66011_pir__DEIS3C glyceraldehyde-3-phosphate dehydrogenase (EC 1.2.1.12), cytosolic - white mustard >gi_21143_emb_CAA27844_ (X04301) GAPDH (aa 1-338) [Sinapis alba]

Seq. No.	159808
Seq. ID	LIB3176-116-P2-K1-C8
Method	BLASTX
NCBI GI	g120667
BLAST score	281
E value	3.0e-25
Match length	69
% identity	81
NCBI Description	GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE, CYTOSOLIC >gi_81622_pir__JQ1287 glyceraldehyde-3-phosphate dehydrogenase (EC 1.2.1.12), cytosolic - Arabidopsis thaliana >gi_166706 (M64116) cystolic glyceraldehyde-3-phosphate dehydrogenase [Arabidopsis thaliana] >gi_166710 (M64119) glyceraldehyde-3-phosphate

dehydrogenase [Arabidopsis thaliana]

Seq. No.	159809
Seq. ID	LIB3176-116-P2-K1-C9
Method	BLASTX
NCBI GI	g4580394
BLAST score	274
E value	3.0e-24
Match length	127
% identity	43
NCBI Description	(AC007171) putative fatty acid elongase [Arabidopsis thaliana]

Seq. No.	159810
Seq. ID	LIB3176-116-P2-K1-D1
Method	BLASTX
NCBI GI	g2982262
BLAST score	384
E value	4.0e-37
Match length	131
% identity	56
NCBI Description	(AF051214) probable glutathione S-transferase [Picea mariana]

Seq. No.	159811
Seq. ID	LIB3176-116-P2-K1-D10
Method	BLASTX
NCBI GI	g2129774
BLAST score	733
E value	5.0e-78
Match length	136
% identity	98
NCBI Description	xyloglucan endotransglycosylase-related protein XTR4 - Arabidopsis thaliana (fragment) >gi_1244754 (U43486) xyloglucan endotransglycosylase-related protein [Arabidopsis thaliana]

Seq. No.	159812
Seq. ID	LIB3176-116-P2-K1-D7
Method	BLASTX
NCBI GI	g4263712
BLAST score	391
E value	5.0e-38
Match length	104
% identity	75
NCBI Description	(AC006223) putative ribosomal protein S12 [Arabidopsis thaliana]

Seq. No.	159813
Seq. ID	LIB3176-116-P2-K1-E1
Method	BLASTN
NCBI GI	g4678291
BLAST score	167
E value	6.0e-89
Match length	339
% identity	100
NCBI Description	Arabidopsis thaliana DNA chromosome 3, BAC clone F28P10

(ESSA project)

Seq. No.	159814
Seq. ID	LIB3176-116-P2-K1-E10
Method	BLASTX
NCBI GI	g3128228
BLAST score	780
E value	2.0e-83
Match length	149
% identity	99
NCBI Description	(AC004077) putative ribosomal protein L18A [Arabidopsis thaliana] >gi_3337376 (AC004481) putative ribosomal protein L18A [Arabidopsis thaliana]

Seq. No.	159815
Seq. ID	LIB3176-116-P2-K1-E11
Method	BLASTX
NCBI GI	g4006934
BLAST score	569
E value	7.0e-59
Match length	108
% identity	99
NCBI Description	(AJ012571) glutathione transferase [Arabidopsis thaliana]

Seq. No.	159816
Seq. ID	LIB3176-116-P2-K1-E2
Method	BLASTX
NCBI GI	g3341685
BLAST score	306
E value	6.0e-28
Match length	87
% identity	70
NCBI Description	(AC003672) unknown protein [Arabidopsis thaliana]

Seq. No.	159817
Seq. ID	LIB3176-116-P2-K1-E3
Method	BLASTX
NCBI GI	g2459420
BLAST score	692
E value	3.0e-73
Match length	137
% identity	98
NCBI Description	(AC002332) putative ribosomal protein L17 [Arabidopsis thaliana]

Seq. No.	159818
Seq. ID	LIB3176-116-P2-K1-E4
Method	BLASTX
NCBI GI	g2062158
BLAST score	50
E value	2.0e-30
Match length	100
% identity	42
NCBI Description	(AC001645) jasmonate inducible protein isolog [Arabidopsis thaliana]

Seq. No. 159819

Seq. ID	LIB3176-116-P2-K1-E5
Method	BLASTN
NCBI GI	g4539353
BLAST score	387
E value	0.0e+00
Match length	411
% identity	98
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F25I24 (ESSA project)

Seq. No.	159820
Seq. ID	LIB3176-116-P2-K1-E6
Method	BLASTX
NCBI GI	g2911057
BLAST score	634
E value	2.0e-66
Match length	137
% identity	91
NCBI Description	(AL021961) caffeoyl-CoA O-methyltransferase - like protein [Arabidopsis thaliana]

Seq. No.	159821
Seq. ID	LIB3176-116-P2-K1-E7
Method	BLASTN
NCBI GI	g2264317
BLAST score	240
E value	1.0e-132
Match length	252
% identity	99
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MUG13, complete sequence [Arabidopsis thaliana]

Seq. No.	159822
Seq. ID	LIB3176-116-P2-K1-E8
Method	BLASTX
NCBI GI	g444340
BLAST score	579
E value	4.0e-60
Match length	106
% identity	98
NCBI Description	catalase [Arabidopsis thaliana]

Seq. No.	159823
Seq. ID	LIB3176-116-P2-K1-E9
Method	BLASTX
NCBI GI	g4587552
BLAST score	460
E value	5.0e-46
Match length	90
% identity	99
NCBI Description	(AC006577) Strong similarity to gb_S77096 aldehyde dehydrogenase homolog from Brassica napus and is a member of PF_00171 Aldehyde dehydrogenase family. ESTs gb_T46213, gb_T42164, gb_T43682, gb_N96380, gb_T42973, gb

Seq. No.	159824
Seq. ID	LIB3176-116-P2-K1-F10

Method	BLASTX
NCBI GI	g2369714
BLAST score	434
E value	1.0e-45
Match length	115
% identity	89
NCBI Description	(Z97178) elongation factor 2 [Beta vulgaris]

Seq. No.	159825
Seq. ID	LIB3176-116-P2-K1-F11
Method	BLASTN
NCBI GI	g2645198
BLAST score	262
E value	1.0e-145
Match length	440
% identity	99
NCBI Description	Arabidopsis thaliana chromosome I BAC T26J12 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	159826
Seq. ID	LIB3176-116-P2-K1-F12
Method	BLASTN
NCBI GI	g4732169
BLAST score	259
E value	1.0e-144
Match length	365
% identity	99
NCBI Description	Arabidopsis thaliana BAC T3E15

Seq. No.	159827
Seq. ID	LIB3176-116-P2-K1-F2
Method	BLASTN
NCBI GI	g2829274
BLAST score	199
E value	1.0e-108
Match length	231
% identity	97
NCBI Description	Arabidopsis thaliana nucleoside diphosphate kinase 3 (ndpk3) mRNA, complete cds

Seq. No.	159828
Seq. ID	LIB3176-116-P2-K1-F3
Method	BLASTX
NCBI GI	g3319354
BLAST score	51
E value	5.0e-45
Match length	125
% identity	80
NCBI Description	(AF077407) contains similarity to sugar transporters (Pfam: sugar_tr.hmm, score: 395.39) [Arabidopsis thaliana]

Seq. No.	159829
Seq. ID	LIB3176-116-P2-K1-F4
Method	BLASTX
NCBI GI	g2911057
BLAST score	198
E value	2.0e-15

Match length	67
% identity	67
NCBI Description	(AL021961) caffeoyl-CoA O-methyltransferase - like protein [Arabidopsis thaliana]

Seq. No.	159830
Seq. ID	LIB3176-116-P2-K1-F6
Method	BLASTX
NCBI GI	g2262167
BLAST score	726
E value	3.0e-77
Match length	141
% identity	99
NCBI Description	(AC002329) cytosolic ribosomal protein S4 [Arabidopsis thaliana]

Seq. No.	159831
Seq. ID	LIB3176-116-P2-K1-F8
Method	BLASTX
NCBI GI	g114421
BLAST score	420
E value	1.0e-41
Match length	88
% identity	94
NCBI Description	ATP SYNTHASE BETA CHAIN, MITOCHONDRIAL PRECURSOR >gi_82133_pir__A24355 H+-transporting ATP synthase (EC 3.6.1.34) beta-1 chain, mitochondrial - curled-leaved tobacco >gi_19685_emb_CAA26620_ (X02868) ATP synthase beta subunit [Nicotiana plumbaginifolia]

Seq. No.	159832
Seq. ID	LIB3176-116-P2-K1-F9
Method	BLASTN
NCBI GI	g2924733
BLAST score	40
E value	2.0e-13
Match length	63
% identity	90
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MUF9, complete sequence [Arabidopsis thaliana]

Seq. No.	159833
Seq. ID	LIB3176-116-P2-K1-G1
Method	BLASTX
NCBI GI	g3738261
BLAST score	177
E value	8.0e-14
Match length	101
% identity	56
NCBI Description	(AB018412) chloroplast phosphoglycerate kinase [Populus nigra]

Seq. No.	159834
Seq. ID	LIB3176-116-P2-K1-G11
Method	BLASTN
NCBI GI	g4584339
BLAST score	218

E value	1.0e-119
Match length	403
% identity	100
NCBI Description	Arabidopsis thaliana chromosome II BAC T23A1 genomic sequence, complete sequence

Seq. No.	159835
Seq. ID	LIB3176-116-P2-K1-G2
Method	BLASTX
NCBI GI	g4218120
BLAST score	397
E value	1.0e-38
Match length	135
% identity	61
NCBI Description	(AL035353) Proline-rich APG-like protein [Arabidopsis thaliana]

Seq. No.	159836
Seq. ID	LIB3176-116-P2-K1-G3
Method	BLASTN
NCBI GI	g2262155
BLAST score	49
E value	1.0e-18
Match length	68
% identity	93
NCBI Description	DNA sequence of Arabidopsis thaliana BAC F5J6 from chromosome IV, complete sequence [Arabidopsis thaliana]

Seq. No.	159837
Seq. ID	LIB3176-116-P2-K1-G4
Method	BLASTX
NCBI GI	g1041825
BLAST score	147
E value	3.0e-09
Match length	145
% identity	27
NCBI Description	(U26175) LPG2 [Leishmania donovani] >gi_1583457_prf__2120442A LPG2 gene [Leishmania donovani]

Seq. No.	159838
Seq. ID	LIB3176-116-P2-K1-G5
Method	BLASTN
NCBI GI	g4063735
BLAST score	215
E value	1.0e-118
Match length	251
% identity	96
NCBI Description	Arabidopsis thaliana BAC F18G18 from chromosome V near 60.5 cM, complete sequence [Arabidopsis thaliana]

Seq. No.	159839
Seq. ID	LIB3176-116-P2-K1-G6
Method	BLASTX
NCBI GI	g2119846
BLAST score	767
E value	6.0e-82
Match length	146

% identity	99
NCBI Description	chlorophyll a/b-binding protein type I precursor Lhb1B2 - Arabidopsis thaliana >gi_16364_emb_CAA45790_ (X64460) photosystem II type I chlorophyll a /b binding protein [Arabidopsis thaliana] >gi_3128230 (AC004077) photosystem II type I chlorophyll a/b binding protein [Arabidopsis thaliana] >gi_3337371 (AC004481) photosystem II type I chlorophyll a/b binding protein [Arabidopsis thaliana]
Seq. No.	159840
Seq. ID	LIB3176-116-P2-K1-G7
Method	BLASTX
NCBI GI	g132863
BLAST score	542
E value	9.0e-56
Match length	103
% identity	97
NCBI Description	CHLOROPLAST 50S RIBOSOMAL PROTEIN L2 >gi_12214_emb_CAA46568_ (X65615) ribosomal protein L2 [Sinapis alba]
Seq. No.	159841
Seq. ID	LIB3176-116-P2-K1-G8
Method	BLASTX
NCBI GI	g1702872
BLAST score	624
E value	3.0e-65
Match length	125
% identity	98
NCBI Description	(Y09667) ferredoxin-dependent glutamate synthase [Arabidopsis thaliana]
Seq. No.	159842
Seq. ID	LIB3176-116-P2-K1-G9
Method	BLASTN
NCBI GI	g4586098
BLAST score	200
E value	1.0e-108
Match length	284
% identity	93
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F16J13 (ESSA project)
Seq. No.	159843
Seq. ID	LIB3176-116-P2-K1-H10
Method	BLASTX
NCBI GI	g399013
BLAST score	335
E value	2.0e-31
Match length	75
% identity	89
NCBI Description	ADP,ATP CARRIER PROTEIN 1 PRECURSOR (ADP/ATP TRANSLOCASE 1) (ADENINE NUCLEOTIDE TRANSLOCATOR 1) (ANT 1) >gi_99658_pir__S21313 ADP,ATP carrier protein - Arabidopsis thaliana (fragment) >gi_16175_emb_CAA46518_ (X65549) adenylate translocator [Arabidopsis thaliana] >gi_445607_prf__1909354A adenylate translocator

[Arabidopsis thaliana]

Seq. No.	159844
Seq. ID	LIB3176-116-P2-K1-H11
Method	BLASTX
NCBI GI	g3334141
BLAST score	276
E value	1.0e-24
Match length	77
% identity	64
NCBI Description	CENTROMERE/MICROTUBULE BINDING PROTEIN CBF5 (CENTROMERE-BINDING FACTOR 5) (NUCLEOLAR PROTEIN CBF5) >gi_2737890 (U59149) nucleolar protein CaCbf5p [Candida albicans]

Seq. No.	159845
Seq. ID	LIB3176-116-P2-K1-H12
Method	BLASTX
NCBI GI	g3142294
BLAST score	589
E value	4.0e-61
Match length	116
% identity	96
NCBI Description	(AC002411) Strong similarity to initiation factor eIF-2, gb_U37354 from S. pombe. ESTs gb_T41979, gb_N37284 and gb_N37529 come from this gene. [Arabidopsis thaliana]

Seq. No.	159846
Seq. ID	LIB3176-116-P2-K1-H2
Method	BLASTN
NCBI GI	g2961370
BLAST score	408
E value	0.0e+00
Match length	412
% identity	100
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F23E13 (ESSAII project)

Seq. No.	159847
Seq. ID	LIB3176-116-P2-K1-H3
Method	BLASTN
NCBI GI	g2961370
BLAST score	259
E value	1.0e-144
Match length	295
% identity	97
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F23E13 (ESSAII project)

Seq. No.	159848
Seq. ID	LIB3176-116-P2-K1-H4
Method	BLASTX
NCBI GI	g2286069
BLAST score	574
E value	2.0e-59
Match length	118
% identity	91

NCBI Description (U72155) beta-glucosidase [Arabidopsis thaliana]

Seq. No. 159849
Seq. ID LIB3176-116-P2-K1-H5
Method BLASTX
NCBI GI g399013
BLAST score 364
E value 7.0e-35
Match length 83
% identity 88
NCBI Description ADP,ATP CARRIER PROTEIN 1 PRECURSOR (ADP/ATP TRANSLOCASE 1) (ADENINE NUCLEOTIDE TRANSLOCATOR 1) (ANT 1) >gi_99658_pir__S21313 ADP,ATP carrier protein - Arabidopsis thaliana (fragment) >gi_16175_emb_CAA46518_ (X65549) adenylate translocator [Arabidopsis thaliana] >gi_445607_prf__1909354A adenylate translocator [Arabidopsis thaliana]

Seq. No. 159850
Seq. ID LIB3176-116-P2-K1-H6
Method BLASTX
NCBI GI g3142294
BLAST score 586
E value 9.0e-61
Match length 114
% identity 98
NCBI Description (AC002411) Strong similarity to initiation factor eIF-2, gb_U37354 from S. pombe. ESTs gb_T41979, gb_N37284 and gb_N37529 come from this gene. [Arabidopsis thaliana]

Seq. No. 159851
Seq. ID LIB3176-116-P2-K1-H7
Method BLASTX
NCBI GI g2738248
BLAST score 62
E value 3.0e-43
Match length 95
% identity 96
NCBI Description (U97200) cobalamin-independent methionine synthase [Arabidopsis thaliana]

Seq. No. 159852
Seq. ID LIB3176-116-P2-K1-H8
Method BLASTX
NCBI GI g282865
BLAST score 666
E value 4.0e-70
Match length 141
% identity 69
NCBI Description chlorophyll a/b-binding protein - Arabidopsis thaliana >gi_16207_emb_CAA39534_ (X56062) chlorophyll A/B-binding protein [Arabidopsis thaliana] >gi_166644 (M85150) chlorophyll a/b-binding protein [Arabidopsis thaliana] >gi_4678304_emb_CAB41095.1_ (AL049655) chlorophyll a/b-binding protein [Arabidopsis thaliana]

Seq. No. 159853

Seq. ID	LIB3176-117-P2-K1-A1
Method	BLASTX
NCBI GI	g477819
BLAST score	400
E value	3.0e-39
Match length	99
% identity	77
NCBI Description	mitochondrial processing peptidase (EC 3.4.99.41) beta chain precursor - potato >gi_410634_bbs_136741 cytochrome c reductase-processing peptidase subunit II, MPP subunit II, P53 [potatoes, var. Marfona, tuber, Peptide Mitochondrial, 530 aa]

Seq. No.	159854
Seq. ID	LIB3176-117-P2-K1-A12
Method	BLASTX
NCBI GI	g1531762
BLAST score	195
E value	6.0e-15
Match length	51
% identity	75
NCBI Description	(Y07765) S-adenosylmethionine decarboxylase [Arabidopsis thaliana]

Seq. No.	159855
Seq. ID	LIB3176-117-P2-K1-A2
Method	BLASTX
NCBI GI	g3122288
BLAST score	143
E value	7.0e-09
Match length	39
% identity	72
NCBI Description	IMPORTIN ALPHA-1 SUBUNIT (KARYOPHERIN ALPHA-1 SUBUNIT) (KAP ALPHA) >gi_1568635 (U69533) AtKAP alpha [Arabidopsis thaliana]

Seq. No.	159856
Seq. ID	LIB3176-117-P2-K1-A3
Method	BLASTN
NCBI GI	g2760829
BLAST score	173
E value	2.0e-92
Match length	369
% identity	99
NCBI Description	Arabidopsis thaliana chromosome II BAC F18A8 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	159857
Seq. ID	LIB3176-117-P2-K1-A4
Method	BLASTX
NCBI GI	g2062158
BLAST score	702
E value	2.0e-74
Match length	148
% identity	48
NCBI Description	(AC001645) jasmonate inducible protein isolog [Arabidopsis thaliana]

Seq. No.	159858
Seq. ID	LIB3176-117-P2-K1-A5
Method	BLASTX
NCBI GI	g4512664
BLAST score	209
E value	3.0e-22
Match length	74
% identity	76
NCBI Description	(AC006931) putative ribose phosphate pyrophosphokinase [Arabidopsis thaliana] >gi_4544471_gb_AAD22378.1_AC006580_10 (AC006580) putative ribose phosphate pyrophosphokinase [Arabidopsis thaliana]

Seq. No.	159859
Seq. ID	LIB3176-117-P2-K1-A7
Method	BLASTX
NCBI GI	g2078350
BLAST score	369
E value	1.0e-35
Match length	83
% identity	87
NCBI Description	(U95923) transaldolase [Solanum tuberosum]

Seq. No.	159860
Seq. ID	LIB3176-117-P2-K1-A8
Method	BLASTX
NCBI GI	g1053057
BLAST score	349
E value	3.0e-33
Match length	74
% identity	95
NCBI Description	(U38422) histone H3 [Triticum aestivum]

Seq. No.	159861
Seq. ID	LIB3176-117-P2-K1-A9
Method	BLASTX
NCBI GI	g4586101
BLAST score	539
E value	3.0e-55
Match length	117
% identity	90
NCBI Description	(AL049638) putative protein [Arabidopsis thaliana]

Seq. No.	159862
Seq. ID	LIB3176-117-P2-K1-B1
Method	BLASTX
NCBI GI	g4585978
BLAST score	775
E value	7.0e-83
Match length	147
% identity	99
NCBI Description	(AC005287) NADP specific isocitrate dehydrogenase [Arabidopsis thaliana]

Seq. No.	159863
Seq. ID	LIB3176-117-P2-K1-B2

Method	BLASTX
NCBI GI	g2851508
BLAST score	752
E value	3.0e-80
Match length	153
% identity	95
NCBI Description	60S RIBOSOMAL PROTEIN L21 >gi_2160162 (AC000132) Similar to ribosomal protein L21 (gb_L38826). ESTs gb_AA395597,gb_ATTS5197 come from this gene. [Arabidopsis thaliana] >gi_3482935 (AC003970) Putative ribosomal protein L21 [Arabidopsis thaliana]

Seq. No.	159864
Seq. ID	LIB3176-117-P2-K1-B4
Method	BLASTX
NCBI GI	g2500347
BLAST score	425
E value	7.0e-42
Match length	128
% identity	69
NCBI Description	NHP2/RS6 FAMILY PROTEIN YEL026W HOMOLOG >gi_3878691_emb_CAA90127_ (Z49911) similar [illegible] bosomal protein (L7AE family); cDNA EST EMBL:D73957 [illegible]s from this gene; cDNA EST EMBL:D71298 comes from this gene; cDNA EST EMBL:D74077 comes from this gene; cDNA EST EMBL:D71393 comes from this gene; cD

Seq. No.	159865
Seq. ID	LIB3176-117-P2-K1-B5
Method	BLASTN
NCBI GI	g3128137
BLAST score	272
E value	1.0e-151
Match length	379
% identity	94
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K9I9, complete sequence [Arabidopsis thaliana]

Seq. No.	159866
Seq. ID	LIB3176-117-P2-K1-B7
Method	BLASTN
NCBI GI	g3702736
BLAST score	404
E value	0.0e+00
Match length	412
% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MRI1, complete sequence [Arabidopsis thaliana]

Seq. No.	159867
Seq. ID	LIB3176-117-P2-K1-B8
Method	BLASTN
NCBI GI	g2191157
BLAST score	462
E value	0.0e+00
Match length	466
% identity	100

NCBI Description Arabidopsis thaliana BAC IG002P16

Seq. No. 159868
Seq. ID LIB3176-117-P2-K1-B9
Method BLASTX
NCBI GI g1350680
BLAST score 364
E value 1.0e-34
Match length 121
% identity 71
NCBI Description 60S RIBOSOMAL PROTEIN L1

Seq. No. 159869
Seq. ID LIB3176-117-P2-K1-C1
Method BLASTX
NCBI GI g1350680
BLAST score 765
E value 1.0e-81
Match length 151
% identity 99
NCBI Description 60S RIBOSOMAL PROTEIN L1

Seq. No. 159870
Seq. ID LIB3176-117-P2-K1-C10
Method BLASTX
NCBI GI g1363489
BLAST score 638
E value 7.0e-67
Match length 120
% identity 98
NCBI Description thioglucosidase (EC 3.2.3.1) 3D precursor - Arabidopsis thaliana >gi_984052_emb_CAA61592_ (X89413) thioglucoside glucohydrolase [Arabidopsis thaliana]

Seq. No. 159871
Seq. ID LIB3176-117-P2-K1-C12
Method BLASTX
NCBI GI g3212877
BLAST score 612
E value 4.0e-72
Match length 143
% identity 99
NCBI Description (AC004005) Lea-like protein [Arabidopsis thaliana]

Seq. No. 159872
Seq. ID LIB3176-117-P2-K1-C2
Method BLASTN
NCBI GI g2914688
BLAST score 77
E value 6.0e-36
Match length 81
% identity 99
NCBI Description Arabidopsis thaliana chromosome II BAC F24L7 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No. 159873
Seq. ID LIB3176-117-P2-K1-C3

Method	BLASTX
NCBI GI	g3402487
BLAST score	529
E value	4.0e-54
Match length	140
% identity	78
NCBI Description	(AB015138) Vacuolar proton pyrophosphatase [Arabidopsis thaliana]

Seq. No.	159874
Seq. ID	LIB3176-117-P2-K1-C4
Method	BLASTN
NCBI GI	g2244829
BLAST score	455
E value	0.0e+00
Match length	455
% identity	100
NCBI Description	Arabidopsis thaliana DNA chromosome 4, ESSA I contig fragment No

Seq. No.	159875
Seq. ID	LIB3176-117-P2-K1-C6
Method	BLASTX
NCBI GI	g232031
BLAST score	332
E value	5.0e-31
Match length	115
% identity	54
NCBI Description	ELONGATION FACTOR 1 BETA' >gi_322851_pir__S29224 translation elongation factor eEF-1 beta' chain - rice >gi_218161_dbj_BAA02253_ (D12821) elongation factor 1 beta' [Oryza sativa]

Seq. No.	159876
Seq. ID	LIB3176-117-P2-K1-C7
Method	BLASTN
NCBI GI	g4741184
BLAST score	158
E value	1.0e-83
Match length	294
% identity	100
NCBI Description	Arabidopsis thaliana DNA chromosome 3, BAC clone T23J7 (ESSA project)

Seq. No.	159877
Seq. ID	LIB3176-117-P2-K1-C8
Method	BLASTX
NCBI GI	g2326372
BLAST score	692
E value	4.0e-73
Match length	153
% identity	88
NCBI Description	(Y14404) putative arabinose kinase [Arabidopsis thaliana]

Seq. No.	159878
Seq. ID	LIB3176-117-P2-K1-C9
Method	BLASTN

NCBI GI	g3600045
BLAST score	204
E value	1.0e-111
Match length	282
% identity	97
NCBI Description	Arabidopsis thaliana BAC F2P3

Seq. No.	159879
Seq. ID	LIB3176-117-P2-K1-D10
Method	BLASTX
NCBI GI	g2642429
BLAST score	220
E value	7.0e-18
Match length	139
% identity	12
NCBI Description	(AC002391) putative poly(A)-binding protein [Arabidopsis thaliana]

Seq. No.	159880
Seq. ID	LIB3176-117-P2-K1-D11
Method	BLASTN
NCBI GI	g2642427
BLAST score	69
E value	1.0e-30
Match length	101
% identity	92
NCBI Description	Arabidopsis thaliana chromosome II BAC T20D16 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	159881
Seq. ID	LIB3176-117-P2-K1-D2
Method	BLASTX
NCBI GI	g1702986
BLAST score	685
E value	2.0e-72
Match length	140
% identity	99
NCBI Description	14-3-3-LIKE PROTEIN GF14 CHI >gi_1255987 (U09377) GF14chi isoform [Arabidopsis thaliana] >gi_1256534 (L09112) GF14 chi chain [Arabidopsis thaliana]

Seq. No.	159882
Seq. ID	LIB3176-117-P2-K1-D3
Method	BLASTX
NCBI GI	g1652975
BLAST score	149
E value	2.0e-09
Match length	76
% identity	42
NCBI Description	(D90910) hypothetical protein [Synechocystis sp.]

Seq. No.	159883
Seq. ID	LIB3176-117-P2-K1-D4
Method	BLASTN
NCBI GI	g2642427
BLAST score	50
E value	4.0e-19

Match length	109
% identity	86
NCBI Description	Arabidopsis thaliana chromosome II BAC T20D16 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	159884
Seq. ID	LIB3176-117-P2-K1-D5
Method	BLASTN
NCBI GI	g4159703
BLAST score	143
E value	1.0e-74
Match length	392
% identity	98
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K5F14, complete sequence

Seq. No.	159885
Seq. ID	LIB3176-117-P2-K1-D6
Method	BLASTX
NCBI GI	g1363489
BLAST score	819
E value	5.0e-88
Match length	153
% identity	99
NCBI Description	thioglucosidase (EC 3.2.3.1) 3D precursor - Arabidopsis thaliana >gi_984052_emb_CAA61592_ (X89413) thioglucoside glucohydrolase [Arabidopsis thaliana]

Seq. No.	159886
Seq. ID	LIB3176-117-P2-K1-D7
Method	BLASTX
NCBI GI	g1732570
BLAST score	213
E value	3.0e-17
Match length	56
% identity	73
NCBI Description	(U72153) beta-glucosidase [Arabidopsis thaliana]

Seq. No.	159887
Seq. ID	LIB3176-117-P2-K1-D8
Method	BLASTX
NCBI GI	g228408
BLAST score	385
E value	3.0e-37
Match length	78
% identity	54
NCBI Description	calmodulin 1 [Arabidopsis thaliana]

Seq. No.	159888
Seq. ID	LIB3176-117-P2-K1-E1
Method	BLASTX
NCBI GI	g4454479
BLAST score	362
E value	2.0e-34
Match length	72
% identity	100
NCBI Description	(AC006234) putative riboflavin synthase alpha chain

[Arabidopsis thaliana]

Seq. No.	159889
Seq. ID	LIB3176-117-P2-K1-E5
Method	BLASTX
NCBI GI	g4587542
BLAST score	261
E value	4.0e-23
Match length	64
% identity	80
NCBI Description	(AC006577) Belongs to the PF_00657 Lipase/Acylhydrolase with GDSL-motif family. ESTs gb_T45815, gb_T45130 and gb_Z38046 come from this gene. [Arabidopsis thaliana]

Seq. No.	159890
Seq. ID	LIB3176-117-P2-K1-E7
Method	BLASTX
NCBI GI	g4337175
BLAST score	517
E value	1.0e-52
Match length	127
% identity	80
NCBI Description	(AC006416) ESTs gb_T20589, gb_T04648, gb_AA597906, gb_T04111, gb_R84180, gb_R65428, gb_T44439, gb_T76570, gb_R90004, gb_T45020, gb_T42457, gb_T20921, gb_AA042762 and gb_AA720210 come from this gene. [Arabidopsis thaliana]

Seq. No.	159891
Seq. ID	LIB3176-117-P2-K1-E8
Method	BLASTX
NCBI GI	g4755193
BLAST score	564
E value	3.0e-58
Match length	121
% identity	94
NCBI Description	(AC007018) putative ribosomal protein S17 [Arabidopsis thaliana]

Seq. No.	159892
Seq. ID	LIB3176-117-P2-K1-E9
Method	BLASTX
NCBI GI	g3273743
BLAST score	617
E value	2.0e-64
Match length	118
% identity	99
NCBI Description	(AF057357) lipid transfer protein 2 precursor [Arabidopsis thaliana] >gi_3786019 (AC005499) unknown protein [Arabidopsis thaliana]

Seq. No.	159893
Seq. ID	LIB3176-117-P2-K1-F1
Method	BLASTX
NCBI GI	g2809256
BLAST score	385
E value	3.0e-37
Match length	79

% identity	95
NCBI Description	(AC002560) F21B7.25 [Arabidopsis thaliana]
Seq. No.	159894
Seq. ID	LIB3176-117-P2-K1-F10
Method	BLASTX
NCBI GI	g4056469
BLAST score	482
E value	1.0e-48
Match length	95
% identity	99
NCBI Description	(AC005990) Strong similarity to gb_M95166 ADP-ribosylation factor from Arabidopsis thaliana. ESTs gb_Z25826, gb_R90191, gb_N65697, gb_AA713150, gb_T46332, gb_AA040967, gb_AA712956, gb_T46403, gb_T46050, gb_AI100391 and gb_Z25043 come from t
Seq. No.	159895
Seq. ID	LIB3176-117-P2-K1-F11
Method	BLASTX
NCBI GI	g4056469
BLAST score	571
E value	5.0e-59
Match length	115
% identity	97
NCBI Description	(AC005990) Strong similarity to gb_M95166 ADP-ribosylation factor from Arabidopsis thaliana. ESTs gb_Z25826, gb_R90191, gb_N65697, gb_AA713150, gb_T46332, gb_AA040967, gb_AA712956, gb_T46403, gb_T46050, gb_AI100391 and gb_Z25043 come from t
Seq. No.	159896
Seq. ID	LIB3176-117-P2-K1-F12
Method	BLASTX
NCBI GI	g4490737
BLAST score	562
E value	6.0e-58
Match length	123
% identity	89
NCBI Description	(AL035708) putative protein [Arabidopsis thaliana]
Seq. No.	159897
Seq. ID	LIB3176-117-P2-K1-F2
Method	BLASTX
NCBI GI	g134889
BLAST score	162
E value	5.0e-11
Match length	112
% identity	37
NCBI Description	SIGNAL RECOGNITION PARTICLE 68 KD PROTEIN (SRP68) >gi_108065_pir__S12981 68K protein - gray wolf >gi_227342_prf__1702226A SRP68 protein [Canis familiaris]
Seq. No.	159898
Seq. ID	LIB3176-117-P2-K1-F3
Method	BLASTX
NCBI GI	g2492519

BLAST score	484
E value	9.0e-49
Match length	109
% identity	85
NCBI Description	26S PROTEASE REGULATORY SUBUNIT 7 (26S PROTEASOME SUBUNIT 7) >gi_1395191_dbj_BAA13021_ (D86121) 26S proteasome ATPase subunit [Spinacia oleracea]

Seq. No.	159899
Seq. ID	LIB3176-117-P2-K1-F6
Method	BLASTX
NCBI GI	g4539408
BLAST score	387
E value	2.0e-37
Match length	132
% identity	65
NCBI Description	(AL049524) putative alpha NAC [Arabidopsis thaliana]

Seq. No.	159900
Seq. ID	LIB3176-117-P2-K1-F7
Method	BLASTX
NCBI GI	g2982303
BLAST score	401
E value	4.0e-39
Match length	91
% identity	78
NCBI Description	(AF051236) hypothetical protein [Picea mariana]

Seq. No.	159901
Seq. ID	LIB3176-117-P2-K1-F8
Method	BLASTN
NCBI GI	g2618602
BLAST score	171
E value	3.0e-91
Match length	452
% identity	97
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MSJ1, complete sequence [Arabidopsis thaliana]

Seq. No.	159902
Seq. ID	LIB3176-117-P2-K1-G1
Method	BLASTN
NCBI GI	g3241926
BLAST score	214
E value	1.0e-117
Match length	432
% identity	99
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MSG15, complete sequence [Arabidopsis thaliana]

Seq. No.	159903
Seq. ID	LIB3176-117-P2-K1-G10
Method	BLASTX
NCBI GI	g132074
BLAST score	803
E value	3.0e-86
Match length	151

% identity	99
NCBI Description	RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN 1A PRECURSOR (RUBISCO SMALL SUBUNIT 1A) >gi_68063_pir__RKMUA1 ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain A1 precursor - Arabidopsis thaliana
Seq. No.	159904
Seq. ID	LIB3176-117-P2-K1-G11
Method	BLASTX
NCBI GI	g132074
BLAST score	254
E value	3.0e-22
Match length	71
% identity	75
NCBI Description	RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN 1A PRECURSOR (RUBISCO SMALL SUBUNIT 1A) >gi_68063_pir__RKMUA1 ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain A1 precursor - Arabidopsis thaliana
Seq. No.	159905
Seq. ID	LIB3176-117-P2-K1-G12
Method	BLASTN
NCBI GI	g3193282
BLAST score	186
E value	1.0e-100
Match length	430
% identity	74
NCBI Description	Arabidopsis thaliana BAC T14P8
Seq. No.	159906
Seq. ID	LIB3176-117-P2-K1-G2
Method	BLASTN
NCBI GI	g2564051
BLAST score	175
E value	1.0e-93
Match length	432
% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MWD9, complete sequence [Arabidopsis thaliana]
Seq. No.	159907
Seq. ID	LIB3176-117-P2-K1-G4
Method	BLASTN
NCBI GI	g2924651
BLAST score	404
E value	0.0e+00
Match length	430
% identity	99
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K2A18, complete sequence [Arabidopsis thaliana]
Seq. No.	159908
Seq. ID	LIB3176-117-P2-K1-G5
Method	BLASTX
NCBI GI	g2911057
BLAST score	619
E value	1.0e-64

Match length	135
% identity	90
NCBI Description	(AL021961) caffeoyl-CoA O-methyltransferase - like protein [Arabidopsis thaliana]

Seq. No.	159909
Seq. ID	LIB3176-117-P2-K1-G6
Method	BLASTX
NCBI GI	g1346756
BLAST score	439
E value	1.0e-43
Match length	86
% identity	99
NCBI Description	SERINE/THREONINE PROTEIN PHOSPHATASE PP1 ISOZYME 3 >gi_421852_pir__S31087 phosphoprotein phosphatase (EC 3.1.3.16) 1 catalytic chain (clone TOPP3) - Arabidopsis thaliana >gi_166799 (M93410) phosphoprotein phosphatase 1 [Arabidopsis thaliana]

Seq. No.	159910
Seq. ID	LIB3176-117-P2-K1-G7
Method	BLASTX
NCBI GI	g629602
BLAST score	337
E value	1.0e-31
Match length	114
% identity	55
NCBI Description	probable imbibition protein - wild cabbage >gi_488787_emb_CAA55893_ (X79330) putative imbibition protein [Brassica oleracea]

Seq. No.	159911
Seq. ID	LIB3176-117-P2-K1-G8
Method	BLASTX
NCBI GI	g2914700
BLAST score	545
E value	4.0e-56
Match length	114
% identity	59
NCBI Description	(AC003974) tRNA-processing protein SEN3-like [Arabidopsis thaliana]

Seq. No.	159912
Seq. ID	LIB3176-117-P2-K1-G9
Method	BLASTN
NCBI GI	g4490717
BLAST score	140
E value	9.0e-73
Match length	429
% identity	100
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone (ESSA project)

Seq. No.	159913
Seq. ID	LIB3176-117-P2-K1-H10
Method	BLASTX
NCBI GI	g3122753

BLAST score	566
E value	2.0e-58
Match length	105
% identity	99
NCBI Description	60S RIBOSOMAL PROTEIN L44 >gi_2244789_emb_CAB10211.1_ (Z97336) ribosomal protein [Arabidopsis thaliana]

Seq. No.	159914
Seq. ID	LIB3176-117-P2-K1-H11
Method	BLASTX
NCBI GI	g3122753
BLAST score	520
E value	4.0e-53
Match length	102
% identity	96
NCBI Description	60S RIBOSOMAL PROTEIN L44 >gi_2244789_emb_CAB10211.1_ (Z97336) ribosomal protein [Arabidopsis thaliana]

Seq. No.	159915
Seq. ID	LIB3176-117-P2-K1-H12
Method	BLASTX
NCBI GI	g2244749
BLAST score	653
E value	1.0e-68
Match length	123
% identity	100
NCBI Description	(Z97335) hydroxymethyltransferase [Arabidopsis thaliana]

Seq. No.	159916
Seq. ID	LIB3176-117-P2-K1-H2
Method	BLASTX
NCBI GI	g3281868
BLAST score	237
E value	7.0e-20
Match length	46
% identity	98
NCBI Description	(AL031004) putative protein [Arabidopsis th a]

Seq. No.	159917
Seq. ID	LIB3176-117-P2-K1-H3
Method	BLASTX
NCBI GI	g1363489
BLAST score	691
E value	4.0e-73
Match length	143
% id	92
NCBI	sidase (EC ? idopsis _CAA61592_ (A69415) thioglucoside glucohydr idopsis thaliana]

Seq. No.	159918
Seq. ID	LIB3176-117-P2-K1-H4
Method	BLASTX
NCBI GI	g1706261
BLAST score	666
E value	4.0e-70
Match length	150

% identity	83
NCBI Description	CYSTEINE PROTEINASE 2 PRECURSOR >gi_2118129_pir__S59598 cysteine proteinase 2 precursor - maize >gi_644490_dbj_BAA08245_ (D45403) cysteine proteinase [Zea mays]

Seq. No.	159919
Seq. ID	LIB3176-117-P2-K1-H5
Method	BLASTX
NCBI GI	g2493144
BLAST score	437
E value	3.0e-43
Match length	140
% identity	67
NCBI Description	VACUOLAR ATP SYNTHASE 16 KD PROTEOLIPID SUBUNIT (V-ATPASE 16 KD PROTEOLIPID SUBUNIT) >gi_2118221_pir__S60132 H+-transporting ATPase (EC 3.6.1.35), vacuolar, 16K chain (clone AVA-P2) - Arabidopsis thaliana >gi_926937 (L44585) vacuolar H+-pumping ATPase 16 kDa proteolipid [Arabidopsis thaliana]

Seq. No.	159920
Seq. ID	LIB3176-117-P2-K1-H6
Method	BLASTX
NCBI GI	g4538942
BLAST score	144
E value	6.0e-09
Match length	101
% identity	40
NCBI Description	(AL049483) uncharacterized protein [Arabidopsis thaliana]

Seq. No.	159921
Seq. ID	LIB3176-117-P2-K1-H7
Method	BLASTX
NCBI GI	g2499811
BLAST score	611
E value	9.0e-64
Match length	118
% identity	99
NCBI Description	PROFILIN 2 >gi_1353766 (U43323) profilin 2 [Arabidopsis thaliana] >gi_1353772 (U43326) profilin 2 [Arabidopsis thaliana]

Seq. No.	159922
Seq. ID	LIB3176-117-P2-K1-H8
Method	BLASTX
NCBI GI	g3080411
BLAST score	209
E value	1.0e-16
Match length	77
% identity	47
NCBI Description	(AL022604) putative protein [Arabidopsis thaliana]

Seq. No.	159923
Seq. ID	LIB3176-118-P2-K1-A1
Method	BLASTX
NCBI GI	g2281090

BLAST score 333
E value 3.0e-41
Match length 128
% identity 69
NCBI Description (AC002333) hypothetical protein [Arabidopsis thaliana]

Seq. No. 159924
Seq. ID LIB3176-118-P2-K1-A11
Method BLASTX
NCBI GI g399013
BLAST score 220
E value 3.0e-18
Match length 47
% identity 94
NCBI Description ADP,ATP CARRIER PROTEIN 1 PRECURSOR (ADP/ATP TRANSLOCASE 1) (ADENINE NUCLEOTIDE TRANSLOCATOR 1) (ANT 1) >gi_99658_pir__S21313 ADP,ATP carrier protein - Arabidopsis thaliana (fragment) >gi_16175_emb_CAA46518_ (X65549) adenylate translocator [Arabidopsis thaliana] >gi_445607_prf__1909354A adenylate translocator [Arabidopsis thaliana]

Seq. No. 159925
Seq. ID LIB3176-118-P2-K1-A12
Method BLASTX
NCBI GI g2494041
BLAST score 274
E value 3.0e-24
Match length 66
% identity 76
NCBI Description DIAMINOPIMELATE EPIMERASE >gi_1653875_dbj_BAA18785_ (D90917) diaminopimelate epimerase [Synechocystis sp.]

Seq. No. 159926
Seq. ID LIB3176-118-P2-K1-A2
Method BLASTX
NCBI GI g99735
BLAST score 638
E value 7.0e-67
Match length 125
% identity 97
NCBI Description L-ascorbate peroxidase (EC 1.11.1.11) precursor - Arabidopsis thaliana (fragment)

Seq. No. 159927
Seq. ID LIB3176-118-P2-K1-A3
Method BLASTX
NCBI GI g3738291
BLAST score 416
E value 6.0e-41
Match length 120
% identity 72
NCBI Description (AC005309) unknown protein [Arabidopsis thaliana]

Seq. No. 159928
Seq. ID LIB3176-118-P2-K1-A4
Method BLASTX

NCBI GI	g3123271
BLAST score	491
E value	1.0e-49
Match length	115
% identity	83
NCBI Description	40S RIBOSOMAL PROTEIN S6 >gi_2224751_emb_CAA74381_ (Y14052) ribosomal protein S6 [Arabidopsis thaliana]

Seq. No.	159929
Seq. ID	LIB3176-118-P2-K1-A5
Method	BLASTN
NCBI GI	g4558586
BLAST score	257
E value	1.0e-142
Match length	462
% identity	94
NCBI Description	Arabidopsis thaliana chromosome 1 BAC T5I8 sequence, complete sequence

Seq. No.	159930
Seq. ID	LIB3176-118-P2-K1-A6
Method	BLASTN
NCBI GI	g2264314
BLAST score	154
E value	2.0e-81
Match length	170
% identity	98
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MQK4, complete sequence [Arabidopsis thaliana]

Seq. No.	159931
Seq. ID	LIB3176-118-P2-K1-A7
Method	BLASTX
NCBI GI	g1710530
BLAST score	400
E value	2.0e-54
Match length	108
% identity	97
NCBI Description	60S RIBOSOMAL PROTEIN L27A >gi_2129719_pir__S71256 ribosomal protein L27a - Arabidopsis thaliana >gi_1107487_emb_CAA63025_ (X91959) 60S ribosomal protein L27a [Arabidopsis thaliana]

Seq. No.	159932
Seq. ID	LIB3176-118-P2-K1-A8
Method	BLASTN
NCBI GI	g4757402
BLAST score	180
E value	8.0e-97
Match length	257
% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MIG5, complete sequence

Seq. No.	159933
Seq. ID	LIB3176-118-P2-K1-B1
Method	BLASTX

NCBI GI	g3695383
BLAST score	535
E value	7.0e-55
Match length	105
% identity	97
NCBI Description	(AF096370) similar to inorganic pyrophosphatase (Pfam: PF00719 Pyrophosphatase, E-value: 2.7e-88) [Arabidopsis thaliana]

Seq. No.	159934
Seq. ID	LIB3176-118-P2-K1-B10
Method	BLASTX
NCBI GI	g1669387
BLAST score	153
E value	2.0e-24
Match length	62
% identity	82
NCBI Description	(U41998) actin 2 [Arabidopsis thaliana]

Seq. No.	159935
Seq. ID	LIB3176-118-P2-K1-B11
Method	BLASTX
NCBI GI	g2558962
BLAST score	407
E value	1.0e-39
Match length	83
% identity	99
NCBI Description	(AF025667) histone H2B1 [Gossypium hirsutum]

Seq. No.	159936
Seq. ID	LIB3176-118-P2-K1-B3
Method	BLASTX
NCBI GI	g119350
BLAST score	631
E value	5.0e-66
Match length	125
% identity	98
NCBI Description	ENOLASE (2-PHOSPHOGLYCERATE DEHYDRATASE) (2-PHOSPHO-D-GLYCERATE HYDRO-LYASE) >gi_81608_pir__JQ1187 phosphopyruvate hydratase (EC 4.2.1.11) - Arabidopsis thaliana >gi_16271_emb_CAA41114_ (X58107) enolase [Arabidopsis thaliana] >gi_4581151_gb_AAD24635.1_AC006919_13 (AC006919) enolase (2-phospho-D-glycerate hydroylase);identical to P25696 [Arabidopsis thaliana]

Seq. No.	159937
Seq. ID	LIB3176-118-P2-K1-B4
Method	BLASTN
NCBI GI	g3128142
BLAST score	351
E value	0.0e+00
Match length	452
% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MQN23, complete sequence [Arabidopsis thaliana]

Seq. No.	159938
Seq. ID	LIB3176-118-P2-K1-B5
Method	BLASTX
NCBI GI	g116392
BLAST score	645
E value	1.0e-67
Match length	130
% identity	95
NCBI Description	CHALCONE SYNTHASE (NARINGENIN-CHALCONE SYNTHASE) >gi_66543_pir__SYMUCN naringenin-chalcone synthase (EC 2.3.1.74) - Arabidopsis thaliana >gi_166670 (M20308) chalcone synthase [Arabidopsis thaliana]

Seq. No.	159939
Seq. ID	LIB3176-118-P2-K1-B6
Method	BLASTX
NCBI GI	g3037045
BLAST score	70
E value	2.0e-12
Match length	116
% identity	35
NCBI Description	(AF052621) hypothetical protein COX4AL [Mus musculus]

Seq. No.	159940
Seq. ID	LIB3176-118-P2-K1-B7
Method	BLASTX
NCBI GI	g136739
BLAST score	271
E value	7.0e-24
Match length	94
% identity	57
NCBI Description	UTP--GLUCOSE-1-PHOSPHATE URIDYLYLTRANSFERASE (UDP-GLUCOSE PYROPHOSPHORYLASE) (UDPGP) >gi_67061_pir__XNPOU UTP--glucose-1-phosphate uridylyltransferase (EC 2.7.7.9) - potato >gi_218001_dbj_BAA00570_ (D00667) UDP-glucose pyrophosphorylase precursor [Solanum tuberosum]

Seq. No.	159941
Seq. ID	LIB3176-118-P2-K1-B8
Method	BLASTX
NCBI GI	g2062161
BLAST score	669
E value	2.0e-71
Match length	138
% identity	52
NCBI Description	(AC001645) jasmonate inducible protein isolog [Arabidopsis thaliana]

Seq. No.	159942
Seq. ID	LIB3176-118-P2-K1-B9
Method	BLASTX
NCBI GI	g2529665
BLAST score	312
E value	3.0e-29
Match length	72
% identity	90
NCBI Description	(AC002535) putative ribosomal protein L7A [Arabidopsis

thaliana]

Seq. No.	159943
Seq. ID	LIB3176-118-P2-K1-C1
Method	BLASTX
NCBI GI	g584867
BLAST score	232
E value	2.0e-19
Match length	80
% identity	53
NCBI Description	CYTOCHROME P450 77A2 (CYPLXXVIIA2) (P-450EG5) >gi_481959_pir__S40266 gene CYP77A2 protein - eggplant >gi_542071_pir__S41598 cytochrome P450 77A2 - eggplant >gi_438241_emb_CAA50646_ (X71655) CYP77A2 [Solanum melongena]

Seq. No.	159944
Seq. ID	LIB3176-118-P2-K1-C10
Method	BLASTX
NCBI GI	g3080393
BLAST score	287
E value	1.0e-25
Match length	93
% identity	66
NCBI Description	(AL022603) NADH dehydrogenase like protein [Arabidopsis thaliana]

Seq. No.	159945
Seq. ID	LIB3176-118-P2-K1-C11
Method	BLASTN
NCBI GI	g3335331
BLAST score	290
E value	1.0e-162
Match length	461
% identity	98
NCBI Description	Arabidopsis thaliana chromosome 1 BAC T8F5 sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	159946
Seq. ID	LIB3176-118-P2-K1-C2
Method	BLASTN
NCBI GI	g2275194
BLAST score	445
E value	0.0e+00
Match length	470
% identity	98
NCBI Description	Arabidopsis thaliana chromosome II BAC T08I13 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	159947
Seq. ID	LIB3176-118-P2-K1-C3
Method	BLASTX
NCBI GI	g4049348
BLAST score	334
E value	7.0e-32
Match length	72
% identity	82

NCBI Description	(AL034567) putative protein [Arabidopsis thaliana]
Seq. No.	159948
Seq. ID	LIB3176-118-P2-K1-C7
Method	BLASTX
NCBI GI	g2832649
BLAST score	674
E value	5.0e-71
Match length	132
% identity	100
NCBI Description	(AL021710) adenylosuccinate lyase - like protein [Arabidopsis thaliana]
Seq. No.	159949
Seq. ID	LIB3176-118-P2-K1-C8
Method	BLASTX
NCBI GI	g2760362
BLAST score	671
E value	1.0e-70
Match length	132
% identity	100
NCBI Description	(AF016511) 15.9 kDa subunit of RNA polymerase II [Arabidopsis thaliana]
Seq. No.	159950
Seq. ID	LIB3176-118-P2-K1-C9
Method	BLASTX
NCBI GI	g1136793
BLAST score	70
E value	2.1e+00
Match length	97
% identity	46
NCBI Description	(X91486) PMSR protein [Brassica napus]
Seq. No.	159951
Seq. ID	LIB3176-118-P2-K1-D1
Method	BLASTX
NCBI GI	g3023848
BLAST score	463
E value	3.0e-46
Match length	111
% identity	31
NCBI Description	GUANINE NUCLEOTIDE-BINDING PROTEIN BETA SUBUNIT-LIKE PROTEIN (WD-40 REPEAT AUXIN-DEPENDENT PROTEIN ARCA) >gi_2289095 (U77381) WD-40 repeat protein [Arabidopsis thaliana]
Seq. No.	159952
Seq. ID	LIB3176-118-P2-K1-D10
Method	BLASTX
NCBI GI	g1486472
BLAST score	508
E value	1.0e-51
Match length	115
% identity	87
NCBI Description	(X99853) oxoglutarate malate translocator [Solanum tuberosum]

Seq. No.	159953
Seq. ID	LIB3176-118-P2-K1-D11
Method	BLASTN
NCBI GI	g3386593
BLAST score	72
E value	4.0e-32
Match length	144
% identity	88
NCBI Description	Arabidopsis thaliana chromosome II BAC F4I18 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	159954
Seq. ID	LIB3176-118-P2-K1-D12
Method	BLASTN
NCBI GI	g287378
BLAST score	75
E value	6.0e-34
Match length	79
% identity	99
NCBI Description	Oryza sativa mitochondrial gene for tRNA-Arg, complete sequence, clone:pMTVSCT4

Seq. No.	159955
Seq. ID	LIB3176-118-P2-K1-D3
Method	BLASTX
NCBI GI	g113026
BLAST score	680
E value	9.0e-72
Match length	145
% identity	89
NCBI Description	ISOCITRATE LYASE (ISOCITRASE) (ISOCITRATASE) (ICL) >gi_68211_pir__WZRPI isocitrate lyase (EC 4.1.3.1) - rape >gi_255220_bbs_112862 isocitrate lyase, threo-D S-isocitrate glyoxylate-lyase, IL {EC 4.1.3.1} [Brassica napus, seedlings, Peptide, 576 aa] >gi_167144 (L08482) isocitrate lyase [Brassica napus] >gi_447142_prf__1913424A isocitrate lyase [Brassica napus]

Seq. No.	159956
Seq. ID	LIB3176-118-P2-K1-D4
Method	BLASTX
NCBI GI	g113026
BLAST score	611
E value	1.0e-63
Match length	132
% identity	89
NCBI Description	ISOCITRATE LYASE (ISOCITRASE) (ISOCITRATASE) (ICL) >gi_68211_pir__WZRPI isocitrate lyase (EC 4.1.3.1) - rape >gi_255220_bbs_112862 isocitrate lyase, threo-D S-isocitrate glyoxylate-lyase, IL {EC 4.1.3.1} [Brassica napus, seedlings, Peptide, 576 aa] >gi_167144 (L08482) isocitrate lyase [Brassica napus] >gi_447142_prf__1913424A isocitrate lyase [Brassica napus]

Seq. No.	159957
Seq. ID	LIB3176-118-P2-K1-D5

Method	BLASTN
NCBI GI	g2058281
BLAST score	50
E value	1.0e-19
Match length	74
% identity	92
NCBI Description	A.thaliana mRNA for AtRanBP1a protein

Seq. No.	159958
Seq. ID	LIB3176-118-P2-K1-D6
Method	BLASTX
NCBI GI	g3738284
BLAST score	165
E value	2.0e-11
Match length	43
% identity	70
NCBI Description	(AC005309) unknown protein [Arabidopsis thaliana]

Seq. No.	159959
Seq. ID	LIB3176-118-P2-K1-D7
Method	BLASTX
NCBI GI	g3184272
BLAST score	787
E value	2.0e-84
Match length	141
% identity	48
NCBI Description	(AC004136) hypothetical protein [Arabidopsis thaliana]

Seq. No.	159960
Seq. ID	LIB3176-118-P2-K1-D8
Method	BLASTX
NCBI GI	g1169278
BLAST score	326
E value	2.0e-30
Match length	129
% identity	57
NCBI Description	DEHYDRIN ERD14 >gi_556474_dbj_BAA04569_ (D17715) ERD14 protein [Arabidopsis thaliana]

Seq. No.	159961
Seq. ID	LIB3176-118-P2-K1-E1
Method	BLASTX
NCBI GI	g280386
BLAST score	313
E value	4.0e-29
Match length	60
% identity	98
NCBI Description	ubiquitin / ribosomal protein CEP52 - Arabidopsis thaliana >gi_166930 (J05507) ubiquitin extension protein (UBQ1) [Arabidopsis thaliana] >gi_166932 (J05508) ubiquitin extension protein (UBQ2) [Arabidopsis thaliana] >gi_4678227_gb_AAD26972.1_AC007135_8 (AC007135) ubiquitin/ribosomal protein CEP52 [Arabidopsis thaliana]

Seq. No.	159962
Seq. ID	LIB3176-118-P2-K1-E10
Method	BLASTX

NCBI GI	g4567260
BLAST score	765
E value	9.0e-82
Match length	145
% identity	100
NCBI Description	(AC006841) putative NADPH dependent mannose 6-phosphate reductase [Arabidopsis thaliana] >gi_4582440_gb_AAD24825.1_AC007142_3 (AC007142) putative NADPH-dependent mannose-6-phosphate reductase [Arabidopsis thaliana]

Seq. No.	159963
Seq. ID	LIB3176-118-P2-K1-E11
Method	BLASTX
NCBI GI	g119143
BLAST score	660
E value	2.0e-69
Match length	126
% identity	100
NCBI Description	ELONGATION FACTOR 1-ALPHA (EF-1-ALPHA) >gi_81606_pir__S06724 translation elongation factor eEF-1 alpha chain - Arabidopsis thaliana >gi_295788_emb_CAA34453_ (X16430) elongation factor 1-alpha [Arabidopsis thaliana] >gi_1369927_emb_CAA34454_ (X16431) elongation factor 1-alpha [Arabidopsis thaliana] >gi_1369928_emb_CAA34455_ (X16431) elongation factor 1-alpha [Arabidopsis thaliana] >gi_1532172 (U63815) EF-1alpha-A1 [Arabidopsis thaliana] >gi_1532173 (U63815) EF-1alpha-A2 [Arabidopsis thaliana] >gi_1532174 (U63815) EF-1alpha-A3 [Arabidopsis thaliana]

Seq. No.	159964
Seq. ID	LIB3176-118-P2-K1-E2
Method	BLASTN
NCBI GI	g2245031
BLAST score	40
E value	2.0e-13
Match length	182
% identity	99
NCBI Description	Arabidopsis thaliana DNA chromosome 4, ESSA I contig fragment No

Seq. No.	159965
Seq. ID	LIB3176-118-P2-K1-E3
Method	BLASTX
NCBI GI	g4263525
BLAST score	576
E value	1.0e-59
Match length	134
% identity	85
NCBI Description	(AC004044) putative photosystem I reaction center subunit II precursor [Arabidopsis thaliana]

Seq. No.	159966
Seq. ID	LIB3176-118-P2-K1-E5
Method	BLASTN
NCBI GI	g2191126
BLAST score	90

E value	3.0e-43
Match length	236
% identity	97
NCBI Description	Arabidopsis thaliana BAC IG002N01

Seq. No.	159967
Seq. ID	LIB3176-118-P2-K1-E6
Method	BLASTN
NCBI GI	g2352491
BLAST score	207
E value	1.0e-113
Match length	271
% identity	93
NCBI Description	Arabidopsis thaliana transport inhibitor response 1 (TIR1) gene, complete cds

Seq. No.	159968
Seq. ID	LIB3176-118-P2-K1-E8
Method	BLASTN
NCBI GI	g3264774
BLAST score	236
E value	1.0e-130
Match length	392
% identity	100
NCBI Description	Arabidopsis thaliana BAC T8A17 chromosome IV, complete sequence [Arabidopsis thaliana]

Seq. No.	159969
Seq. ID	LIB3176-118-P2-K1-E9
Method	BLASTN
NCBI GI	g2702261
BLAST score	152
E value	3.0e-80
Match length	196
% identity	94
NCBI Description	Arabidopsis thaliana chromosome II BAC T21L14 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	159970
Seq. ID	LIB3176-118-P2-K1-F10
Method	BLASTN
NCBI GI	g2695704
BLAST score	262
E value	1.0e-145
Match length	375
% identity	99
NCBI Description	A.thaliana constans gene

Seq. No.	159971
Seq. ID	LIB3176-118-P2-K1-F11
Method	BLASTX
NCBI GI	g3150415
BLAST score	592
E value	2.0e-61
Match length	120
% identity	35
NCBI Description	(AC004165) sec13-related protein [Arabidopsis thaliana]

	>gi_3420046 (AC004680) sec13-related protein [Arabidopsis thaliana]
Seq. No.	159972
Seq. ID	LIB3176-118-P2-K1-F12
Method	BLASTX
NCBI GI	g170352
BLAST score	396
E value	2.0e-38
Match length	80
% identity	17
NCBI Description	(M74101) hexameric polyubiquitin [Nicotiana sylvestris] >gi_870792 (L05361) polyubiquitin [Arabidopsis thaliana] >gi_4115333 (L81139) ubiquitin [Pisum sativum] >gi_4115335 (L81140) ubiquitin [Pisum sativum]
Seq. No.	159973
Seq. ID	LIB3176-118-P2-K1-F2
Method	BLASTX
NCBI GI	g2618701
BLAST score	728
E value	2.0e-77
Match length	141
% identity	99
NCBI Description	(AC002510) hypothetical protein [Arabidopsis thaliana]
Seq. No.	159974
Seq. ID	LIB3176-118-P2-K1-F3
Method	BLASTX
NCBI GI	g3914535
BLAST score	174
E value	5.0e-13
Match length	44
% identity	80
NCBI Description	60S RIBOSOMAL PROTEIN L13A >gi_2791948_emb_CAA11283_ (AJ223363) ribosomal protein L13a [Lupinus luteus]
Seq. No.	159975
Seq. ID	LIB3176-118-P2-K1-F5
Method	BLASTX
NCBI GI	g4455235
BLAST score	262
E value	5.0e-23
Match length	69
% identity	80
NCBI Description	(AL035523) PROTEIN TRANSPORT PROTEIN SEC61 GAMMA SUBUNIT-like [Arabidopsis thaliana]
Seq. No.	159976
Seq. ID	LIB3176-118-P2-K1-F6
Method	BLASTX
NCBI GI	g2104535
BLAST score	229
E value	3.0e-35
Match length	87
% identity	92
NCBI Description	(AF001308) T10M13.13 [Arabidopsis thaliana]

Seq. No.	159977
Seq. ID	LIB3176-118-P2-K1-F7
Method	BLASTX
NCBI GI	g3169171
BLAST score	550
E value	1.0e-56
Match length	123
% identity	80
NCBI Description	(AC004401) putative serine carboxypeptidase I [Arabidopsis thaliana] >gi_3445213 (AC004786) putative serine carboxypeptidase I [Arabidopsis thaliana]

Seq. No.	159978
Seq. ID	LIB3176-118-P2-K1-F8
Method	BLASTN
NCBI GI	g2244747
BLAST score	315
E value	1.0e-177
Match length	395
% identity	99
NCBI Description	Arabidopsis thaliana DNA chromosome 4, ESSA I contig fragment No

Seq. No.	159979
Seq. ID	LIB3176-118-P2-K1-F9
Method	BLASTX
NCBI GI	g3482978
BLAST score	579
E value	5.0e-60
Match length	123
% identity	89
NCBI Description	(AL031369) putative protein [Arabidopsis thaliana]

Seq. No.	159980
Seq. ID	LIB3176-118-P2-K1-G1
Method	BLASTN
NCBI GI	g3449326
BLAST score	71
E value	9.0e-32
Match length	122
% identity	91
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K19M22, complete sequence [Arabidopsis thaliana]

Seq. No.	159981
Seq. ID	LIB3176-118-P2-K1-G10
Method	BLASTX
NCBI GI	g4006883
BLAST score	510
E value	6.0e-52
Match length	122
% identity	81
NCBI Description	(Z99707) cysteine proteinase [Arabidopsis thaliana]

Seq. No.	159982
Seq. ID	LIB3176-118-P2-K1-G12

Method	BLASTX
NCBI GI	g3149952
BLAST score	281
E value	5.0e-25
Match length	62
% identity	81
NCBI Description	(AB010259) DRH1 [Arabidopsis thaliana]

Seq. No.	159983
Seq. ID	LIB3176-118-P2-K1-G2
Method	BLASTN
NCBI GI	g2351065
BLAST score	156
E value	2.0e-82
Match length	356
% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MHF15, complete sequence [Arabidopsis thaliana]

Seq. No.	159984
Seq. ID	LIB3176-118-P2-K1-G3
Method	BLASTX
NCBI GI	g1363489
BLAST score	204
E value	1.0e-16
Match length	44
% identity	89
NCBI Description	thioglucosidase (EC 3.2.3.1) 3D precursor - Arabidopsis thaliana >gi_984052_emb_CAA61592_ (X89413) thioglucoside glucohydrolase [Arabidopsis thaliana]

Seq. No.	159985
Seq. ID	LIB3176-118-P2-K1-G4
Method	BLASTX
NCBI GI	g1172873
BLAST score	306
E value	4.0e-31
Match length	87
% identity	91
NCBI Description	CYSTEINE PROTEINASE RD21A PRECURSOR >gi_541857_pir__JN0719 drought-inducible cysteine proteinase (EC 3.4.22.-) RD21A precursor - Arabidopsis thaliana >gi_435619_dbj_BAA02374_ (D13043) thiol protease [Arabidopsis thaliana]

Seq. No.	159986
Seq. ID	LIB3176-118-P2-K1-G5
Method	BLASTX
NCBI GI	g4584110
BLAST score	143
E value	9.0e-09
Match length	52
% identity	56
NCBI Description	(AJ133639) SAH7 protein [Arabidopsis thaliana]

Seq. No.	159987
Seq. ID	LIB3176-118-P2-K1-G6
Method	BLASTX

NCBI GI	g4335737
BLAST score	220
E value	8.0e-18
Match length	136
% identity	26
NCBI Description	(AC006248) putative serine/threonine kinase [Arabidopsis thaliana]

Seq. No.	159988
Seq. ID	LIB3176-118-P2-K1-G7
Method	BLASTN
NCBI GI	g3449326
BLAST score	301
E value	1.0e-169
Match length	337
% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K19M22, complete sequence [Arabidopsis thaliana]

Seq. No.	159989
Seq. ID	LIB3176-118-P2-K1-G8
Method	BLASTX
NCBI GI	g2738248
BLAST score	547
E value	2.0e-56
Match length	111
% identity	99
NCBI Description	(U97200) cobalamin-independent methionine synthase [Arabidopsis thaliana]

Seq. No.	159990
Seq. ID	LIB3176-118-P2-K1-G9
Method	BLASTX
NCBI GI	g2262098
BLAST score	630
E value	5.0e-66
Match length	130
% identity	97
NCBI Description	(AC002343) HSP90 isolog [Arabidopsis thaliana]

Seq. No.	159991
Seq. ID	LIB3176-118-P2-K1-H10
Method	BLASTX
NCBI GI	g2654122
BLAST score	327
E value	1.0e-30
Match length	101
% identity	67
NCBI Description	(AF034694) ribosomal protein L23a [Arabidopsis thaliana]

Seq. No.	159992
Seq. ID	LIB3176-118-P2-K1-H11
Method	BLASTX
NCBI GI	g4490732
BLAST score	421
E value	6.0e-42
Match length	78

% identity	97
NCBI Description	(AL035709) phosphoenolpyruvate carboxykinase (ATP)-like protein [Arabidopsis thaliana]

Seq. No.	159993
Seq. ID	LIB3176-118-P2-K1-H12
Method	BLASTN
NCBI GI	g4510338
BLAST score	293
E value	1.0e-164
Match length	326
% identity	97
NCBI Description	Arabidopsis thaliana chromosome II BAC F2H17 genomic sequence, complete sequence

Seq. No.	159994
Seq. ID	LIB3176-118-P2-K1-H2
Method	BLASTX
NCBI GI	g120667
BLAST score	178
E value	5.0e-13
Match length	65
% identity	62
NCBI Description	GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE, CYTOSOLIC >gi_81622_pir__JQ1287 glyceraldehyde-3-phosphate dehydrogenase (EC 1.2.1.12), cytosolic - Arabidopsis thaliana >gi_166706 (M64116) cystolic glyceraldehyde-3-phosphate dehydrogenase [Arabidopsis thaliana] >gi_166710 (M64119) glyceraldehyde-3-phosphate dehydrogenase [Arabidopsis thaliana]

Seq. No.	159995
Seq. ID	LIB3176-118-P2-K1-H3
Method	BLASTX
NCBI GI	g4006883
BLAST score	772
E value	1.0e-82
Match length	146
% identity	99
NCBI Description	(Z99707) cysteine proteinase [Arabidopsis thaliana]

Seq. No.	159996
Seq. ID	LIB3176-118-P2-K1-H4
Method	BLASTX
NCBI GI	g4586249
BLAST score	317
E value	3.0e-29
Match length	130
% identity	57
NCBI Description	(AL049640) putative pollen surface protein [Arabidopsis thaliana]

Seq. No.	159997
Seq. ID	LIB3176-118-P2-K1-H5
Method	BLASTX
NCBI GI	g2244750
BLAST score	701

E value	3.0e-74
Match length	143
% identity	90
NCBI Description	(Z97335) adenosylhomocysteinase [Arabidopsis thaliana] >gi_3088579 (AF059581) S-adenosyl-L-homocysteine hydrolase [Arabidopsis thaliana]

Seq. No.	159998
Seq. ID	LIB3176-118-P2-K1-H6
Method	BLASTX
NCBI GI	g2058282
BLAST score	350
E value	3.0e-33
Match length	96
% identity	76
NCBI Description	(X97377) atranbp1a [Arabidopsis thaliana]

Seq. No.	159999
Seq. ID	LIB3176-118-P2-K1-H7
Method	BLASTN
NCBI GI	g2264316
BLAST score	52
E value	3.0e-20
Match length	406
% identity	38
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MRO11, complete sequence [Arabidopsis thaliana]

Seq. No.	160000
Seq. ID	LIB3176-118-P2-K1-H8
Method	BLASTX
NCBI GI	g166765
BLAST score	592
E value	2.0e-61
Match length	116
% identity	97
NCBI Description	(M23106) heat shock protein HSP70-1 [Arabidopsis thaliana]

Seq. No.	160001
Seq. ID	LIB3176-118-P2-K1-H9
Method	BLASTX
NCBI GI	g2832625
BLAST score	450
E value	8.0e-45
Match length	99
% identity	85
NCBI Description	(AL021711) putative protein [Arabidopsis thaliana]

Seq. No.	160002
Seq. ID	LIB3176-119-P2-K1-A10
Method	BLASTX
NCBI GI	g2961372
BLAST score	713
E value	1.0e-75
Match length	137
% identity	99
NCBI Description	(AL022141) putative ribosomal protein L8 [Arabidopsis

	thaliana] >gi_3036817_emb_CAA18507_ (AL022373) ribosomal protein L2 [Arabidopsis thaliana]
Seq. No.	160003
Seq. ID	LIB3176-119-P2-K1-A11
Method	BLASTN
NCBI GI	g3036791
BLAST score	39
E value	2.0e-12
Match length	131
% identity	82
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone T19K4 (ESSAII project)
Seq. No.	160004
Seq. ID	LIB3176-119-P2-K1-A2
Method	BLASTX
NCBI GI	g1350981
BLAST score	146
E value	1.0e-09
Match length	46
% identity	63
NCBI Description	40S RIBOSOMAL PROTEIN S3A (S PHASE SPECIFIC PROTEIN BIS289) >gi_480282_pir__S36622 hypothetical protein - turnip >gi_387909 (L23553) S-phase-specific protein [Brassica rapa] >gi_397401_emb_CAA81030_ (Z25769) putative product [Brassica rapa]
Seq. No.	160005
Seq. ID	LIB3176-119-P2-K1-A6
Method	BLASTX
NCBI GI	g2829526
BLAST score	177
E value	9.0e-13
Match length	68
% identity	51
NCBI Description	GUANYLATE KINASE (GMP KINASE) >gi_1542897_emb_CAB02172_ (Z80108) gmk [Mycobacterium tuberculosis]
Seq. No.	160006
Seq. ID	LIB3176-119-P2-K1-A7
Method	BLASTN
NCBI GI	g3766106
BLAST score	137
E value	6.0e-71
Match length	149
% identity	98
NCBI Description	Arabidopsis thaliana chromosome 1 BAC F9K20 sequence, complete sequence [Arabidopsis thaliana]
Seq. No.	160007
Seq. ID	LIB3176-119-P2-K1-A8
Method	BLASTN
NCBI GI	g4678340
BLAST score	270
E value	1.0e-150
Match length	290

% identity	98
NCBI Description	Arabidopsis thaliana DNA chromosome 3, BAC clone T29H11 (ESSA project)

Seq. No.	160008
Seq. ID	LIB3176-119-P2-K1-A9
Method	BLASTN
NCBI GI	g4455229
BLAST score	439
E value	0.0e+00
Match length	446
% identity	100
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F13M23 (ESSAII project)

Seq. No.	160009
Seq. ID	LIB3176-119-P2-K1-B10
Method	BLASTX
NCBI GI	g4210334
BLAST score	639
E value	6.0e-67
Match length	146
% identity	90
NCBI Description	(AJ223804) 2-oxoglutarate dehydrogenase, E3 subunit [Arabidopsis thaliana]

Seq. No.	160010
Seq. ID	LIB3176-119-P2-K1-B11
Method	BLASTN
NCBI GI	g3641835
BLAST score	135
E value	8.0e-70
Match length	402
% identity	100
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone T4L20 (ESSAII project)

Seq. No.	160011
Seq. ID	LIB3176-119-P2-K1-B2
Method	BLASTX
NCBI GI	g99698
BLAST score	523
E value	2.0e-53
Match length	100
% identity	99
NCBI Description	glutamate--ammonia ligase (EC 6.3.1.2), cytosolic (clone lambdaAtgskb6) - Arabidopsis thaliana

Seq. No.	160012
Seq. ID	LIB3176-119-P2-K1-B4
Method	BLASTX
NCBI GI	g3834328
BLAST score	777
E value	4.0e-83
Match length	146
% identity	99
NCBI Description	(AC005679) Strong similarity to glycoprotein EP1 gb_L16983

Daucus carota and a member of S locus glycoprotein family PF_00954. [Arabidopsis thaliana]

Seq. No.	160013
Seq. ID	LIB3176-119-P2-K1-B5
Method	BLASTX
NCBI GI	g3377797
BLAST score	201
E value	3.0e-16
Match length	58
% identity	74
NCBI Description	(AF075597) Similar to 60S ribosome protein L19; coded for by A. thaliana cDNA T04719; coded for by A. thaliana cDNA H36046; coded for by A. thaliana cDNA T44067; coded for by A. thaliana cDNA T14056; coded for by A. thaliana cDNA R90691 [Ara

Seq. No.	160014
Seq. ID	LIB3176-119-P2-K1-B6
Method	BLASTX
NCBI GI	g3785996
BLAST score	445
E value	3.0e-44
Match length	89
% identity	58
NCBI Description	(AC005499) putative annexin [Arabidopsis thaliana]

Seq. No.	160015
Seq. ID	LIB3176-119-P2-K1-B8
Method	BLASTX
NCBI GI	g281807
BLAST score	575
E value	2.0e-59
Match length	145
% identity	71
NCBI Description	adenylosuccinate lyase - Escherichia coli

Seq. No.	160016
Seq. ID	LIB3176-119-P2-K1-B9
Method	BLASTX
NCBI GI	g1350680
BLAST score	266
E value	1.0e-23
Match length	70
% identity	80
NCBI Description	60S RIBOSOMAL PROTEIN L1

Seq. No.	160017
Seq. ID	LIB3176-119-P2-K1-C1
Method	BLASTX
NCBI GI	g3892056
BLAST score	394
E value	1.0e-38
Match length	89
% identity	90
NCBI Description	(AC002330) putative vacuolar ATPase [Arabidopsis thaliana]

Seq. No.	160018
Seq. ID	LIB3176-119-P2-K1-C10
Method	BLASTX
NCBI GI	g4539297
BLAST score	375
E value	5.0e-36
Match length	137
% identity	58
NCBI Description	(AL049480) putative pathogenesis-related protein [Arabidopsis thaliana]

Seq. No.	160019
Seq. ID	LIB3176-119-P2-K1-C11
Method	BLASTX
NCBI GI	g2129533
BLAST score	552
E value	6.0e-57
Match length	112
% identity	96
NCBI Description	adenine nucleotide translocase - Arabidopsis thaliana >gi_1051109_emb_CAA89201_ (Z49227) adenine nucleotide translocase [Arabidopsis thaliana]

Seq. No.	160020
Seq. ID	LIB3176-119-P2-K1-C12
Method	BLASTX
NCBI GI	g4580920
BLAST score	362
E value	1.0e-34
Match length	89
% identity	79
NCBI Description	(AF113545) vacuole-associated annexin VCaB42 [Nicotiana tabacum]

Seq. No.	160021
Seq. ID	LIB3176-119-P2-K1-C4
Method	BLASTX
NCBI GI	g2160174
BLAST score	368
E value	2.0e-35
Match length	92
% identity	84
NCBI Description	(AC000132) Identical to A. thaliana PUR2 (gb_X74766). ESTs gb_ATTS3927,gb_N96446 come from this gene. [Arabidopsis thaliana]

Seq. No.	160022
Seq. ID	LIB3176-119-P2-K1-C6
Method	BLASTX
NCBI GI	g2244750
BLAST score	548
E value	2.0e-56
Match length	113
% identity	94
NCBI Description	(Z97335) adenosylhomocysteinase [Arabidopsis thaliana] >gi_3088579 (AF059581) S-adenosyl-L-homocysteine hydrolase [Arabidopsis thaliana]

Seq. No.	160023
Seq. ID	LIB3176-119-P2-K1-C7
Method	BLASTX
NCBI GI	g3892056
BLAST score	442
E value	6.0e-44
Match length	92
% identity	99
NCBI Description	(AC002330) putative vacuolar ATPase [Arabidopsis thaliana]

Seq. No.	160024
Seq. ID	LIB3176-119-P2-K1-C8
Method	BLASTX
NCBI GI	g3913653
BLAST score	730
E value	1.0e-77
Match length	151
% identity	88
NCBI Description	FERREDOXIN--NADP REDUCTASE, EMBRYO ISOZYME PRECURSOR (FNR) >gi_1778686_dbj_BAA13417_ (D87547) precursor ferredoxin-NADP+ oxidoreductase [Oryza sativa]

Seq. No.	160025
Seq. ID	LIB3176-119-P2-K1-D1
Method	BLASTN
NCBI GI	g498913
BLAST score	161
E value	1.0e-85
Match length	177
% identity	98
NCBI Description	Arabidopsis thaliana Columbia glutamate-1-semialdehyde aminotransferase (gsa2) gene, complete cds

Seq. No.	160026
Seq. ID	LIB3176-119-P2-K1-D10
Method	BLASTN
NCBI GI	g2477521
BLAST score	32
E value	3.0e-08
Match length	378
% identity	11
NCBI Description	Arabidopsis thaliana chromosome I BAC F22K20 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	160027
Seq. ID	LIB3176-119-P2-K1-D11
Method	BLASTX
NCBI GI	g1351272
BLAST score	270
E value	7.0e-24
Match length	78
% identity	72
NCBI Description	TRIOSEPHOSPHATE ISOMERASE, CYTOSOLIC (TIM) >gi_414550 (U02949) cytosolic triose phosphate isomerase [Arabidopsis thaliana] >gi_742408_prf__2009415A triose phosphate isomerase [Arabidopsis thaliana]

D0E3404.400

Seq. No.	160028
Seq. ID	LIB3176-119-P2-K1-D12
Method	BLASTX
NCBI GI	g2146731
BLAST score	398
E value	9.0e-39
Match length	120
% identity	32
NCBI Description	FK506-binding protein - Arabidopsis thaliana >gi_1354207 (U49453) rof1 [Arabidopsis thaliana]

Seq. No.	160029
Seq. ID	LIB3176-119-P2-K1-D3
Method	BLASTN
NCBI GI	g3228389
BLAST score	181
E value	3.0e-97
Match length	208
% identity	100
NCBI Description	Genomic sequence for Arabidopsis thaliana BAC F17L21, complete sequence [Arabidopsis thaliana]

Seq. No.	160030
Seq. ID	LIB3176-119-P2-K1-D4
Method	BLASTX
NCBI GI	g3342802
BLAST score	375
E value	3.0e-36
Match length	100
% identity	75
NCBI Description	(AF061838) putative cytosolic 6-phosphogluconate dehydrogenase [Zea mays]

Seq. No.	160031
Seq. ID	LIB3176-119-P2-K1-D6
Method	BLASTX
NCBI GI	g132074
BLAST score	661
E value	1.0e-69
Match length	126
% identity	98
NCBI Description	RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN 1A PRECURSOR (RUBISCO SMALL SUBUNIT 1A) >gi_68063_pir__RKMUA1 ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain A1 precursor - Arabidopsis thaliana

Seq. No.	160032
Seq. ID	LIB3176-119-P2-K1-D7
Method	BLASTN
NCBI GI	g1532162
BLAST score	51
E value	8.0e-20
Match length	361
% identity	55
NCBI Description	Arabidopsis thaliana AT.I.24-1, AT.I.24-2, AT.I.24-3, AT.I.24-4, AT.I.24-5, AT.I.24-6, AT.I.24-9 and AT.I.24-14

genes, partial cds, AT.I.24-7, ascorbate peroxidase (ATHAPX1), EF-1alpha-A1, -A2 and -A3 (EF-1alpha) and AT.I

Seq. No.	160033
Seq. ID	LIB3176-119-P2-K1-D8
Method	BLASTN
NCBI GI	g1732514
BLAST score	450
E value	0.0e+00
Match length	450
% identity	100
NCBI Description	Arabidopsis thaliana myosin heavy chain-like protein mRNA, complete cds

Seq. No.	160034
Seq. ID	LIB3176-119-P2-K1-D9
Method	BLASTX
NCBI GI	g2119012
BLAST score	148
E value	7.0e-10
Match length	75
% identity	43
NCBI Description	histone 3.3A - chicken >gi_211851 (M11667) histone 3.3A [Gallus gallus]

Seq. No.	160035
Seq. ID	LIB3176-119-P2-K1-E1
Method	BLASTX
NCBI GI	g122085
BLAST score	522
E value	2.0e-53
Match length	122
% identity	86
NCBI Description	HISTONE H3 >gi_81641_pir__S06250 histone H3 - Arabidopsis thaliana >gi_82482_pir__S04099 histone H3 (variant H3R-21) - rice >gi_1362194_pir__S57626 histone H3 - maize >gi_20251_emb_CAA31969_ (X13678) histone H3 (AA 1-136) [Oryza sativa] >gi_20253_emb_CAA31970_ (X13680) histone H3 (AA 1-136) [Oryza sativa] >gi_168493 (M36658) histone H3 (H3C3) [Zea mays] >gi_168495 (M13378) histone H3 [Zea mays] >gi_168497 (M13379) histone H3 [Zea mays] >gi_168506 (M35388) histone H3 [Zea mays] >gi_169655 (M77493) histone H3 [Petroselinum crispum] >gi_169657 (M77494) histone H3 [Petroselinum crispum] >gi_169659 (M77495) histone H3 [Petroselinum crispum] >gi_387565 (M17130) histone H3 [Arabidopsis thaliana] >gi_387567 (M17131) histone H3 [Arabidopsis thaliana] >gi_886738_emb_CAA59111_ (X84377) histone 3 [Zea mays] >gi_1040764 (M35387) histone H3 [Arabidopsis thaliana] >gi_1314779 (U54827) histone H3 homolog [Brassica napus] >gi_1531754_emb_CAA57811_ (X82414) Histone H3 [Asparagus officinalis] >gi_1667592 (U77296) histone 3 [Oryza sativa] >gi_3249101 (AC003114) Match to histone H3 gene gb_M17131 and gb_M35387 from A. thaliana. ESTs gb_H76511 gb_H76255, gb_AA712452, gb_N65260 and gb_T42306 come from this gene. [Arabidopsis thaliana] >gi_225459_prf__1303352A histone H3 [Helicoverpa zea] >gi_225839_prf__1314298B histone H3 [Arabidopsis thaliana]

Seq. No.	160036
Seq. ID	LIB3176-119-P2-K1-E10
Method	BLASTX
NCBI GI	g1363487
BLAST score	517
E value	8.0e-53
Match length	107
% identity	97
NCBI Description	IAA7 protein - Arabidopsis thaliana >gi_972917 (U18409) IAA7 [Arabidopsis thaliana]

Seq. No.	160037
Seq. ID	LIB3176-119-P2-K1-E12
Method	BLASTX
NCBI GI	g4454036
BLAST score	555
E value	3.0e-57
Match length	103
% identity	99
NCBI Description	(AL035394) putative major latex protein [Arabidopsis thaliana]

Seq. No.	160038
Seq. ID	LIB3176-119-P2-K1-E2
Method	BLASTN
NCBI GI	g1322277
BLAST score	32
E value	1.0e-08
Match length	60
% identity	88
NCBI Description	Arabidopsis thaliana cyclophilin (ROC4) gene, nuclear gene encoding chloroplast protein, complete cds

Seq. No.	160039
Seq. ID	LIB3176-119-P2-K1-E3
Method	BLASTN
NCBI GI	g4159712
BLAST score	81
E value	2.0e-38
Match length	81
% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MWI23, complete sequence

Seq. No.	160040
Seq. ID	LIB3176-119-P2-K1-E5
Method	BLASTX
NCBI GI	g2529665
BLAST score	176
E value	2.0e-13
Match length	50
% identity	68
NCBI Description	(AC002535) putative ribosomal protein L7A [Arabidopsis thaliana]

Seq. No.	160041

Seq. ID	LIB3176-119-P2-K1-E7
Method	BLASTN
NCBI GI	g4757409
BLAST score	269
E value	1.0e-150
Match length	277
% identity	99
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MVC8, complete sequence

Seq. No.	160042
Seq. ID	LIB3176-119-P2-K1-E8
Method	BLASTN
NCBI GI	g3297806
BLAST score	80
E value	1.0e-37
Match length	88
% identity	98
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F17I5 (ESSA project)

Seq. No.	160043
Seq. ID	LIB3176-119-P2-K1-F10
Method	BLASTX
NCBI GI	g2924779
BLAST score	630
E value	6.0e-66
Match length	126
% identity	98
NCBI Description	(AC002334) putative 3-ketoacyl-CoA thiolase [Arabidopsis thaliana] >gi_2981616_dbj_BAA25248_ (AB008854) 3-ketoacyl-CoA thiolase [Arabidopsis thaliana] >gi_2981618_dbj_BAA25249_ (AB008855) 3-ketoacyl-CoA thiolase [Arabidopsis thaliana]

Seq. No.	160044
Seq. ID	LIB3176-119-P2-K1-F11
Method	BLASTN
NCBI GI	g1742952
BLAST score	135
E value	6.0e-70
Match length	175
% identity	93
NCBI Description	A.thaliana mRNA for CLC-a chloride channel protein

Seq. No.	160045
Seq. ID	LIB3176-119-P2-K1-F12
Method	BLASTX
NCBI GI	g4220514
BLAST score	329
E value	1.0e-30
Match length	141
% identity	51
NCBI Description	(AL035356) putative protein [Arabidopsis thaliana]

Seq. No.	160046
Seq. ID	LIB3176-119-P2-K1-F2

Method	BLASTX
NCBI GI	g1785851
BLAST score	148
E value	8.0e-10
Match length	53
% identity	55
NCBI Description	(D50692) c-myc binding protein [Homo sapiens] >gi_2443310_dbj_BAA22408_ (AB007191) AMY-1 [Homo sapiens]

Seq. No.	160047
Seq. ID	LIB3176-119-P2-K1-F3
Method	BLASTN
NCBI GI	g4309683
BLAST score	228
E value	1.0e-125
Match length	248
% identity	98
NCBI Description	Arabidopsis thaliana chromosome 1 BAC T31J12 sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	160048
Seq. ID	LIB3176-119-P2-K1-F4
Method	BLASTX
NCBI GI	g2244909
BLAST score	736
E value	2.0e-78
Match length	147
% identity	99
NCBI Description	(Z97339) pyruvate,orthophosphate dikinase [Arabidopsis thaliana]

Seq. No.	160049
Seq. ID	LIB3176-119-P2-K1-F5
Method	BLASTX
NCBI GI	g3600058
BLAST score	202
E value	4.0e-16
Match length	46
% identity	93
NCBI Description	(AF080120) similar to vacuolar ATPases [Arabidopsis thaliana]

Seq. No.	160050
Seq. ID	LIB3176-119-P2-K1-F6
Method	BLASTX
NCBI GI	g132863
BLAST score	614
E value	4.0e-64
Match length	123
% identity	93
NCBI Description	CHLOROPLAST 50S RIBOSOMAL PROTEIN L2 >gi_12214_emb_CAA46568_ (X65615) ribosomal protein L2 [Sinapis alba]

Seq. No.	160051
Seq. ID	LIB3176-119-P2-K1-F7
Method	BLASTX

NCBI GI	g4432859
BLAST score	251
E value	2.0e-21
Match length	86
% identity	59
NCBI Description	(AC006300) unknown protein [Arabidopsis thaliana]

Seq. No.	160052
Seq. ID	LIB3176-119-P2-K1-F8
Method	BLASTX
NCBI GI	g2829869
BLAST score	346
E value	8.0e-33
Match length	83
% identity	86
NCBI Description	(AC002396) pyruvate dehydrogenase E1 alpha subunit [Arabidopsis thaliana]

Seq. No.	160053
Seq. ID	LIB3176-119-P2-K1-G1
Method	BLASTX
NCBI GI	g2459420
BLAST score	640
E value	3.0e-67
Match length	126
% identity	98
NCBI Description	(AC002332) putative ribosomal protein L17 [Arabidopsis thaliana]

Seq. No.	160054
Seq. ID	LIB3176-119-P2-K1-G10
Method	BLASTX
NCBI GI	g1170040
BLAST score	318
E value	6.0e-30
Match length	61
% identity	100
NCBI Description	GLUTATHIONE REDUCTASE, CHLOROPLAST PRECURSOR (GR) (GRASE) >gi_451198_dbj_BAA03137_ (D14049) glutathione reductase precursor [Arabidopsis thaliana] >gi_1944448_dbj_BAA19653_ (D89620) glutathione reductase precursor [Arabidopsis thaliana] >gi_740576_prf__2005376A glutathione reductase [Arabidopsis thaliana]

Seq. No.	160055
Seq. ID	LIB3176-119-P2-K1-G11
Method	BLASTX
NCBI GI	g2894596
BLAST score	580
E value	5.0e-60
Match length	115
% identity	97
NCBI Description	(AL021889) putative protein [Arabidopsis thaliana]

Seq. No.	160056
Seq. ID	LIB3176-119-P2-K1-G12
Method	BLASTX

NCBI GI	g2462746
BLAST score	391
E value	5.0e-38
Match length	98
% identity	80
NCBI Description	(AC002292) Similar to ATP-citrate-lyase [Arabidopsis thaliana]

Seq. No.	160057
Seq. ID	LIB3176-119-P2-K1-G2
Method	BLASTX
NCBI GI	g132074
BLAST score	624
E value	3.0e-65
Match length	114
% identity	99
NCBI Description	RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN 1A PRECURSOR (RUBISCO SMALL SUBUNIT 1A) >gi_68063_pir__RKMUA1 ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain A1 precursor - Arabidopsis thaliana

Seq. No.	160058
Seq. ID	LIB3176-119-P2-K1-G4
Method	BLASTX
NCBI GI	g3193323
BLAST score	609
E value	2.0e-63
Match length	122
% identity	98
NCBI Description	(AF069299) similar to ribosomal protein S13 (Pfam; S15.hmm, score: 78.35); identical to Arabidopsis 40S ribosomal protein S13 (fragment) (SW: P49203A) except the first 32 amino acids are different [Arabidopsis thaliana]

Seq. No.	160059
Seq. ID	LIB3176-119-P2-K1-G5
Method	BLASTX
NCBI GI	g3334123
BLAST score	373
E value	8.0e-36
Match length	107
% identity	77
NCBI Description	ATP SYNTHASE GAMMA CHAIN, MITOCHONDRIAL PRECURSOR >gi_1655480_dbj_BAA13599_ (D88374) gamma subunit of mitochondrial F1-ATPase [Arabidopsis thaliana] >gi_2924787 (AC002334) mitochondrial F1-ATPase, gamma subunit [Arabidopsis thaliana]

Seq. No.	160060
Seq. ID	LIB3176-119-P2-K1-G6
Method	BLASTX
NCBI GI	g4582787
BLAST score	533
E value	1.0e-54
Match length	145
% identity	69
NCBI Description	(AJ012281) adenosine kinase [Zea mays]

Seq. No.	160061
Seq. ID	LIB3176-119-P2-K1-G7
Method	BLASTX
NCBI GI	g1710581
BLAST score	554
E value	5.0e-57
Match length	124
% identity	90
NCBI Description	60S RIBOSOMAL PROTEIN L9 >gi_2129720_pir__S71255 ribosomal protein L9 - Arabidopsis thaliana >gi_1107489_emb_CAA63024_ (X91958) 60S ribosomal protein L9 [Arabidopsis thaliana]

Seq. No.	160062
Seq. ID	LIB3176-119-P2-K1-G8
Method	BLASTX
NCBI GI	g3894178
BLAST score	362
E value	2.0e-37
Match length	80
% identity	90
NCBI Description	(AC005312) putative nucleic acid binding protein [Arabidopsis thaliana]

Seq. No.	160063
Seq. ID	LIB3176-119-P2-K1-H1
Method	BLASTX
NCBI GI	g3319350
BLAST score	484
E value	5.0e-49
Match length	98
% identity	98
NCBI Description	(AF077407) No definition line found [Arabidopsis thaliana]

Seq. No.	160064
Seq. ID	LIB3176-119-P2-K1-H12
Method	BLASTN
NCBI GI	g2244747
BLAST score	173
E value	8.0e-93
Match length	185
% identity	98
NCBI Description	Arabidopsis thaliana DNA chromosome 4, ESSA I contig fragment No

Seq. No.	160065
Seq. ID	LIB3176-119-P2-K1-H2
Method	BLASTN
NCBI GI	g4220635
BLAST score	190
E value	1.0e-102
Match length	258
% identity	97
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MDB19, complete sequence [Arabidopsis thaliana]

Seq. No.	160066

Seq. ID	LIB3176-119-P2-K1-H4
Method	BLASTX
NCBI GI	g3953473
BLAST score	564
E value	3.0e-58
Match length	114
% identity	100
NCBI Description	(AC002328) F22O2.18 [Arabidopsis thaliana]

Seq. No.	160067
Seq. ID	LIB3176-119-P2-K1-H5
Method	BLASTX
NCBI GI	g2262167
BLAST score	590
E value	3.0e-61
Match length	112
% identity	100
NCBI Description	(AC002329) cytosolic ribosomal protein S4 [Arabidopsis thaliana]

Seq. No.	160068
Seq. ID	LIB3176-119-P2-K1-H6
Method	BLASTN
NCBI GI	g4583545
BLAST score	311
E value	1.0e-175
Match length	315
% identity	100
NCBI Description	Arabidopsis thaliana mRNA for chloroplast GrpE protein

Seq. No.	160069
Seq. ID	LIB3176-119-P2-K1-H8
Method	BLASTX
NCBI GI	g3776561
BLAST score	519
E value	4.0e-53
Match length	107
% identity	100
NCBI Description	(AC005388) Identical to DNA for acyl carrier protein (ACP) gene A2 gb_X57699 from A. thaliana. ESTs gb_W43252, gb_T42821, gb_N65229, gb_N97267, gb_F15491 and gb_AA040955 come from this gene. [Arabidopsis thaliana]

Seq. No.	160070
Seq. ID	LIB3176-119-P2-K1-H9
Method	BLASTN
NCBI GI	g3869072
BLAST score	185
E value	1.0e-99
Match length	193
% identity	99
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MJB24, complete sequence [Arabidopsis thaliana]

Seq. No.	160071
Seq. ID	LIB3176-120-P2-K1-A1
Method	BLASTN

NCBI GI	g4662609
BLAST score	446
E value	0.0e+00
Match length	467
% identity	99
NCBI Description	Genomic sequence for Arabidopsis thaliana BAC F10A5, complete sequence

Seq. No.	160072
Seq. ID	LIB3176-120-P2-K1-A11
Method	BLASTN
NCBI GI	g2454181
BLAST score	193
E value	1.0e-104
Match length	248
% identity	98
NCBI Description	Arabidopsis thaliana pyruvate dehydrogenase E1 alpha subunit mRNA, nuclear gene encoding plastid protein, complete cds

Seq. No.	160073
Seq. ID	LIB3176-120-P2-K1-A4
Method	BLASTX
NCBI GI	g58299
BLAST score	231
E value	9.0e-20
Match length	56
% identity	86
NCBI Description	(X68342) modified transit peptide for chloroplast targeting of the CryIA(c) protein [synthetic construct]

Seq. No.	160074
Seq. ID	LIB3176-120-P2-K1-A5
Method	BLASTN
NCBI GI	g2244991
BLAST score	395
E value	0.0e+00
Match length	395
% identity	100
NCBI Description	Arabidopsis thaliana DNA chromosome 4, ESSA I contig fragment No

Seq. No.	160075
Seq. ID	LIB3176-120-P2-K1-A7
Method	BLASTX
NCBI GI	g2864622
BLAST score	690
E value	6.0e-73
Match length	158
% identity	91
NCBI Description	(AL021811) putative protein [Arabidopsis thaliana]

Seq. No.	160076
Seq. ID	LIB3176-120-P2-K1-B1
Method	BLASTX
NCBI GI	g121075
BLAST score	514

E value	3.0e-52
Match length	132
% identity	79
NCBI Description	GLYCINE CLEAVAGE SYSTEM H PROTEIN PRECURSOR >gi_166725 (M82921) H-Protein precursor [Arabidopsis thaliana] >gi_861215 (U27144) glycine decarboxylase complex H-protein precursor [Arabidopsis thaliana] >gi_3608151 (AC005314) glycine decarboxylase complex H-protein [Arabidopsis thaliana] >gi_445119_prf__1908425A Gly decarboxylase:SUBUNIT=H protein [Arabidopsis thaliana]
Seq. No.	160077
Seq. ID	LIB3176-120-P2-K1-B11
Method	BLASTX
NCBI GI	g548355
BLAST score	307
E value	3.0e-28
Match length	91
% identity	66
NCBI Description	NITRATE REDUCTASE 1 (NR1) >gi_486751_pir__S35228 nitrate reductase (NADH) (EC 1.6.6.1) 1 - Arabidopsis thaliana >gi_22757_emb_CAA79494_ (Z19050) nitrate reductase [Arabidopsis thaliana] >gi_448286_prf__1916406A nitrate reductase [Arabidopsis thaliana]
Seq. No.	160078
Seq. ID	LIB3176-120-P2-K1-B12
Method	BLASTX
NCBI GI	g132110
BLAST score	427
E value	2.0e-42
Match length	83
% identity	99
NCBI Description	RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN 3B PRECURSOR (RUBISCO SMALL SUBUNIT 3B) >gi_68060_pir__RKMUB3 ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain B3 precursor - Arabidopsis thaliana >gi_16195_emb_CAA32702_ (X14564) ribulose bisphosphate carboxylase [Arabidopsis thaliana]
Seq. No.	160079
Seq. ID	LIB3176-120-P2-K1-B2
Method	BLASTX
NCBI GI	g267073
BLAST score	533
E value	1.0e-54
Match length	100
% identity	98
NCBI Description	TUBULIN BETA-2/BETA-3 CHAIN >gi_320184_pir__JQ1587 tubulin beta chain - Arabidopsis thaliana >gi_166898 (M84700) beta-2 tubulin [Arabidopsis thaliana] >gi_166900 (M84701) beta-3 tubulin [Arabidopsis thaliana]
Seq. No.	160080
Seq. ID	LIB3176-120-P2-K1-B3
Method	BLASTX
NCBI GI	g166765

BLAST score	480
E value	1.0e-48
Match length	96
% identity	96
NCBI Description	(M23106) heat shock protein HSP70-1 [Arabidopsis thaliana]

Seq. No.	160081
Seq. ID	LIB3176-120-P2-K1-B6
Method	BLASTN
NCBI GI	g4753195
BLAST score	210
E value	1.0e-114
Match length	218
% identity	99
NCBI Description	Arabidopsis thaliana BAC F15A18 from chromosome V near 68.5 cM, complete sequence

Seq. No.	160082
Seq. ID	LIB3176-120-P2-K1-B7
Method	BLASTX
NCBI GI	g1864017
BLAST score	614
E value	4.0e-64
Match length	120
% identity	98
NCBI Description	(D63396) elongation factor-1 alpha [Nicotiana tabacum]

Seq. No.	160083
Seq. ID	LIB3176-120-P2-K1-B8
Method	BLASTX
NCBI GI	g2146730
BLAST score	776
E value	5.0e-83
Match length	145
% identity	100
NCBI Description	farnesyl diphosphate synthase (EC 2.5.1.10) FPS2 - Arabidopsis thaliana >gi_1146161 (L46350) farnesyl diphosphate synthase [Arabidopsis thaliana] >gi_1146163 (L46349) farnesyl diphosphate synthase [Arabidopsis thaliana] >gi_2245078_emb_CAB10500_ (Z97343) farnesyl diphosphate synthase (FPS2) protein [Arabidopsis thaliana]

Seq. No.	160084
Seq. ID	LIB3176-120-P2-K1-B9
Method	BLASTX
NCBI GI	g2146730
BLAST score	347
E value	1.0e-32
Match length	84
% identity	79
NCBI Description	farnesyl diphosphate synthase (EC 2.5.1.10) FPS2 - Arabidopsis thaliana >gi_1146161 (L46350) farnesyl diphosphate synthase [Arabidopsis thaliana] >gi_1146163 (L46349) farnesyl diphosphate synthase [Arabidopsis thaliana] >gi_2245078_emb_CAB10500_ (Z97343) farnesyl diphosphate synthase (FPS2) protein [Arabidopsis thaliana]

Seq. No.	160085
Seq. ID	LIB3176-120-P2-K1-C10
Method	BLASTX
NCBI GI	g4262174
BLAST score	275
E value	1.0e-24
Match length	65
% identity	90
NCBI Description	(AC005508) 9058 [Arabidopsis thaliana]

Seq. No.	160086
Seq. ID	LIB3176-120-P2-K1-C11
Method	BLASTX
NCBI GI	g1350965
BLAST score	159
E value	2.0e-11
Match length	36
% identity	81
NCBI Description	40S RIBOSOMAL PROTEIN S23 (S12)

Seq. No.	160087
Seq. ID	LIB3176-120-P2-K1-C12
Method	BLASTX
NCBI GI	g3790102
BLAST score	505
E value	3.0e-51
Match length	120
% identity	75
NCBI Description	(AF095521) pyrophosphate-dependent phosphofructokinase alpha subunit [Citrus X paradisi]

Seq. No.	160088
Seq. ID	LIB3176-120-P2-K1-C3
Method	BLASTX
NCBI GI	g1905876
BLAST score	286
E value	3.0e-26
Match length	58
% identity	98
NCBI Description	(U90879) biotin carboxylase subunit [Arabidopsis thaliana] >gi_1916300 (U91414) heteromeric acetyl-CoA carboxylase biotin carboxylase subunit [Arabidopsis thaliana] >gi_3047099 (AF058826) Arabidopsis thaliana biotin carboxylase subunit (GB:U90879) [Arabidopsis thaliana]

Seq. No.	160089
Seq. ID	LIB3176-120-P2-K1-C4
Method	BLASTX
NCBI GI	g2191128
BLAST score	299
E value	9.0e-28
Match length	70
% identity	90
NCBI Description	(AF007269) belongs to the L5P family of ribosomal proteins [Arabidopsis thaliana]

Seq. No.	160090

Seq. ID	LIB3176-120-P2-K1-C5
Method	BLASTX
NCBI GI	g399013
BLAST score	391
E value	5.0e-38
Match length	75
% identity	100
NCBI Description	ADP,ATP CARRIER PROTEIN 1 PRECURSOR (ADP/ATP TRANSLOCASE 1) (ADENINE NUCLEOTIDE TRANSLOCATOR 1) (ANT 1) >gi_99658_pir__S21313 ADP,ATP carrier protein - Arabidopsis thaliana (fragment) >gi_16175_emb_CAA46518_ (X65549) adenylate translocator [Arabidopsis thaliana] >gi_445607_prf__1909354A adenylate translocator [Arabidopsis thaliana]

Seq. No.	160091
Seq. ID	LIB3176-120-P2-K1-C6
Method	BLASTX
NCBI GI	g2826811
BLAST score	439
E value	8.0e-44
Match length	85
% identity	100
NCBI Description	(AJ002892) AtGRP2 [Arabidopsis thaliana]

Seq. No.	160092
Seq. ID	LIB3176-120-P2-K1-C7
Method	BLASTN
NCBI GI	g3510340
BLAST score	45
E value	1.0e-16
Match length	57
% identity	95
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MDN11, complete sequence [Arabidopsis thaliana]

Seq. No.	160093
Seq. ID	LIB3176-120-P2-K1-C8
Method	BLASTN
NCBI GI	g2826810
BLAST score	46
E value	2.0e-17
Match length	46
% identity	100
NCBI Description	Arabidopsis thaliana mRNA for glycine-rich RNA-binding protein (AtGRP2)

Seq. No.	160094
Seq. ID	LIB3176-120-P2-K1-C9
Method	BLASTX
NCBI GI	g1732570
BLAST score	164
E value	7.0e-12
Match length	31
% identity	100
NCBI Description	(U72153) beta-glucosidase [Arabidopsis thaliana]

Seq. No.	160095
Seq. ID	LIB3176-120-P2-K1-D10
Method	BLASTN
NCBI GI	g4580744
BLAST score	54
E value	6.0e-22
Match length	106
% identity	59
NCBI Description	Sequence of BAC F15I1 from Arabidopsis thaliana chromosome 1, complete sequence

Seq. No.	160096
Seq. ID	LIB3176-120-P2-K1-D11
Method	BLASTN
NCBI GI	g16174
BLAST score	66
E value	7.0e-29
Match length	90
% identity	93
NCBI Description	A.thaliana ANT1 mRNA for adenylate translocator

Seq. No.	160097
Seq. ID	LIB3176-120-P2-K1-D12
Method	BLASTX
NCBI GI	g3421123
BLAST score	533
E value	1.0e-54
Match length	110
% identity	95
NCBI Description	(AF043538) 20S proteasome beta subunit PBG1 [Arabidopsis thaliana]

Seq. No.	160098
Seq. ID	LIB3176-120-P2-K1-D2
Method	BLASTX
NCBI GI	g4544432
BLAST score	250
E value	2.0e-21
Match length	59
% identity	80
NCBI Description	(AC006955) putative mannose-1-phosphate guanyltransferase [Arabidopsis thaliana]

Seq. No.	160099
Seq. ID	LIB3176-120-P2-K1-D3
Method	BLASTN
NCBI GI	g2244870
BLAST score	288
E value	1.0e-161
Match length	288
% identity	93
NCBI Description	Arabidopsis thaliana DNA chromosome 4, ESSA I contig fragment No

Seq. No.	160100
Seq. ID	LIB3176-120-P2-K1-D6
Method	BLASTN

NCBI GI	g3046853
BLAST score	137
E value	3.0e-71
Match length	222
% identity	93
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MRA19, complete sequence [Arabidopsis thaliana]

Seq. No.	160101
Seq. ID	LIB3176-120-P2-K1-D7
Method	BLASTN
NCBI GI	g1235717
BLAST score	54
E value	6.0e-22
Match length	113
% identity	95
NCBI Description	Arabidopsis thaliana mRNA for calcium-dependent protein kinase (CDPK), complete cds

Seq. No.	160102
Seq. ID	LIB3176-120-P2-K1-D8
Method	BLASTN
NCBI GI	g2564050
BLAST score	237
E value	1.0e-131
Match length	257
% identity	98
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MUA22, complete sequence [Arabidopsis thaliana]

Seq. No.	160103
Seq. ID	LIB3176-120-P2-K1-D9
Method	BLASTX
NCBI GI	g3273743
BLAST score	253
E value	2.0e-22
Match length	59
% identity	85
NCBI Description	(AF057357) lipid transfer protein 2 precursor [Arabidopsis thaliana] >gi_3786019 (AC005499) unknown protein [Arabidopsis thaliana]

Seq. No.	160104
Seq. ID	LIB3176-120-P2-K1-E1
Method	BLASTX
NCBI GI	g4559327
BLAST score	162
E value	4.0e-11
Match length	77
% identity	48
NCBI Description	(AC007087) hypothetical protein [Arabidopsis thaliana]

Seq. No.	160105
Seq. ID	LIB3176-120-P2-K1-E10
Method	BLASTX
NCBI GI	g4835233
BLAST score	633

E value	2.0e-66
Match length	126
% identity	100
NCBI Description	(AL049862) putative protein 1 photosystem II oxygen-evolving complex [Arabidopsis thaliana]

Seq. No.	160106
Seq. ID	LIB3176-120-P2-K1-E11
Method	BLASTX
NCBI GI	g2493045
BLAST score	636
E value	1.0e-66
Match length	145
% identity	86
NCBI Description	ATP SYNTHASE DELTA' CHAIN, MITOCHONDRIAL PRECURSOR >gi_1655484_dbj_BAA13601_ (D88376) delta-prime subunit of mitochondrial F1-ATPase [Arabidopsis thaliana]

Seq. No.	160107
Seq. ID	LIB3176-120-P2-K1-E12
Method	BLASTX
NCBI GI	g4454036
BLAST score	402
E value	2.0e-39
Match length	86
% identity	91
NCBI Description	(AL035394) putative major latex protein [Arabidopsis thaliana]

Seq. No.	160108
Seq. ID	LIB3176-120-P2-K1-E2
Method	BLASTN
NCBI GI	g1769906
BLAST score	239
E value	1.0e-132
Match length	283
% identity	96
NCBI Description	A.thaliana mRNA for xyloglucan endo-transglycosylase

Seq. No.	160109
Seq. ID	LIB3176-120-P2-K1-E3
Method	BLASTX
NCBI GI	g119143
BLAST score	218
E value	1.0e-17
Match length	46
% identity	91
NCBI Description	ELONGATION FACTOR 1-ALPHA (EF-1-ALPHA) >gi_81606_pir__S06724 translation elongation factor eEF-1 alpha chain - Arabidopsis thaliana >gi_295788_emb_CAA34453_ (X16430) elongation factor 1-alpha [Arabidopsis thaliana] >gi_1369927_emb_CAA34454_ (X16431) elongation factor 1-alpha [Arabidopsis thaliana] >gi_1369928_emb_CAA34455_ (X16431) elongation factor 1-alpha [Arabidopsis thaliana] >gi_1532172 (U63815) EF-1alpha-A1 [Arabidopsis thaliana] >gi_1532173 (U63815) EF-1alpha-A2 [Arabidopsis thaliana] >gi_1532174 (U63815) EF-1alpha-A3 [Arabidopsis thaliana]

Seq. No.	160110
Seq. ID	LIB3176-120-P2-K1-E7
Method	BLASTN
NCBI GI	g298035
BLAST score	85
E value	5.0e-40
Match length	97
% identity	97
NCBI Description	A.thaliana Lhcb4 gene

Seq. No.	160111
Seq. ID	LIB3176-120-P2-K1-E8
Method	BLASTN
NCBI GI	g2760316
BLAST score	175
E value	1.0e-93
Match length	336
% identity	98
NCBI Description	The sequence of BAC F1N21 from Arabidopsis thaliana chromosome 1, complete sequence [Arabidopsis thaliana]

Seq. No.	160112
Seq. ID	LIB3176-120-P2-K1-E9
Method	BLASTN
NCBI GI	g2264314
BLAST score	291
E value	1.0e-163
Match length	311
% identity	98
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MQK4, complete sequence [Arabidopsis thaliana]

Seq. No.	160113
Seq. ID	LIB3176-120-P2-K1-F11
Method	BLASTN
NCBI GI	g4753195
BLAST score	385
E value	0.0e+00
Match length	433
% identity	97
NCBI Description	Arabidopsis thaliana BAC F15A18 from chromosome V near 68.5 cM, complete sequence

Seq. No.	160114
Seq. ID	LIB3176-120-P2-K1-F12
Method	BLASTX
NCBI GI	g2982783
BLAST score	182
E value	2.0e-13
Match length	95
% identity	41
NCBI Description	(AE000670) 3-hydroxyisobutyrate dehydrogenase [Aquifex aeolicus]

Seq. No.	160115
Seq. ID	LIB3176-120-P2-K1-F2

Method	BLASTX
NCBI GI	g1906826
BLAST score	490
E value	2.0e-49
Match length	110
% identity	87
NCBI Description	(Y11827) heat shock protein [Arabidopsis thaliana]

Seq. No.	160116
Seq. ID	LIB3176-120-P2-K1-F3
Method	BLASTX
NCBI GI	g133409
BLAST score	267
E value	5.0e-24
Match length	67
% identity	75
NCBI Description	DNA-DIRECTED RNA POLYMERASE ALPHA CHAIN >gi_66962_pir__RNNTA DNA-directed RNA polymerase (EC 2.7.7.6) alpha chain - common tobacco chloroplast >gi_11860_emb_CAA77376_ (Z00044) RNA polymerase alpha subunit [Nicotiana tabacum] >gi_225228_prf__1211235BK RNA polymerase alpha [Nicotiana tabacum]

Seq. No.	160117
Seq. ID	LIB3176-120-P2-K1-F4
Method	BLASTX
NCBI GI	g2982283
BLAST score	159
E value	1.0e-10
Match length	45
% identity	62
NCBI Description	(AF051226) PREG-like protein [Picea mariana]

Seq. No.	160118
Seq. ID	LIB3176-120-P2-K1-F5
Method	BLASTN
NCBI GI	g4678371
BLAST score	208
E value	1.0e-113
Match length	421
% identity	98
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone T6G15 (ESSA project)

Seq. No.	160119
Seq. ID	LIB3176-120-P2-K1-F7
Method	BLASTX
NCBI GI	g2832672
BLAST score	256
E value	3.0e-22
Match length	58
% identity	88
NCBI Description	(AL021712) nifU-like protein [Arabidopsis thaliana]

Seq. No.	160120
Seq. ID	LIB3176-120-P2-K1-F9
Method	BLASTX

NCBI GI	g4467097
BLAST score	199
E value	1.0e-15
Match length	45
% identity	89
NCBI Description	(AL035538) heat shock protein 70 like protein [Arabidopsis thaliana]

Seq. No.	160121
Seq. ID	LIB3176-120-P2-K1-G10
Method	BLASTN
NCBI GI	g2191157
BLAST score	38
E value	9.0e-13
Match length	74
% identity	97
NCBI Description	Arabidopsis thaliana BAC IG002P16

Seq. No.	160122
Seq. ID	LIB3176-120-P2-K1-G11
Method	BLASTN
NCBI GI	g3399678
BLAST score	87
E value	1.0e-41
Match length	134
% identity	94
NCBI Description	Arabidopsis thaliana chromosome 1 BAC F13M7 sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	160123
Seq. ID	LIB3176-120-P2-K1-G12
Method	BLASTX
NCBI GI	g1170373
BLAST score	296
E value	2.0e-27
Match length	62
% identity	97
NCBI Description	HEAT SHOCK COGNATE 70 KD PROTEIN 1 >gi_1072473_pir__S46302 heat shock cognate protein 70-1 - Arabidopsis thaliana >gi_397482_emb_CAA52684_ (X74604) heat shock protein 70 cognate [Arabidopsis thaliana]

Seq. No.	160124
Seq. ID	LIB3176-120-P2-K1-G2
Method	BLASTX
NCBI GI	g2232354
BLAST score	232
E value	3.0e-19
Match length	118
% identity	42
NCBI Description	(AF006081) UDPG glucosyltransferase [Solanum berthaultii]

Seq. No.	160125
Seq. ID	LIB3176-120-P2-K1-G5
Method	BLASTX
NCBI GI	g4567207
BLAST score	736

E value	2.0e-78
Match length	140
% identity	99
NCBI Description	(AC007168) unknown protein [Arabidopsis thaliana]

Seq. No.	160126
Seq. ID	LIB3176-120-P2-K1-G6
Method	BLASTX
NCBI GI	g115767
BLAST score	677
E value	2.0e-71
Match length	144
% identity	90
NCBI Description	CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR (CAB-165/180) (LHCP) >gi_81603_pir__A29280 chlorophyll a/b-binding protein ab165 - Arabidopsis thaliana >gi_16368_emb_CAA27540_ (X03907) chlorophyll a/b binding protein (LHCP AB 65) [Arabidopsis thaliana] >gi_16372_emb_CAA27541_ (X03908) chlorophyll a/b binding protein (LHCP AB 180) [Arabidopsis thaliana]

Seq. No.	160127
Seq. ID	LIB3176-120-P2-K1-G7
Method	BLASTX
NCBI GI	g113026
BLAST score	543
E value	9.0e-56
Match length	122
% identity	86
NCBI Description	ISOCITRATE LYASE (ISOCITRASE) (ISOCITRATASE) (ICL) >gi_68211_pir__WZRPI isocitrate lyase (EC 4.1.3.1) - rape >gi_255220_bbs_112862 isocitrate lyase, threo-D S-isocitrate glyoxylate-lyase, IL {EC 4.1.3.1} [Brassica napus, seedlings, Peptide, 576 aa] >gi_167144 (L08482) isocitrate lyase [Brassica napus] >gi_447142_prf__1913424A isocitrate lyase [Brassica napus]

Seq. No.	160128
Seq. ID	LIB3176-120-P2-K1-G8
Method	BLASTN
NCBI GI	g2351064
BLAST score	73
E value	4.0e-33
Match length	168
% identity	99
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MDJ22, complete sequence [Arabidopsis thaliana]

Seq. No.	160129
Seq. ID	LIB3176-120-P2-K1-H1
Method	BLASTX
NCBI GI	g3176668
BLAST score	513
E value	2.0e-52
Match length	101
% identity	98
NCBI Description	(AC004393) Similar to ribosomal protein L17 gb_X62724 from

	Hordeum vulgare. ESTs gb_Z34728, gb_F19974, gb_T75677 and gb_Z33937 come from this gene. [Arabidopsis thaliana]
Seq. No.	160130
Seq. ID	LIB3176-120-P2-K1-H12
Method	BLASTN
NCBI GI	g1402897
BLAST score	81
E value	8.0e-38
Match length	170
% identity	89
NCBI Description	A.thaliana gst6 gene
Seq. No.	160131
Seq. ID	LIB3176-120-P2-K1-H2
Method	BLASTN
NCBI GI	g2244991
BLAST score	106
E value	7.0e-53
Match length	142
% identity	94
NCBI Description	Arabidopsis thaliana DNA chromosome 4, ESSA I contig fragment No
Seq. No.	160132
Seq. ID	LIB3176-120-P2-K1-H3
Method	BLASTX
NCBI GI	g2317729
BLAST score	574
E value	2.0e-59
Match length	109
% identity	98
NCBI Description	(AF013627) reversibly glycosylated polypeptide-1 [Arabidopsis thaliana]
Seq. No.	160133
Seq. ID	LIB3176-120-P2-K1-H4
Method	BLASTX
NCBI GI	g3193317
BLAST score	172
E value	7.0e-13
Match length	67
% identity	57
NCBI Description	(AF069299) similar to plant chalcone and stilbene synthases [Arabidopsis thaliana]
Seq. No.	160134
Seq. ID	LIB3176-120-P2-K1-H5
Method	BLASTX
NCBI GI	g1592677
BLAST score	284
E value	1.0e-25
Match length	88
% identity	69
NCBI Description	(X91912) LEA76 homologue type2 [Arabidopsis thaliana]
Seq. No.	160135

Seq. ID	LIB3176-120-P2-K1-H6
Method	BLASTX
NCBI GI	g1168547
BLAST score	334
E value	3.0e-31
Match length	83
% identity	83
NCBI Description	HOMEOBOX-LEUCINE ZIPPER PROTEIN ATHB-6 (HD-ZIP PROTEIN ATHB-6) >gi_629505_pir__S47136 homeotic protein Athb-6 - Arabidopsis thaliana >gi_499162_emb_CAA47427_ (X67034) Athb-6 [Arabidopsis thaliana]

Seq. No.	160136
Seq. ID	LIB3176-120-P2-K1-H7
Method	BLASTX
NCBI GI	g1352347
BLAST score	275
E value	9.0e-25
Match length	57
% identity	95
NCBI Description	ELONGATION FACTOR 1-BETA A1 (EF-1-BETA) >gi_480620_pir__S37103 translation elongation factor eEF-1 beta-A1 chain - Arabidopsis thaliana (cv. Colombia) >gi_398608_emb_CAA52751_ (X74733) elongation factor-1 beta A1 [Arabidopsis thaliana]

Seq. No.	160137
Seq. ID	LIB3176-120-P2-K1-H8
Method	BLASTN
NCBI GI	g4584519
BLAST score	201
E value	1.0e-109
Match length	237
% identity	96
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F11C18 (ESSA project)

Seq. No.	160138
Seq. ID	LIB3176-120-P2-K1-H9
Method	BLASTN
NCBI GI	g3461810
BLAST score	144
E value	2.0e-75
Match length	144
% identity	100
NCBI Description	Arabidopsis thaliana chromosome II BAC T17M13 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	160139
Seq. ID	LIB3176-121-P2-K1-A1
Method	BLASTN
NCBI GI	g3449330
BLAST score	49
E value	1.0e-18
Match length	69
% identity	94
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:

MDJ14, complete sequence [Arabidopsis thaliana]

Seq. No.	160140
Seq. ID	LIB3176-121-P2-K1-A11
Method	BLASTX
NCBI GI	g4580513
BLAST score	121
E value	3.0e-35
Match length	85
% identity	96
NCBI Description	(AF036300) scarecrow-like 1 [Arabidopsis thaliana]

Seq. No.	160141
Seq. ID	LIB3176-121-P2-K1-A12
Method	BLASTX
NCBI GI	g2146730
BLAST score	117
E value	5.0e-06
Match length	101
% identity	72
NCBI Description	farnesyl diphosphate synthase (EC 2.5.1.10) FPS2 - Arabidopsis thaliana >gi_1146161 (L46350) farnesyl diphosphate synthase [Arabidopsis thaliana] >gi_1146163 (L46349) farnesyl diphosphate synthase [Arabidopsis thaliana] >gi_2245078_emb_CAB10500_ (Z97343) farnesyl diphosphate synthase (FPS2) protein [Arabidopsis thaliana]

Seq. No.	160142
Seq. ID	LIB3176-121-P2-K1-A4
Method	BLASTX
NCBI GI	g3024022
BLAST score	493
E value	7.0e-50
Match length	103
% identity	89
NCBI Description	INITIATION FACTOR 5A-5 (EIF-5A) (EIF-4D) >gi_2225885_dbj_BAA20879_ (AB004826) eukaryotic initiation factor 5A5 [Solanum tuberosum]

Seq. No.	160143
Seq. ID	LIB3176-121-P2-K1-A6
Method	BLASTX
NCBI GI	g3482928
BLAST score	125
E value	2.0e-53
Match length	121
% identity	90
NCBI Description	(AC003970) Unknown protein [Arabidopsis thaliana] >gi_3929586 (AF100166) phytochrome interacting factor 3 [Arabidopsis thaliana]

Seq. No.	160144
Seq. ID	LIB3176-121-P2-K1-A7
Method	BLASTX
NCBI GI	g2826811
BLAST score	225
E value	2.0e-18

Match length	92
% identity	54
NCBI Description	(AJ002892) AtGRP2 [Arabidopsis thaliana]

Seq. No.	160145
Seq. ID	LIB3176-121-P2-K1-B1
Method	BLASTX
NCBI GI	g189422
BLAST score	164
E value	9.0e-12
Match length	70
% identity	51
NCBI Description	(M32110) proliferating cell nuclear protein P120 [Homo sapiens]

Seq. No.	160146
Seq. ID	LIB3176-121-P2-K1-B10
Method	BLASTX
NCBI GI	g231536
BLAST score	48
E value	2.0e-44
Match length	102
% identity	96
NCBI Description	CYTOSOL AMINOPEPTIDASE (LEUCINE AMINOPEPTIDASE) (LAP) (LEUCYL AMINOPEPTIDASE) (PROLINE AMINOPEPTIDASE) (PROLYL AMINOPEPTIDASE) >gi_99683_pir__S22399 leucyl aminopeptidase (EC 3.4.11.1) - Arabidopsis thaliana >gi_16394_emb_CAA45040_ (X63444) leucine aminopeptidase [Arabidopsis thaliana] >gi_4115380 (AC005967) putative leucine aminopeptidase [Arabidopsis thaliana]

Seq. No.	160147
Seq. ID	LIB3176-121-P2-K1-B2
Method	BLASTX
NCBI GI	g4490758
BLAST score	98
E value	8.0e-24
Match length	147
% identity	47
NCBI Description	(AL035708) putative protein [Arabidopsis thaliana]

Seq. No.	160148
Seq. ID	LIB3176-121-P2-K1-B3
Method	BLASTX
NCBI GI	g113026
BLAST score	74
E value	4.0e-64
Match length	127
% identity	98
NCBI Description	ISOCITRATE LYASE (ISOCITRASE) (ISOCITRATASE) (ICL) >gi_68211_pir__WZRPI isocitrate lyase (EC 4.1.3.1) - rape >gi_255220_bbs_112862 isocitrate lyase, threo-D S-isocitrate glyoxylate-lyase, IL (EC 4.1.3.1) [Brassica napus, seedlings, Peptide, 576 aa] >gi_167144 (L08482) isocitrate lyase [Brassica napus] >gi_447142_prf__1913424A isocitrate lyase [Brassica napus]

Seq. No.	160149
Seq. ID	LIB3176-121-P2-K1-B6
Method	BLASTX
NCBI GI	g2864615
BLAST score	334
E value	3.0e-31
Match length	70
% identity	99
NCBI Description	(AL021811) putative protein [Arabidopsis thaliana]

Seq. No.	160150
Seq. ID	LIB3176-121-P2-K1-B7
Method	BLASTN
NCBI GI	g472876
BLAST score	99
E value	8.0e-49
Match length	130
% identity	95
NCBI Description	A.thaliana mRNA for plasma membrane intrinsic protein 2a

Seq. No.	160151
Seq. ID	LIB3176-121-P2-K1-C1
Method	BLASTX
NCBI GI	g2459445
BLAST score	186
E value	6.0e-14
Match length	50
% identity	32
NCBI Description	(AC002332) putative ribonucleoprotein [Arabidopsis thaliana]

Seq. No.	160152
Seq. ID	LIB3176-121-P2-K1-C10
Method	BLASTX
NCBI GI	g1304215
BLAST score	251
E value	2.0e-21
Match length	55
% identity	47
NCBI Description	(D84392) precursor of rice 22 kDa protein of photosystem II (PSII-S) [Oryza sativa]

Seq. No.	160153
Seq. ID	LIB3176-121-P2-K1-C11
Method	BLASTX
NCBI GI	g3738259
BLAST score	482
E value	1.0e-48
Match length	111
% identity	85
NCBI Description	(AB018411) cytosolic phosphoglycerate kinase 1 [Populus nigra]

Seq. No.	160154
Seq. ID	LIB3176-121-P2-K1-C12
Method	BLASTX
NCBI GI	g3928543

BLAST score	54
E value	2.0e-71
Match length	135
% identity	100
NCBI Description	(AB016819) UDP-glucose glucosyltransferase [Arabidopsis thaliana]

Seq. No.	160155
Seq. ID	LIB3176-121-P2-K1-C2
Method	BLASTN
NCBI GI	g2864607
BLAST score	100
E value	5.0e-49
Match length	331
% identity	98
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F10M6 (ESSAII project)

Seq. No.	160156
Seq. ID	LIB3176-121-P2-K1-C3
Method	BLASTN
NCBI GI	g4582444
BLAST score	57
E value	3.0e-23
Match length	107
% identity	96
NCBI Description	Arabidopsis thaliana chromosome II BAC T9H9 genomic sequence, complete sequence

Seq. No.	160157
Seq. ID	LIB3176-121-P2-K1-C4
Method	BLASTX
NCBI GI	g2529673
BLAST score	264
E value	6.0e-23
Match length	137
% identity	42
NCBI Description	(AC002535) hypothetical protein [Arabidopsis thaliana]

Seq. No.	160158
Seq. ID	LIB3176-121-P2-K1-C5
Method	BLASTX
NCBI GI	g3617741
BLAST score	76
E value	1.0e-56
Match length	124
% identity	95
NCBI Description	(AC005687) L3 cytoplasmic ribosomal protein [Arabidopsis thaliana]

Seq. No.	160159
Seq. ID	LIB3176-121-P2-K1-C6
Method	BLASTX
NCBI GI	g4337175
BLAST score	78
E value	4.0e-56
Match length	134

% identity	88
NCBI Description	(AC006416) ESTs gb_T20589, gb_T04648, gb_AA597906, gb_T04111, gb_R84180, gb_R65428, gb_T44439, gb_T76570, gb_R90004, gb_T45020, gb_T42457, gb_T20921, gb_AA042762 and gb_AA720210 come from this gene. [Arabidopsis thaliana]
Seq. No.	160160
Seq. ID	LIB3176-121-P2-K1-C7
Method	BLASTN
NCBI GI	g4539402
BLAST score	47
E value	4.0e-18
Match length	63
% identity	94
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F7L13 (ESSA project)
Seq. No.	160161
Seq. ID	LIB3176-121-P2-K1-D1
Method	BLASTX
NCBI GI	g2062161
BLAST score	87
E value	2.0e-65
Match length	127
% identity	53
NCBI Description	(AC001645) jasmonate inducible protein isolog [Arabidopsis thaliana]
Seq. No.	160162
Seq. ID	LIB3176-121-P2-K1-D10
Method	BLASTX
NCBI GI	g1170373
BLAST score	229
E value	6.0e-22
Match length	55
% identity	98
NCBI Description	HEAT SHOCK COGNATE 70 KD PROTEIN 1 >gi_1072473_pir__S46302 heat shock cognate protein 70-1 - Arabidopsis thaliana >gi_397482_emb_CAA52684_ (X74604) heat shock protein 70 cognate [Arabidopsis thaliana]
Seq. No.	160163
Seq. ID	LIB3176-121-P2-K1-D11
Method	BLASTN
NCBI GI	g1245217
BLAST score	36
E value	9.0e-12
Match length	52
% identity	92
NCBI Description	Oryza sativa subsp. indica large ribosomal RNA gene, chloroplast gene encoding chloroplast rRNA, partial sequence
Seq. No.	160164
Seq. ID	LIB3176-121-P2-K1-D12
Method	BLASTX
NCBI GI	g625977

BLAST score	624
E value	3.0e-65
Match length	121
% identity	100
NCBI Description	p40 protein homolog - Arabidopsis thaliana >gi_402904 (U01955) laminin receptor-like protein [Arabidopsis thaliana]

Seq. No.	160165
Seq. ID	LIB3176-121-P2-K1-D3
Method	BLASTN
NCBI GI	g4757414
BLAST score	39
E value	1.0e-12
Match length	71
% identity	89
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MYF24, complete sequence

Seq. No.	160166
Seq. ID	LIB3176-121-P2-K1-D4
Method	BLASTX
NCBI GI	g3914658
BLAST score	50
E value	8.0e-60
Match length	123
% identity	98
NCBI Description	50S RIBOSOMAL PROTEIN L24, CHLOROPLAST PRECURSOR >gi_1694974_emb_CAA70851_ (Y09635) plastid ribosomal protein [Arabidopsis thaliana]

Seq. No.	160167
Seq. ID	LIB3176-121-P2-K1-D5
Method	BLASTX
NCBI GI	g1490554
BLAST score	488
E value	3.0e-49
Match length	113
% identity	89
NCBI Description	(U63633) S-adenosylmethionine decarboxylase [Arabidopsis thaliana]

Seq. No.	160168
Seq. ID	LIB3176-121-P2-K1-D6
Method	BLASTN
NCBI GI	g3763915
BLAST score	143
E value	2.0e-74
Match length	407
% identity	74
NCBI Description	Arabidopsis thaliana chromosome II BAC F14B2 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	160169
Seq. ID	LIB3176-121-P2-K1-D7
Method	BLASTN
NCBI GI	g4455168

BLAST score	46
E value	5.0e-17
Match length	66
% identity	92
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F10M10 (ESSAII project)

Seq. No.	160170
Seq. ID	LIB3176-121-P2-K1-D8
Method	BLASTX
NCBI GI	g480450
BLAST score	116
E value	1.0e-64
Match length	126
% identity	98
NCBI Description	ketol-acid reductoisomerase (EC 1.1.1.86) - Arabidopsis thaliana >gi_402552_emb_CAA49506_ (X69880) ketol-acid reductoisomerase [Arabidopsis thaliana]

Seq. No.	160171
Seq. ID	LIB3176-121-P2-K1-E11
Method	BLASTN
NCBI GI	g4469002
BLAST score	103
E value	1.0e-50
Match length	405
% identity	95
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone T29A15 (ESSA project)

Seq. No.	160172
Seq. ID	LIB3176-121-P2-K1-E2
Method	BLASTX
NCBI GI	g4335745
BLAST score	338
E value	7.0e-32
Match length	113
% identity	58
NCBI Description	(AC006284) putative hydrolase (contains an esterase/lipase/thioesterase active site serine domain (prosite: PS50187) [Arabidopsis thaliana]

Seq. No.	160173
Seq. ID	LIB3176-121-P2-K1-E4
Method	BLASTN
NCBI GI	g4199934
BLAST score	310
E value	1.0e-174
Match length	357
% identity	35
NCBI Description	Genomic sequence for Arabidopsis thaliana BAC T3P18, complete sequence [Arabidopsis thaliana]

Seq. No.	160174
Seq. ID	LIB3176-121-P2-K1-E5
Method	BLASTN
NCBI GI	g2924768

BLAST score	68
E value	2.0e-30
Match length	91
% identity	95
NCBI Description	Arabidopsis thaliana chromosome II BAC F25I18 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	160175
Seq. ID	LIB3176-121-P2-K1-E6
Method	BLASTN
NCBI GI	g3449317
BLAST score	198
E value	1.0e-107
Match length	266
% identity	93
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MKM21, complete sequence [Arabidopsis thaliana]

Seq. No.	160176
Seq. ID	LIB3176-121-P2-K1-E7
Method	BLASTN
NCBI GI	g3668073
BLAST score	171
E value	2.0e-91
Match length	253
% identity	97
NCBI Description	Arabidopsis thaliana chromosome II BAC T4C15 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	160177
Seq. ID	LIB3176-121-P2-K1-E8
Method	BLASTN
NCBI GI	g2191157
BLAST score	42
E value	3.0e-15
Match length	58
% identity	93
NCBI Description	Arabidopsis thaliana BAC IG002P16

Seq. No.	160178
Seq. ID	LIB3176-121-P2-K1-E9
Method	BLASTN
NCBI GI	g1546697
BLAST score	182
E value	3.0e-98
Match length	193
% identity	99
NCBI Description	A.thaliana mRNA for peroxidase ATP3a

Seq. No.	160179
Seq. ID	LIB3176-121-P2-K1-F11
Method	BLASTN
NCBI GI	g4757405
BLAST score	134
E value	3.0e-69
Match length	401
% identity	99

NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MOJ10, complete sequence
Seq. No.	160180
Seq. ID	LIB3176-121-P2-K1-F12
Method	BLASTX
NCBI GI	g132110
BLAST score	665
E value	5.0e-70
Match length	124
% identity	98
NCBI Description	RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN 3B PRECURSOR (RUBISCO SMALL SUBUNIT 3B) >gi_68060_pir__RKMUB3 ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain B3 precursor - Arabidopsis thaliana >gi_16195_emb_CAA32702_ (X14564) ribulose bisphosphate carboxylase [Arabidopsis thaliana]
Seq. No.	160181
Seq. ID	LIB3176-121-P2-K1-F2
Method	BLASTN
NCBI GI	g3228389
BLAST score	233
E value	1.0e-128
Match length	280
% identity	98
NCBI Description	Genomic sequence for Arabidopsis thaliana BAC F17L21, complete sequence [Arabidopsis thaliana]
Seq. No.	160182
Seq. ID	LIB3176-121-P2-K1-F3
Method	BLASTX
NCBI GI	g132939
BLAST score	76
E value	5.0e-12
Match length	38
% identity	97
NCBI Description	60S RIBOSOMAL PROTEIN L3 >gi_81657_pir__JQ0771 ribosomal protein L3 (ARP1) - Arabidopsis thaliana >gi_166858 (M32654) ribosomal protein [Arabidopsis thaliana]
Seq. No.	160183
Seq. ID	LIB3176-121-P2-K1-F4
Method	BLASTX
NCBI GI	g3057150
BLAST score	145
E value	1.0e-09
Match length	40
% identity	85
NCBI Description	(AF059037) chaperonin 10 [Arabidopsis thaliana]
Seq. No.	160184
Seq. ID	LIB3176-121-P2-K1-F5
Method	BLASTX
NCBI GI	g3927837
BLAST score	51
E value	1.0e-67

Match length	136
% identity	99
NCBI Description	(AC005727) putative core protein [Arabidopsis thaliana]

Seq. No.	160185
Seq. ID	LIB3176-121-P2-K1-F6
Method	BLASTX
NCBI GI	g4582787
BLAST score	119
E value	1.0e-10
Match length	45
% identity	74
NCBI Description	(AJ012281) adenosine kinase [Zea mays]

Seq. No.	160186
Seq. ID	LIB3176-121-P2-K1-F7
Method	BLASTN
NCBI GI	g3641835
BLAST score	126
E value	2.0e-64
Match length	291
% identity	98
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone T4L20 (ESSAII project)

Seq. No.	160187
Seq. ID	LIB3176-121-P2-K1-F8
Method	BLASTX
NCBI GI	g121075
BLAST score	159
E value	5.0e-11
Match length	59
% identity	54
NCBI Description	GLYCINE CLEAVAGE SYSTEM H PROTEIN PRECURSOR >gi_166725 (M82921) H-Protein precursor [Arabidopsis thaliana] >gi_861215 (U27144) glycine decarboxylase complex H-protein precursor [Arabidopsis thaliana] >gi_3608151 (AC005314) glycine decarboxylase complex H-protein [Arabidopsis thaliana] >gi_445119_prf__1908425A Gly decarboxylase:SUBUNIT=H protein [Arabidopsis thaliana]

Seq. No.	160188
Seq. ID	LIB3176-121-P2-K1-F9
Method	BLASTN
NCBI GI	g4587641
BLAST score	37
E value	6.0e-12
Match length	76
% identity	88
NCBI Description	Arabidopsis thaliana chromosome I BAC F20D21 genomic sequence, complete sequence

Seq. No.	160189
Seq. ID	LIB3176-121-P2-K1-G10
Method	BLASTX
NCBI GI	g445613
BLAST score	155

E value	3.0e-10
Match length	105
% identity	33
NCBI Description	ribosomal protein L7 [Solanum tuberosum]

Seq. No.	160190
Seq. ID	LIB3176-121-P2-K1-G11
Method	BLASTN
NCBI GI	g2121272
BLAST score	107
E value	4.0e-53
Match length	143
% identity	94
NCBI Description	Arabidopsis thaliana dihydroorotase (pyr4) mRNA, complete cds

Seq. No.	160191
Seq. ID	LIB3176-121-P2-K1-G2
Method	BLASTX
NCBI GI	g1923256
BLAST score	295
E value	6.0e-27
Match length	73
% identity	84
NCBI Description	(U86782) 26S proteasome-associated pad1 homolog [Homo sapiens]

Seq. No.	160192
Seq. ID	LIB3176-121-P2-K1-G3
Method	BLASTN
NCBI GI	g4432847
BLAST score	282
E value	1.0e-157
Match length	289
% identity	100
NCBI Description	Arabidopsis thaliana chromosome II BAC F13B15 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	160193
Seq. ID	LIB3176-121-P2-K1-G4
Method	BLASTX
NCBI GI	g1710401
BLAST score	43
E value	4.0e-29
Match length	89
% identity	79
NCBI Description	RIBONUCLEOSIDE-DIPHOSPHATE REDUCTASE SMALL CHAIN (RIBONUCLEOTIDE REDUCTASE) (R2 SUBUNIT) >gi_1044912_emb_CAA63194_ (X92443) ribonucleotide reductase R2 [Nicotiana tabacum]

Seq. No.	160194
Seq. ID	LIB3176-121-P2-K1-G5
Method	BLASTX
NCBI GI	g2341034
BLAST score	424
E value	3.0e-43

Match length	104
% identity	85
NCBI Description	(AC000104) F19P19.13 [Arabidopsis thaliana]

Seq. No.	160195
Seq. ID	LIB3176-121-P2-K1-G7
Method	BLASTX
NCBI GI	g132110
BLAST score	665
E value	5.0e-70
Match length	122
% identity	99
NCBI Description	RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN 3B PRECURSOR (RUBISCO SMALL SUBUNIT 3B) >gi_68060_pir__RKMUB3 ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain B3 precursor - Arabidopsis thaliana >gi_16195_emb_CAA32702_ (X14564) ribulose bisphosphate carboxylase [Arabidopsis thaliana]

Seq. No.	160196
Seq. ID	LIB3176-121-P2-K1-G8
Method	BLASTN
NCBI GI	g499161
BLAST score	125
E value	3.0e-64
Match length	172
% identity	94
NCBI Description	A.thaliana mRNA Athb-6

Seq. No.	160197
Seq. ID	LIB3176-121-P2-K1-H1
Method	BLASTX
NCBI GI	g1352347
BLAST score	118
E value	4.0e-49
Match length	108
% identity	97
NCBI Description	ELONGATION FACTOR 1-BETA A1 (EF-1-BETA) >gi_480620_pir__S37103 translation elongation factor eEF-1 beta-A1 chain - Arabidopsis thaliana (cv. Colombia) >gi_398608_emb_CAA52751_ (X74733) elongation factor-1 beta A1 [Arabidopsis thaliana]

Seq. No.	160198
Seq. ID	LIB3176-121-P2-K1-H10
Method	BLASTX
NCBI GI	g2811028
BLAST score	110
E value	7.0e-22
Match length	58
% identity	92
NCBI Description	HYPOTHETICAL 47.9 KD PROTEIN M021B04.12 >gi_2191188 (AF007271) similar to S. cerevisiae SIK1P (PID:g984964) [Arabidopsis thaliana]

Seq. No.	160199
Seq. ID	LIB3176-121-P2-K1-H11

Method	BLASTX
NCBI GI	g99735
BLAST score	287
E value	3.0e-26
Match length	75
% identity	76
NCBI Description	L-ascorbate peroxidase (EC 1.11.1.11) precursor - Arabidopsis thaliana (fragment)

Seq. No.	160200
Seq. ID	LIB3176-121-P2-K1-H12
Method	BLASTN
NCBI GI	g3335356
BLAST score	209
E value	1.0e-114
Match length	303
% identity	93
NCBI Description	Arabidopsis thaliana chromosome II BAC F16M14 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	160201
Seq. ID	LIB3176-121-P2-K1-H2
Method	BLASTX
NCBI GI	g549643
BLAST score	83
E value	1.0e-10
Match length	87
% identity	47
NCBI Description	HYPOTHETICAL 102.7 KD PROTEIN IN PRP16-SRP40 INTERGENIC REGION >gi_539284_pir__S38167 hypothetical protein YKR089c - yeast (Saccharomyces cerevisiae) >gi_415909_emb_CAA81640_ (Z27116) ORF YKR409 [Saccharomyces cerevisiae] >gi_486575_emb_CAA82168_ (Z28314) ORF YKR089c [Saccharomyces cerevisiae]

Seq. No.	160202
Seq. ID	LIB3176-121-P2-K1-H4
Method	BLASTX
NCBI GI	g1771381
BLAST score	189
E value	2.0e-14
Match length	47
% identity	70
NCBI Description	(X95877) phosphoinositide-specific phospholipase C [Nicotiana rustica]

Seq. No.	160203
Seq. ID	LIB3176-121-P2-K1-H5
Method	BLASTN
NCBI GI	g4586098
BLAST score	195
E value	1.0e-106
Match length	239
% identity	96
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F16J13 (ESSA project)

Seq. No.	160204
Seq. ID	LIB3176-121-P2-K1-H6
Method	BLASTN
NCBI GI	g3413696
BLAST score	99
E value	1.0e-48
Match length	117
% identity	97
NCBI Description	Arabidopsis thaliana chromosome II BAC T19L18 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	160205
Seq. ID	LIB3176-121-P2-K1-H9
Method	BLASTN
NCBI GI	g2501811
BLAST score	36
E value	9.0e-11
Match length	72
% identity	90
NCBI Description	Arabidopsis thaliana glycolate oxidase mRNA, partial cds

Seq. No.	160206
Seq. ID	LIB3176-122-P2-K1-A1
Method	BLASTX
NCBI GI	g2454182
BLAST score	249
E value	2.0e-21
Match length	56
% identity	89
NCBI Description	(U80185) pyruvate dehydrogenase E1 alpha subunit [Arabidopsis thaliana]

Seq. No.	160207
Seq. ID	LIB3176-122-P2-K1-A11
Method	BLASTN
NCBI GI	g1483217
BLAST score	158
E value	8.0e-84
Match length	225
% identity	95
NCBI Description	A.thaliana gene induced upon wounding stress

Seq. No.	160208
Seq. ID	LIB3176-122-P2-K1-A12
Method	BLASTX
NCBI GI	g3269284
BLAST score	327
E value	2.0e-30
Match length	117
% identity	62
NCBI Description	(AL030978) histone H2A- like protein [Arabidopsis thaliana]

Seq. No.	160209
Seq. ID	LIB3176-122-P2-K1-A2
Method	BLASTN
NCBI GI	g509264
BLAST score	51

E value	3.0e-20
Match length	67
% identity	94
NCBI Description	B.napus mRNA for acyl-CoA binding protein

Seq. No.	160210
Seq. ID	LIB3176-122-P2-K1-A3
Method	BLASTN
NCBI GI	g4589440
BLAST score	83
E value	2.0e-39
Match length	87
% identity	99
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MSD21, complete sequence

Seq. No.	160211
Seq. ID	LIB3176-122-P2-K1-A4
Method	BLASTN
NCBI GI	g3702731
BLAST score	56
E value	5.0e-23
Match length	117
% identity	91
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MFC19, complete sequence [Arabidopsis thaliana]

Seq. No.	160212
Seq. ID	LIB3176-122-P2-K1-A5
Method	BLASTN
NCBI GI	g3510340
BLAST score	71
E value	5.0e-32
Match length	111
% identity	91
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MDN11, complete sequence [Arabidopsis thaliana]

Seq. No.	160213
Seq. ID	LIB3176-122-P2-K1-A6
Method	BLASTX
NCBI GI	g4581146
BLAST score	253
E value	2.0e-22
Match length	59
% identity	88
NCBI Description	(AC006919) putative fructose-bisphosphate aldolase, cytoplasmic [Arabidopsis thaliana]

Seq. No.	160214
Seq. ID	LIB3176-122-P2-K1-A9
Method	BLASTX
NCBI GI	g2062157
BLAST score	283
E value	7.0e-26
Match length	57
% identity	35

NCBI Description	(AC001645) jasmonate inducible protein isolog [Arabidopsis thaliana]
Seq. No.	160215
Seq. ID	LIB3176-122-P2-K1-B1
Method	BLASTN
NCBI GI	g2829274
BLAST score	307
E value	1.0e-172
Match length	340
% identity	97
NCBI Description	Arabidopsis thaliana nucleoside diphosphate kinase 3 (ndpk3) mRNA, complete cds
Seq. No.	160216
Seq. ID	LIB3176-122-P2-K1-B11
Method	BLASTX
NCBI GI	g945081
BLAST score	295
E value	6.0e-27
Match length	72
% identity	74
NCBI Description	(U31094) P21 [Petunia hybrida]
Seq. No.	160217
Seq. ID	LIB3176-122-P2-K1-B12
Method	BLASTX
NCBI GI	g1350680
BLAST score	280
E value	2.0e-25
Match length	56
% identity	96
NCBI Description	60S RIBOSOMAL PROTEIN L1
Seq. No.	160218
Seq. ID	LIB3176-122-P2-K1-B2
Method	BLASTX
NCBI GI	g3860261
BLAST score	179
E value	1.0e-13
Match length	39
% identity	97
NCBI Description	(AC005824) putative acidic ribosomal protein [Arabidopsis thaliana]
Seq. No.	160219
Seq. ID	LIB3176-122-P2-K1-B4
Method	BLASTX
NCBI GI	g421836
BLAST score	639
E value	5.0e-67
Match length	130
% identity	98
NCBI Description	G-box-binding factor GF14 - Arabidopsis thaliana >gi_553040 (M96855) GF14 [Arabidopsis thaliana]
Seq. No.	160220

Seq. ID	LIB3176-122-P2-K1-B6
Method	BLASTX
NCBI GI	g99688
BLAST score	695
E value	1.0e-73
Match length	142
% identity	94
NCBI Description	translation elongation factor eEF-1 alpha chain (gene A4) - Arabidopsis thaliana >gi_295789_emb_CAA34456_ (X16432) elongation factor 1-alpha [Arabidopsis thaliana]

Seq. No.	160221
Seq. ID	LIB3176-122-P2-K1-B9
Method	BLASTN
NCBI GI	g2564047
BLAST score	222
E value	1.0e-121
Match length	322
% identity	97
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MJB21, complete sequence [Arabidopsis thaliana]

Seq. No.	160222
Seq. ID	LIB3176-122-P2-K1-C1
Method	BLASTX
NCBI GI	g3334123
BLAST score	268
E value	9.0e-24
Match length	78
% identity	77
NCBI Description	ATP SYNTHASE GAMMA CHAIN, MITOCHONDRIAL PRECURSOR >gi_1655480_dbj_BAA13599_ (D88374) gamma subunit of mitochondrial F1-ATPase [Arabidopsis thaliana] >gi_2924787 (AC002334) mitochondrial F1-ATPase, gamma subunit [Arabidopsis thaliana]

Seq. No.	160223
Seq. ID	LIB3176-122-P2-K1-C12
Method	BLASTX
NCBI GI	g4589980
BLAST score	641
E value	3.0e-67
Match length	133
% identity	91
NCBI Description	(AC007195) cyclophilin, 3' partial [Arabidopsis thaliana]

Seq. No.	160224
Seq. ID	LIB3176-122-P2-K1-C2
Method	BLASTX
NCBI GI	g1076678
BLAST score	214
E value	9.0e-18
Match length	43
% identity	100
NCBI Description	ubiquitin / ribosomal protein S27a - potato (fragment)

Seq. No.	160225

Seq. ID LIB3176-122-P2-K1-C3
Method BLASTX
NCBI GI g99696
BLAST score 682
E value 4.0e-72
Match length 121
% identity 99
NCBI Description glutamate--ammonia ligase (EC 6.3.1.2) precursor, chloroplast (clone lambdaAtgsl1) - Arabidopsis thaliana >gi_240070_bbs_69728 (S69727) light-regulated glutamine synthetase isoenzyme [Arabidopsis thaliana, Peptide, 430 aa] [Arabidopsis thaliana] >gi_228453_prf__1804333A Gln synthetase [Arabidopsis thaliana]

Seq. No. 160226
Seq. ID LIB3176-122-P2-K1-C6
Method BLASTX
NCBI GI g2982303
BLAST score 325
E value 4.0e-30
Match length 91
% identity 67
NCBI Description (AF051236) hypothetical protein [Picea mariana]

Seq. No. 160227
Seq. ID LIB3176-122-P2-K1-C7
Method BLASTX
NCBI GI g132863
BLAST score 206
E value 3.0e-16
Match length 126
% identity 29
NCBI Description CHLOROPLAST 50S RIBOSOMAL PROTEIN L2 >gi_12214_emb_CAA46568_ (X65615) ribosomal protein L2 [Sinapis alba]

Seq. No. 160228
Seq. ID LIB3176-122-P2-K1-C8
Method BLASTX
NCBI GI g119143
BLAST score 639
E value 5.0e-67
Match length 123
% identity 99
NCBI Description ELONGATION FACTOR 1-ALPHA (EF-1-ALPHA) >gi_81606_pir__S06724 translation elongation factor eEF-1 alpha chain - Arabidopsis thaliana >gi_295788_emb_CAA34453_ (X16430) elongation factor 1-alpha [Arabidopsis thaliana] >gi_1369927_emb_CAA34454_ (X16431) elongation factor 1-alpha [Arabidopsis thaliana] >gi_1369928_emb_CAA34455_ (X16431) elongation factor 1-alpha [Arabidopsis thaliana] >gi_1532172 (U63815) EF-1alpha-A1 [Arabidopsis thaliana] >gi_1532173 (U63815) EF-1alpha-A2 [Arabidopsis thaliana] >gi_1532174 (U63815) EF-1alpha-A3 [Arabidopsis thaliana]

Seq. No. 160229
Seq. ID LIB3176-122-P2-K1-D1

Method	BLASTX
NCBI GI	g1174844
BLAST score	178
E value	6.0e-13
Match length	49
% identity	76
NCBI Description	UBIQUITIN-CONJUGATING ENZYME E2-17 KD 2 (UBIQUITIN-PROTEIN LIGASE 2) (UBIQUITIN CARRIER PROTEIN 2) >gi_1076426_pir__S43783 ubiquitin-conjugating enzyme UBC2 - Arabidopsis thaliana >gi_431264 (L19353) ubiquitin conjugating enzyme [Arabidopsis thaliana] >gi_2689243_emb_CAA73476_ (Y13031) ubiquitin conjugating enzyme [Arabidopsis thaliana] >gi_2947065 (AC002521) ubiquitin conjugating enzyme [Arabidopsis thaliana]

Seq. No.	160230
Seq. ID	LIB3176-122-P2-K1-D10
Method	BLASTN
NCBI GI	g4510360
BLAST score	224
E value	1.0e-123
Match length	319
% identity	99
NCBI Description	Arabidopsis thaliana chromosome II BAC F11F19 genomic sequence, complete sequence

Seq. No.	160231
Seq. ID	LIB3176-122-P2-K1-D11
Method	BLASTX
NCBI GI	g3157949
BLAST score	196
E value	5.0e-15
Match length	71
% identity	49
NCBI Description	(AC002131) Similar to glucan endo-1,3-beta-D-glucosidase precursor gb_Z28697 from Nicotiana tabacum. ESTs gb_Z18185 and gb_AA605362 come from this gene. [Arabidopsis thaliana]

Seq. No.	160232
Seq. ID	LIB3176-122-P2-K1-D12
Method	BLASTN
NCBI GI	g4539309
BLAST score	279
E value	1.0e-155
Match length	407
% identity	100
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F19H22 (ESSA project)

Seq. No.	160233
Seq. ID	LIB3176-122-P2-K1-D2
Method	BLASTX
NCBI GI	g2088654
BLAST score	388
E value	9.0e-38
Match length	93
% identity	84

NCBI Description	(AF002109) 60S acidic ribosomal protein P0 isolog [Arabidopsis thaliana]
Seq. No.	160234
Seq. ID	LIB3176-122-P2-K1-D4
Method	BLASTN
NCBI GI	g1448916
BLAST score	68
E value	2.0e-30
Match length	76
% identity	97
NCBI Description	Arabidopsis thaliana threonine synthase mRNA, 3' end of cds
Seq. No.	160235
Seq. ID	LIB3176-122-P2-K1-D6
Method	BLASTX
NCBI GI	g1170034
BLAST score	802
E value	4.0e-86
Match length	145
% identity	100
NCBI Description	GLUTAMATE--CYSTEINE LIGASE PRECURSOR (GAMMA-GLUTAMYLCYSTEINE SYNTHETASE) (GAMMA-ECS) (GCS) >gi_2129598_pir__S60128 glutamate--cysteine ligase (EC 6.3.2.2) precursor, chloroplast - Arabidopsis thaliana >gi_488615_emb_CAA82626_ (Z29490) gamma-glutamylcysteine synthetase [Arabidopsis thaliana]
Seq. No.	160236
Seq. ID	LIB3176-122-P2-K1-D7
Method	BLASTX
NCBI GI	g1172806
BLAST score	354
E value	1.0e-47
Match length	116
% identity	82
NCBI Description	60S RIBOSOMAL PROTEIN L10 (WILM'S TUMOR SUPPRESSOR PROTEIN HOMOLOG) >gi_478401_pir__JQ2244 ribosomal protein L10.e, cytosolic - Arabidopsis thaliana >gi_17682_emb_CAA78856_ (Z15157) Wilm's tumor suppressor homologue [Arabidopsis thaliana]
Seq. No.	160237
Seq. ID	LIB3176-122-P2-K1-E1
Method	BLASTX
NCBI GI	g124224
BLAST score	150
E value	3.0e-10
Match length	48
% identity	69
NCBI Description	INITIATION FACTOR 5A-1 (EIF-5A) (EIF-4D) >gi_100345_pir__S21060 translation initiation factor eIF-5A - common tobacco >gi_19887_emb_CAA45105_ (X63543) eukaryotic initiatin factor 5A (3) [Nicotiana tabacum]
Seq. No.	160238
Seq. ID	LIB3176-122-P2-K1-E11

Method	BLASTX
NCBI GI	g3861068
BLAST score	142
E value	1.0e-08
Match length	60
% identity	43
NCBI Description	(AJ235272) unknown [Rickettsia prowazekii]

Seq. No.	160239
Seq. ID	LIB3176-122-P2-K1-E12
Method	BLASTX
NCBI GI	g3249065
BLAST score	586
E value	9.0e-61
Match length	137
% identity	90
NCBI Description	(AC004473) Similar to HAK1 gb_U22945 high affinity potassium transporter from Schwanniomyces occidentalis. [Arabidopsis thaliana]

Seq. No.	160240
Seq. ID	LIB3176-122-P2-K1-E3
Method	BLASTX
NCBI GI	g3152562
BLAST score	156
E value	5.0e-11
Match length	36
% identity	92
NCBI Description	(AC002986) Similar to proteosome component, micropain (multi-catalytic endopeptidase complex) subunit Y7, gb_X56731 from S. cerevisiae. EST gb_Z25719 comes from this gene. [Arabidopsis thaliana]

Seq. No.	160241
Seq. ID	LIB3176-122-P2-K1-E6
Method	BLASTX
NCBI GI	g3341698
BLAST score	645
E value	1.0e-67
Match length	143
% identity	86
NCBI Description	(AC003672) blue copper-binding protein II [Arabidopsis thaliana]

Seq. No.	160242
Seq. ID	LIB3176-122-P2-K1-E9
Method	BLASTX
NCBI GI	g2511574
BLAST score	555
E value	4.0e-57
Match length	112
% identity	100
NCBI Description	(Y13176) multicatalytic endopeptidase [Arabidopsis thaliana] >gi_3421075 (AF043520) 20S proteasome subunit PAB1 [Arabidopsis thaliana]

Seq. No.	160243

Seq. ID	LIB3176-122-P2-K1-F1
Method	BLASTX
NCBI GI	g2511574
BLAST score	476
E value	6.0e-48
Match length	104
% identity	94
NCBI Description	(Y13176) multicatalytic endopeptidase [Arabidopsis thaliana] >gi_3421075 (AF043520) 20S proteasome subunit PAB1 [Arabidopsis thaliana]

Seq. No.	160244
Seq. ID	LIB3176-122-P2-K1-F10
Method	BLASTX
NCBI GI	g2317911
BLAST score	518
E value	6.0e-58
Match length	125
% identity	93
NCBI Description	(U89959) similar to GTP-binding protein [Arabidopsis thaliana]

Seq. No.	160245
Seq. ID	LIB3176-122-P2-K1-F12
Method	BLASTN
NCBI GI	g3413696
BLAST score	395
E value	0.0e+00
Match length	395
% identity	86
NCBI Description	Arabidopsis thaliana chromosome II BAC T19L18 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	160246
Seq. ID	LIB3176-122-P2-K1-F3
Method	BLASTX
NCBI GI	g4417280
BLAST score	338
E value	5.0e-32
Match length	76
% identity	92
NCBI Description	(AC007019) putative ATP synthase [Arabidopsis thaliana]

Seq. No.	160247
Seq. ID	LIB3176-122-P2-K1-F5
Method	BLASTX
NCBI GI	g2232354
BLAST score	206
E value	2.0e-16
Match length	77
% identity	49
NCBI Description	(AF006081) UDPG glucosyltransferase [Solanum berthaultii]

Seq. No.	160248
Seq. ID	LIB3176-122-P2-K1-F6
Method	BLASTX
NCBI GI	g452470

BLAST score	664
E value	7.0e-70
Match length	123
% identity	100
NCBI Description	(U05218) ATP sulfurylase [Arabidopsis thaliana]

Seq. No.	160249
Seq. ID	LIB3176-122-P2-K1-F8
Method	BLASTX
NCBI GI	g2459420
BLAST score	476
E value	3.0e-48
Match length	92
% identity	100
NCBI Description	(AC002332) putative ribosomal protein L17 [Arabidopsis thaliana]

Seq. No.	160250
Seq. ID	LIB3176-122-P2-K1-F9
Method	BLASTX
NCBI GI	g2129550
BLAST score	137
E value	1.0e-08
Match length	74
% identity	39
NCBI Description	calcium-dependent protein kinase (EC 2.7.1.-) CDPK6 - Arabidopsis thaliana >gi_2129554_pir__S71901 calcium-dependent protein kinase 6 - Arabidopsis thaliana >gi_836940 (U20623) calcium-dependent protein kinase [Arabidopsis thaliana] >gi_836944 (U20625) calcium-dependent protein kinase [Arabidopsis thaliana] >gi_4454034_emb_CAA23031.1_ (AL035394) calcium-dependent protein kinase (CDPK6) [Arabidopsis thaliana]

Seq. No.	160251
Seq. ID	LIB3176-122-P2-K1-G10
Method	BLASTX
NCBI GI	g4586038
BLAST score	90
E value	4.0e-09
Match length	52
% identity	67
NCBI Description	(AC007109) putative heat shock protein [Arabidopsis thaliana]

Seq. No.	160252
Seq. ID	LIB3176-122-P2-K1-G11
Method	BLASTN
NCBI GI	g4376087
BLAST score	279
E value	1.0e-156
Match length	279
% identity	100
NCBI Description	Arabidopsis thaliana DNA chromosome 4, ESSA I AP2 contig fragment No

Seq. No.	160253

Seq. ID	LIB3176-122-P2-K1-G12
Method	BLASTX
NCBI GI	g1170373
BLAST score	625
E value	2.0e-65
Match length	119
% identity	100
NCBI Description	HEAT SHOCK COGNATE 70 KD PROTEIN 1 >gi_1072473_pir__S46302 heat shock cognate protein 70-1 - Arabidopsis thaliana >gi_397482_emb_CAA52684_ (X74604) heat shock protein 70 cognate [Arabidopsis thaliana]

Seq. No.	160254
Seq. ID	LIB3176-122-P2-K1-G3
Method	BLASTN
NCBI GI	g4490701
BLAST score	41
E value	6.0e-14
Match length	102
% identity	94
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone T24A18 (ESSA project)

Seq. No.	160255
Seq. ID	LIB3176-122-P2-K1-G4
Method	BLASTX
NCBI GI	g267069
BLAST score	644
E value	1.0e-67
Match length	119
% identity	100
NCBI Description	TUBULIN ALPHA-2/ALPHA-4 CHAIN >gi_320183_pir__JQ1594 tubulin alpha chain - Arabidopsis thaliana >gi_166914 (M84696) apha-2 tubulin [Arabidopsis thaliana] >gi_166916 (M84697) alpha-4 tubulin [Arabidopsis thaliana]

Seq. No.	160256
Seq. ID	LIB3176-122-P2-K1-G5
Method	BLASTX
NCBI GI	g2842490
BLAST score	479
E value	3.0e-48
Match length	147
% identity	66
NCBI Description	(AL021749) heat-shock protein [Arabidopsis thaliana]

Seq. No.	160257
Seq. ID	LIB3176-122-P2-K1-G6
Method	BLASTX
NCBI GI	g1170939
BLAST score	686
E value	2.0e-72
Match length	137
% identity	93
NCBI Description	S-ADENOSYLMETHIONINE SYNTHETASE 3 (METHIONINE ADENOSYLTRANSFERASE 3) (ADOMET SYNTHETASE 3) >gi_1084408_pir__S46540 methionine adenosyltransferase (EC

	2.5.1.6) - tomato >gi_429108_emb_CAA80867_ (Z24743) S-adenosyl-L-methionine synthetase [Lycopersicon esculentum]
Seq. No.	160258
Seq. ID	LIB3176-122-P2-K1-G7
Method	BLASTN
NCBI GI	g2815404
BLAST score	201
E value	1.0e-109
Match length	420
% identity	97
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MMG4, complete sequence [Arabidopsis thaliana]
Seq. No.	160259
Seq. ID	LIB3176-122-P2-K1-G8
Method	BLASTX
NCBI GI	g1084350
BLAST score	642
E value	2.0e-67
Match length	126
% identity	93
NCBI Description	glutamate--ammonia ligase (EC 6.3.1.2) - rape >gi_599656_emb_CAA58118.1_ (X82997) glutamate--ammonia ligase [Brassica napus]
Seq. No.	160260
Seq. ID	LIB3176-122-P2-K1-G9
Method	BLASTX
NCBI GI	g4490705
BLAST score	468
E value	5.0e-47
Match length	110
% identity	90
NCBI Description	(AL035680) ribosomal protein L14-like protein [Arabidopsis thaliana]
Seq. No.	160261
Seq. ID	LIB3176-122-P2-K1-H10
Method	BLASTX
NCBI GI	g4531443
BLAST score	167
E value	3.0e-12
Match length	62
% identity	63
NCBI Description	(AC006224) putative 50s ribosomal protein L3 [Arabidopsis thaliana]
Seq. No.	160262
Seq. ID	LIB3176-122-P2-K1-H11
Method	BLASTX
NCBI GI	g3738092
BLAST score	308
E value	2.0e-28
Match length	63
% identity	92

NCBI Description	(AC005617) similar to glyoxysomal malate dehydrogenase [Arabidopsis thaliana]
Seq. No.	160263
Seq. ID	LIB3176-122-P2-K1-H12
Method	BLASTX
NCBI GI	g4506243
BLAST score	219
E value	1.0e-17
Match length	117
% identity	44
NCBI Description	polypyrimidine tract binding protein (heterogeneous nuclear ribonucleoprotein I) >gi_107220_pir__S26294 polypyrimidine tract-binding protein - human >gi_32354_emb_CAA47386_ (X66975) nuclear ribonucleoprotein [Homo sapiens] >gi_35772_emb_CAA46444_ (X65372) polypirimidine tract binding protein [Homo sapiens]
Seq. No.	160264
Seq. ID	LIB3176-122-P2-K1-H2
Method	BLASTX
NCBI GI	g2500376
BLAST score	421
E value	1.0e-41
Match length	84
% identity	95
NCBI Description	60S RIBOSOMAL PROTEIN L34 >gi_4262177_gb_AAD14494_ (AC005508) 23552 [Arabidopsis thaliana]
Seq. No.	160265
Seq. ID	LIB3176-122-P2-K1-H4
Method	BLASTX
NCBI GI	g2506122
BLAST score	238
E value	6.0e-20
Match length	139
% identity	39
NCBI Description	ATP-DEPENDENT PERMEASE MDL2 >gi_2132334_pir__S65303 MDL2 protein - yeast (Saccharomyces cerevisiae) >gi_1370557_emb_CAA98006_ (Z73626) ORF YPL270w [Saccharomyces cerevisiae]
Seq. No.	160266
Seq. ID	LIB3176-122-P2-K1-H5
Method	BLASTX
NCBI GI	g2062161
BLAST score	584
E value	2.0e-60
Match length	145
% identity	54
NCBI Description	(AC001645) jasmonate inducible protein isolog [Arabidopsis thaliana]
Seq. No.	160267
Seq. ID	LIB3176-122-P2-K1-H6
Method	BLASTX
NCBI GI	g2443357

BLAST score	498
E value	2.0e-50
Match length	99
% identity	97
NCBI Description	(AB004293) SigB [Arabidopsis thaliana] >gi_2597831_emb_CAA75584_ (Y15362) sigma factor [Arabidopsis thaliana] >gi_2879922_dbj_BAA24825_ (AB004820) plastid RNA polymerase sigma-subunit [Arabidopsis thaliana] >gi_3063440 (AC003981) F22O13.2 [Arabidopsis thaliana]

Seq. No.	160268
Seq. ID	LIB3176-122-P2-K1-H8
Method	BLASTX
NCBI GI	g2443357
BLAST score	143
E value	3.0e-09
Match length	33
% identity	76
NCBI Description	(AB004293) SigB [Arabidopsis thaliana] >gi_2597831_emb_CAA75584_ (Y15362) sigma factor [Arabidopsis thaliana] >gi_2879922_dbj_BAA24825_ (AB004820) plastid RNA polymerase sigma-subunit [Arabidopsis thaliana] >gi_3063440 (AC003981) F22O13.2 [Arabidopsis thaliana]

Seq. No.	160269
Seq. ID	LIB3176-122-P2-K1-H9
Method	BLASTN
NCBI GI	g1209241
BLAST score	370
E value	0.0e+00
Match length	421
% identity	97
NCBI Description	Arabidopsis thaliana metallothionein mRNA sequence

Seq. No.	160270
Seq. ID	LIB3176-123-P2-K1-A11
Method	BLASTN
NCBI GI	g3702735
BLAST score	278
E value	1.0e-155
Match length	333
% identity	97
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MQL5, complete sequence [Arabidopsis thaliana]

Seq. No.	160271
Seq. ID	LIB3176-123-P2-K1-A12
Method	BLASTX
NCBI GI	g1724100
BLAST score	86
E value	4.0e-14
Match length	106
% identity	37
NCBI Description	(U79765) porin [Mesembryanthemum crystallinum]

Seq. No.	160272
Seq. ID	LIB3176-123-P2-K1-A3

Method	BLASTX
NCBI GI	g1173187
BLAST score	198
E value	3.0e-35
Match length	82
% identity	99
NCBI Description	40S RIBOSOMAL PROTEIN S23 (S12) >gi_1362041_pir__S56673 ribosomal protein S23.e, cytosolic (clone RJ3) - garden strawberry >gi_643074 (U19940) putative 40S ribosomal protein s12 [Fragaria x ananassa]

Seq. No.	160273
Seq. ID	LIB3176-123-P2-K1-A4
Method	BLASTX
NCBI GI	g3386565
BLAST score	78
E value	3.0e-24
Match length	111
% identity	48
NCBI Description	(AF079588) 1-aminocyclopropane-1-carboxylate oxidase [Sorghum bicolor]

Seq. No.	160274
Seq. ID	LIB3176-123-P2-K1-A5
Method	BLASTX
NCBI GI	g1172995
BLAST score	185
E value	7.0e-14
Match length	77
% identity	53
NCBI Description	60S RIBOSOMAL PROTEIN L22 >gi_1083790_pir__S52084 ribosomal protein L22 - rat >gi_710295_emb_CAA55204_ (X78444) ribosomal protein L22 [Rattus norvegicus] >gi_1093952_prf__2105193A ribosomal protein L22 [Rattus norvegicus]

Seq. No.	160275
Seq. ID	LIB3176-123-P2-K1-A6
Method	BLASTX
NCBI GI	g3688175
BLAST score	395
E value	2.0e-38
Match length	74
% identity	99
NCBI Description	(AL031804) gamma-VPE (vacuolar processing enzyme) [Arabidopsis thaliana]

Seq. No.	160276
Seq. ID	LIB3176-123-P2-K1-A9
Method	BLASTX
NCBI GI	g1173187
BLAST score	116
E value	3.0e-24
Match length	66
% identity	94
NCBI Description	40S RIBOSOMAL PROTEIN S23 (S12) >gi_1362041_pir__S56673 ribosomal protein S23.e, cytosolic (clone RJ3) - garden

strawberry >gi_643074 (U19940) putative 40S ribosomal protein s12 [Fragaria x ananassa]

Seq. No.	160277
Seq. ID	LIB3176-123-P2-K1-B1
Method	BLASTX
NCBI GI	g4587541
BLAST score	99
E value	2.0e-39
Match length	112
% identity	68
NCBI Description	(AC006577) Belongs to the PF_00657 Lipase/Acylhydrolase with GDSL-motif family. ESTs gb_T44453, gb_T04815, gb_T45993, gb_R30138, gb_AI099570 and gb_T22281 come from this gene. [Arabidopsis thaliana]

Seq. No.	160278
Seq. ID	LIB3176-123-P2-K1-B10
Method	BLASTN
NCBI GI	g2760172
BLAST score	172
E value	4.0e-92
Match length	203
% identity	97
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MUB3, complete sequence [Arabidopsis thaliana]

Seq. No.	160279
Seq. ID	LIB3176-123-P2-K1-B11
Method	BLASTN
NCBI GI	g1916349
BLAST score	106
E value	7.0e-53
Match length	177
% identity	90
NCBI Description	Brassica rapa PSI-H subunit (psaH) mRNA, complete cds

Seq. No.	160280
Seq. ID	LIB3176-123-P2-K1-B2
Method	BLASTX
NCBI GI	g1731146
BLAST score	45
E value	1.0e-10
Match length	46
% identity	72
NCBI Description	HYPOTHETICAL 42.1 KD PROTEIN ZK1307.9 IN CHROMOSOME III >gi_3881615_emb_CAA87435_ (Z47358) similar to YJU2 protein [Caenorhabditis elegans]

Seq. No.	160281
Seq. ID	LIB3176-123-P2-K1-B3
Method	BLASTX
NCBI GI	g3695383
BLAST score	431
E value	1.0e-42
Match length	85
% identity	95

NCBI Description	(AF096370) similar to inorganic pyrophosphatase (Pfam: PF00719 Pyrophosphatase, E-value: 2.7e-88) [Arabidopsis thaliana]
Seq. No.	160282
Seq. ID	LIB3176-123-P2-K1-B8
Method	BLASTN
NCBI GI	g4580744
BLAST score	57
E value	9.0e-24
Match length	136
% identity	62
NCBI Description	Sequence of BAC F15I1 from Arabidopsis thaliana chromosome 1, complete sequence
Seq. No.	160283
Seq. ID	LIB3176-123-P2-K1-B9
Method	BLASTX
NCBI GI	g3024019
BLAST score	218
E value	4.0e-18
Match length	54
% identity	81
NCBI Description	INITIATION FACTOR 5A (EIF-5A) (EIF-4D) >gi_2225879_dbj_BAA20876_ (AB004823) eukaryotic initiation factor 5A2 [Solanum tuberosum] >gi_2225887_dbj_BAA20880_ (AB004827) eukaryotic initiation factor 5A1 [Solanum tuberosum]
Seq. No.	160284
Seq. ID	LIB3176-123-P2-K1-C10
Method	BLASTN
NCBI GI	g4662609
BLAST score	229
E value	1.0e-126
Match length	347
% identity	97
NCBI Description	Genomic sequence for Arabidopsis thaliana BAC F10A5, complete sequence
Seq. No.	160285
Seq. ID	LIB3176-123-P2-K1-C11
Method	BLASTN
NCBI GI	g4757392
BLAST score	58
E value	3.0e-24
Match length	154
% identity	95
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, TAC clone: K14A17, complete sequence
Seq. No.	160286
Seq. ID	LIB3176-123-P2-K1-C12
Method	BLASTX
NCBI GI	g4539316
BLAST score	90
E value	3.0e-40

Match length	97
% identity	88
NCBI Description	(AL035679) putative fructose-bisphosphate aldolase [Arabidopsis thaliana]

Seq. No.	160287
Seq. ID	LIB3176-123-P2-K1-C2
Method	BLASTN
NCBI GI	g3212846
BLAST score	78
E value	5.0e-36
Match length	247
% identity	98
NCBI Description	Arabidopsis thaliana chromosome II BAC F6E13 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	160288
Seq. ID	LIB3176-123-P2-K1-C3
Method	BLASTX
NCBI GI	g4580920
BLAST score	88
E value	7.0e-32
Match length	99
% identity	72
NCBI Description	(AF113545) vacuole-associated annexin VCaB42 [Nicotiana tabacum]

Seq. No.	160289
Seq. ID	LIB3176-123-P2-K1-C4
Method	BLASTX
NCBI GI	g1351271
BLAST score	295
E value	1.0e-26
Match length	113
% identity	59
NCBI Description	TRIOSEPHOSPHATE ISOMERASE CHLOROPLAST PRECURSOR (TIM) >gi_1084309_pir__S52032 triose-phosphate isomerase (EC 5.3.1.1) precursor, chloroplast - spinach >gi_806312 (L36387) triosephosphate isomerase, chloroplast isozyme [Spinacia oleracea]

Seq. No.	160290
Seq. ID	LIB3176-123-P2-K1-C5
Method	BLASTN
NCBI GI	g4454447
BLAST score	73
E value	4.0e-33
Match length	117
% identity	57
NCBI Description	Arabidopsis thaliana chromosome II BAC F5H14 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	160291
Seq. ID	LIB3176-123-P2-K1-C7
Method	BLASTX
NCBI GI	g2738248
BLAST score	230

E value	5.0e-19
Match length	48
% identity	96
NCBI Description	(U97200) cobalamin-independent methionine synthase [Arabidopsis thaliana]

Seq. No.	160292
Seq. ID	LIB3176-123-P2-K1-C8
Method	BLASTX
NCBI GI	g730526
BLAST score	149
E value	2.0e-09
Match length	139
% identity	88
NCBI Description	60S RIBOSOMAL PROTEIN L13 (BBC1 PROTEIN HOMOLOG) >gi_480787_pir__S37271 ribosomal protein L13 - Arabidopsis thaliana >gi_404166_emb_CAA53005_ (X75162) BBC1 protein [Arabidopsis thaliana]

Seq. No.	160293
Seq. ID	LIB3176-123-P2-K1-C9
Method	BLASTN
NCBI GI	g2459406
BLAST score	206
E value	1.0e-112
Match length	415
% identity	95
NCBI Description	Arabidopsis thaliana chromosome II BAC F4P9 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	160294
Seq. ID	LIB3176-123-P2-K1-D10
Method	BLASTN
NCBI GI	g1490552
BLAST score	54
E value	3.0e-22
Match length	66
% identity	95
NCBI Description	Arabidopsis thaliana S-adenosylmethionine decarboxylase (SAMdc) mRNA, complete cds

Seq. No.	160295
Seq. ID	LIB3176-123-P2-K1-D11
Method	BLASTX
NCBI GI	g2160185
BLAST score	89
E value	9.0e-23
Match length	107
% identity	51
NCBI Description	(AC000132) Similar to S. pombe ISP4 (gb_D83992). [Arabidopsis thaliana]

Seq. No.	160296
Seq. ID	LIB3176-123-P2-K1-D12
Method	BLASTN
NCBI GI	g3184270
BLAST score	47

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E value	2.0e-17
Match length	103
% identity	86
NCBI Description	Arabidopsis thaliana chromosome II BAC T8K22 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	160297
Seq. ID	LIB3176-123-P2-K1-D2
Method	BLASTN
NCBI GI	g1305409
BLAST score	120
E value	3.0e-61
Match length	147
% identity	96
NCBI Description	Arabidopsis thaliana isopentenyl diphosphate:dimethylallyl diphosphate isomerase (IPP1) gene, complete cds

Seq. No.	160298
Seq. ID	LIB3176-123-P2-K1-D3
Method	BLASTN
NCBI GI	g4519188
BLAST score	143
E value	1.0e-74
Match length	166
% identity	97
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K21L19, complete sequence

Seq. No.	160299
Seq. ID	LIB3176-123-P2-K1-D4
Method	BLASTX
NCBI GI	g1864017
BLAST score	388
E value	7.0e-38
Match length	79
% identity	96
NCBI Description	(D63396) elongation factor-1 alpha [Nicotiana tabacum]

Seq. No.	160300
Seq. ID	LIB3176-123-P2-K1-D5
Method	BLASTN
NCBI GI	g4455339
BLAST score	88
E value	3.0e-42
Match length	116
% identity	62
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone T12J5 (ESSAII project)

Seq. No.	160301
Seq. ID	LIB3176-123-P2-K1-D7
Method	BLASTN
NCBI GI	g166911
BLAST score	55
E value	2.0e-22
Match length	146
% identity	86

NCBI Description	A.thaliana alpha-tubulin gene, complete cds
Seq. No.	160302
Seq. ID	LIB3176-123-P2-K1-D8
Method	BLASTX
NCBI GI	g625977
BLAST score	59
E value	7.0e-40
Match length	90
% identity	92
NCBI Description	p40 protein homolog - Arabidopsis thaliana >gi_402904 (U01955) laminin receptor-like protein [Arabidopsis thaliana]
Seq. No.	160303
Seq. ID	LIB3176-123-P2-K1-D9
Method	BLASTX
NCBI GI	g3176874
BLAST score	172
E value	3.0e-12
Match length	84
% identity	42
NCBI Description	(AF065639) cucumisin-like serine protease [Arabidopsis thaliana]
Seq. No.	160304
Seq. ID	LIB3176-123-P2-K1-E1
Method	BLASTN
NCBI GI	g4432829
BLAST score	100
E value	5.0e-49
Match length	296
% identity	97
NCBI Description	Arabidopsis thaliana chromosome II BAC T1B3 genomic sequence, complete sequence [Arabidopsis thaliana]
Seq. No.	160305
Seq. ID	LIB3176-123-P2-K1-E11
Method	BLASTX
NCBI GI	g2914700
BLAST score	174
E value	2.0e-54
Match length	115
% identity	99
NCBI Description	(AC003974) tRNA-processing protein SEN3-like [Arabidopsis thaliana]
Seq. No.	160306
Seq. ID	LIB3176-123-P2-K1-E12
Method	BLASTN
NCBI GI	g2160155
BLAST score	442
E value	0.0e+00
Match length	457
% identity	99
NCBI Description	Sequence of BAC F21M12 from Arabidopsis thaliana chromosome 1, complete sequence [Arabidopsis thaliana]

Seq. No.	160307
Seq. ID	LIB3176-123-P2-K1-E2
Method	BLASTN
NCBI GI	g3399678
BLAST score	101
E value	1.0e-49
Match length	170
% identity	99
NCBI Description	Arabidopsis thaliana chromosome 1 BAC F13M7 sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	160308
Seq. ID	LIB3176-123-P2-K1-E5
Method	BLASTX
NCBI GI	g119143
BLAST score	66
E value	8.0e-63
Match length	130
% identity	97
NCBI Description	ELONGATION FACTOR 1-ALPHA (EF-1-ALPHA) >gi_81606_pir__S06724 translation elongation factor eEF-1 alpha chain - Arabidopsis thaliana >gi_295788_emb_CAA34453_ (X16430) elongation factor 1-alpha [Arabidopsis thaliana] >gi_1369927_emb_CAA34454_ (X16431) elongation factor 1-alpha [Arabidopsis thaliana] >gi_1369928_emb_CAA34455_ (X16431) elongation factor 1-alpha [Arabidopsis thaliana] >gi_1532172 (U63815) EF-1alpha-A1 [Arabidopsis thaliana] >gi_1532173 (U63815) EF-1alpha-A2 [Arabidopsis thaliana] >gi_1532174 (U63815) EF-1alpha-A3 [Arabidopsis thaliana]

Seq. No.	160309
Seq. ID	LIB3176-123-P2-K1-E6
Method	BLASTN
NCBI GI	g3766106
BLAST score	70
E value	3.0e-31
Match length	95
% identity	96
NCBI Description	Arabidopsis thaliana chromosome 1 BAC F9K20 sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	160310
Seq. ID	LIB3176-123-P2-K1-E7
Method	BLASTN
NCBI GI	g2351073
BLAST score	264
E value	1.0e-147
Match length	324
% identity	97
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MYJ24, complete sequence [Arabidopsis thaliana]

Seq. No.	160311
Seq. ID	LIB3176-123-P2-K1-E8
Method	BLASTN
NCBI GI	g2351068

BLAST score	119
E value	2.0e-60
Match length	233
% identity	97
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MRH10, complete sequence [Arabidopsis thaliana]

Seq. No.	160312
Seq. ID	LIB3176-123-P2-K1-F1
Method	BLASTN
NCBI GI	g4309683
BLAST score	201
E value	1.0e-109
Match length	237
% identity	96
NCBI Description	Arabidopsis thaliana chromosome 1 BAC T31J12 sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	160313
Seq. ID	LIB3176-123-P2-K1-F10
Method	BLASTN
NCBI GI	g2264320
BLAST score	168
E value	2.0e-89
Match length	367
% identity	96
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MXI10, complete sequence [Arabidopsis thaliana]

Seq. No.	160314
Seq. ID	LIB3176-123-P2-K1-F12
Method	BLASTX
NCBI GI	g2959767
BLAST score	197
E value	1.0e-59
Match length	141
% identity	81
NCBI Description	(AJ002584) AtMRP4 [Arabidopsis thaliana] >gi_3738292 (AC005309) glutathione-conjugate transporter AtMRP4 [Arabidopsis thaliana]

Seq. No.	160315
Seq. ID	LIB3176-123-P2-K1-F4
Method	BLASTN
NCBI GI	g2264310
BLAST score	53
E value	7.0e-21
Match length	251
% identity	81
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MKP11, complete sequence [Arabidopsis thaliana]

Seq. No.	160316
Seq. ID	LIB3176-123-P2-K1-F5
Method	BLASTX
NCBI GI	g1168256
BLAST score	438

E value	9.0e-44
Match length	88
% identity	95
NCBI Description	ASPARTATE AMINOTRANSFERASE, MITOCHONDRIAL PRECURSOR (TRANSAMINASE A) >gi_693688 (U15026) aspartate aminotransferase [Arabidopsis thaliana] >gi_3201622 (AC004669) aspartate aminotransferase [Arabidopsis thaliana]

Seq. No.	160317
Seq. ID	LIB3176-123-P2-K1-F6
Method	BLASTN
NCBI GI	g4206762
BLAST score	99
E value	2.0e-48
Match length	246
% identity	86
NCBI Description	Arabidopsis thaliana cell wall-plasma membrane linker protein homolog (CWLP) mRNA, complete cds

Seq. No.	160318
Seq. ID	LIB3176-123-P2-K1-F7
Method	BLASTX
NCBI GI	g4490732
BLAST score	196
E value	1.0e-31
Match length	73
% identity	100
NCBI Description	(AL035709) phosphoenolpyruvate carboxykinase (ATP)-like protein [Arabidopsis thaliana]

Seq. No.	160319
Seq. ID	LIB3176-123-P2-K1-F8
Method	BLASTX
NCBI GI	g116527
BLAST score	175
E value	1.0e-12
Match length	61
% identity	46
NCBI Description	PROBABLE CLPP-LIKE PROTEASE (ENDOPEPTIDASE CLP) (ORF 196) >gi_1143166 (U32397) ClpP protease [Nicotiana tabacum] >gi_2924270_emb_CAA77422_ (Z00044) ATP-dependent protease proteolytic subuni [Nicotiana tabacum]

Seq. No.	160320
Seq. ID	LIB3176-123-P2-K1-G1
Method	BLASTX
NCBI GI	g267069
BLAST score	419
E value	3.0e-41
Match length	87
% identity	91
NCBI Description	TUBULIN ALPHA-2/ALPHA-4 CHAIN >gi_320183_pir__JQ1594 tubulin alpha chain - Arabidopsis thaliana >gi_166914 (M84696) apha-2 tubulin [Arabidopsis thaliana] >gi_166916 (M84697) alpha-4 tubulin [Arabidopsis thaliana]

Seq. No.	160321
Seq. ID	LIB3176-123-P2-K1-G10
Method	BLASTN
NCBI GI	g2341023
BLAST score	55
E value	2.0e-22
Match length	114
% identity	96
NCBI Description	Sequence of BAC F19P19 from Arabidopsis thaliana chromosome 1, complete sequence [Arabidopsis thaliana]

Seq. No.	160322
Seq. ID	LIB3176-123-P2-K1-G12
Method	BLASTN
NCBI GI	g3068702
BLAST score	266
E value	1.0e-148
Match length	454
% identity	99
NCBI Description	Arabidopsis thaliana putative transmembrane protein G1p (AtG1), putative nuclear DNA-binding protein G2p (AtG2), Em1 protein (ATEM1), putative chlorophyll synthetase (AtG4), putative transmembrane protein G5p (AtG5), put

Seq. No.	160323
Seq. ID	LIB3176-123-P2-K1-G2
Method	BLASTX
NCBI GI	g3176676
BLAST score	58
E value	3.0e-23
Match length	63
% identity	100
NCBI Description	(AC003671) Similar to carbonic anhydrase gb_L19255 from Nicotiana tabacum. ESTs gb_AA597643, gb_T45390, gb_T43963 and gb_AA597734 come from this gene. [Arabidopsis thaliana]

Seq. No.	160324
Seq. ID	LIB3176-123-P2-K1-G4
Method	BLASTX
NCBI GI	g3249099
BLAST score	497
E value	2.0e-50
Match length	129
% identity	77
NCBI Description	(AC003114) EST gb_T21244 comes from this gene. [Arabidopsis thaliana] >gi_4220616_dbj_BAA74591_ (AB021936) nicotianamine synthase [Arabidopsis thaliana]

Seq. No.	160325
Seq. ID	LIB3176-123-P2-K1-G5
Method	BLASTN
NCBI GI	g4678705
BLAST score	189
E value	1.0e-102
Match length	204
% identity	99
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F10N7

(ESSA project)

Seq. No.	160326
Seq. ID	LIB3176-123-P2-K1-G6
Method	BLASTN
NCBI GI	g4454447
BLAST score	26
E value	2.0e-05
Match length	111
% identity	53
NCBI Description	Arabidopsis thaliana chromosome II BAC F5H14 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	160327
Seq. ID	LIB3176-123-P2-K1-G9
Method	BLASTX
NCBI GI	g445613
BLAST score	74
E value	2.0e-19
Match length	103
% identity	50
NCBI Description	ribosomal protein L7 [Solanum tuberosum]

Seq. No.	160328
Seq. ID	LIB3176-123-P2-K1-H1
Method	BLASTN
NCBI GI	g4584387
BLAST score	141
E value	2.0e-73
Match length	296
% identity	96
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F7J7 (ESSA project)

Seq. No.	160329
Seq. ID	LIB3176-123-P2-K1-H10
Method	BLASTX
NCBI GI	g4455256
BLAST score	199
E value	1.0e-15
Match length	113
% identity	63
NCBI Description	(AL035523) protein-methionine-S-oxide reductase [Arabidopsis thaliana]

Seq. No.	160330
Seq. ID	LIB3176-123-P2-K1-H11
Method	BLASTN
NCBI GI	g4580744
BLAST score	138
E value	1.0e-71
Match length	242
% identity	51
NCBI Description	Sequence of BAC F15I1 from Arabidopsis thaliana chromosome 1, complete sequence

Seq. No. 160331

Seq. ID	LIB3176-123-P2-K1-H3
Method	BLASTX
NCBI GI	g1872544
BLAST score	309
E value	2.0e-28
Match length	97
% identity	66
NCBI Description	(U89014) early light-induced protein; ELIP [Arabidopsis thaliana]

Seq. No.	160332
Seq. ID	LIB3176-123-P2-K1-H4
Method	BLASTX
NCBI GI	g114527
BLAST score	185
E value	5.0e-58
Match length	133
% identity	90
NCBI Description	ATP SYNTHASE ALPHA CHAIN >gi_67825_pir__PWSPA H+-transporting ATP synthase (EC 3.6.1.34) alpha chain - spinach chloroplast >gi_12261_emb_CAA29346_ (X05916) atpA protein (cf1 alpha) (AA 1-507) [Spinacia oleracea]

Seq. No.	160333
Seq. ID	LIB3176-123-P2-K1-H5
Method	BLASTX
NCBI GI	g1170503
BLAST score	183
E value	3.0e-33
Match length	85
% identity	92
NCBI Description	EUKARYOTIC INITIATION FACTOR 4A-1 (EIF-4A-1) >gi_322503_pir__JC1452 translation initiation factor eIF-4A1 - Arabidopsis thaliana >gi_16554_emb_CAA46188_ (X65052) eukaryotic translation initiation factor 4A-1 [Arabidopsis thaliana]

Seq. No.	160334
Seq. ID	LIB3176-123-P2-K1-H6
Method	BLASTX
NCBI GI	g3342802
BLAST score	325
E value	2.0e-30
Match length	90
% identity	74
NCBI Description	(AF061838) putative cytosolic 6-phosphogluconate dehydrogenase [Zea mays]

Seq. No.	160335
Seq. ID	LIB3176-123-P2-K1-H8
Method	BLASTX
NCBI GI	g1755096
BLAST score	173
E value	9.0e-18
Match length	59
% identity	65
NCBI Description	(U66904) alpha-tubulin [Trichomitus batrachorum]

Seq. No.	160336
Seq. ID	LIB3177-002-Q1-K1-A10
Method	BLASTX
NCBI GI	g2662469
BLAST score	435
E value	2.0e-43
Match length	81
% identity	100
NCBI Description	(AF034217) ribosomal protein S6 [Arabidopsis thaliana]

Seq. No.	160337
Seq. ID	LIB3177-002-Q1-K1-A12
Method	BLASTN
NCBI GI	g2924257
BLAST score	61
E value	9.0e-26
Match length	85
% identity	93
NCBI Description	Tobacco chloroplast genome DNA

Seq. No.	160338
Seq. ID	LIB3177-002-Q1-K1-A4
Method	BLASTN
NCBI GI	g2191157
BLAST score	127
E value	4.0e-65
Match length	300
% identity	100
NCBI Description	Arabidopsis thaliana BAC IG002P16

Seq. No.	160339
Seq. ID	LIB3177-002-Q1-K1-A5
Method	BLASTX
NCBI GI	g3915826
BLAST score	387
E value	1.0e-37
Match length	89
% identity	82
NCBI Description	60S RIBOSOMAL PROTEIN L5

Seq. No.	160340
Seq. ID	LIB3177-002-Q1-K1-A6
Method	BLASTN
NCBI GI	g4263694
BLAST score	139
E value	2.0e-72
Match length	291
% identity	95
NCBI Description	Arabidopsis thaliana chromosome II BAC F22D22 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	160341
Seq. ID	LIB3177-002-Q1-K1-A7
Method	BLASTX
NCBI GI	g1703220
BLAST score	257

E value	2.0e-22
Match length	91
% identity	56
NCBI Description	AIG2 PROTEIN >gi_1127806 (U40857) AIG2 [Arabidopsis thaliana]

Seq. No.	160342
Seq. ID	LIB3177-002-Q1-K1-A8
Method	BLASTN
NCBI GI	g1632775
BLAST score	269
E value	1.0e-150
Match length	295
% identity	99
NCBI Description	A.thaliana t5r gene

Seq. No.	160343
Seq. ID	LIB3177-002-Q1-K1-B1
Method	BLASTX
NCBI GI	g1524370
BLAST score	229
E value	3.0e-19
Match length	85
% identity	49
NCBI Description	(X92491) TOM20 [Solanum tuberosum]

Seq. No.	160344
Seq. ID	LIB3177-002-Q1-K1-B10
Method	BLASTX
NCBI GI	g4454037
BLAST score	469
E value	2.0e-47
Match length	85
% identity	100
NCBI Description	(AL035394) putative major latex protein [Arabidopsis thaliana]

Seq. No.	160345
Seq. ID	LIB3177-002-Q1-K1-B11
Method	BLASTX
NCBI GI	g1169598
BLAST score	295
E value	6.0e-27
Match length	67
% identity	82
NCBI Description	OMEGA-6 FATTY ACID DESATURASE, ENDOPLASMIC RETICULUM (DELTA-12 DESATURASE) >gi_438451 (L26296) delta-12 desaturase [Arabidopsis thaliana]

Seq. No.	160346
Seq. ID	LIB3177-002-Q1-K1-B12
Method	BLASTX
NCBI GI	g4193388
BLAST score	278
E value	6.0e-25
Match length	74
% identity	76

NCBI Description	(AF091455) translationally controlled tumor protein [Hevea brasiliensis]
Seq. No.	160347
Seq. ID	LIB3177-002-Q1-K1-B3
Method	BLASTN
NCBI GI	g4512656
BLAST score	159
E value	3.0e-84
Match length	301
% identity	89
NCBI Description	Arabidopsis thaliana chromosome II BAC F7D19 genomic sequence, complete sequence
Seq. No.	160348
Seq. ID	LIB3177-002-Q1-K1-B4
Method	BLASTN
NCBI GI	g2804259
BLAST score	298
E value	1.0e-167
Match length	298
% identity	100
NCBI Description	Arabidopsis thaliana DNA for phosphoserine aminotransferase, complete cds
Seq. No.	160349
Seq. ID	LIB3177-002-Q1-K1-B5
Method	BLASTX
NCBI GI	g3892702
BLAST score	321
E value	6.0e-30
Match length	56
% identity	100
NCBI Description	(AL033545) extensin like protein [Arabidopsis thaliana]
Seq. No.	160350
Seq. ID	LIB3177-002-Q1-K1-B6
Method	BLASTX
NCBI GI	g4512651
BLAST score	417
E value	3.0e-41
Match length	79
% identity	100
NCBI Description	(AC007048) putative tyrosine transaminase [Arabidopsis thaliana]
Seq. No.	160351
Seq. ID	LIB3177-002-Q1-K1-B8
Method	BLASTN
NCBI GI	g16472
BLAST score	257
E value	1.0e-143
Match length	257
% identity	100
NCBI Description	A.thaliana rRNA repeat unit, most frequent IGR type
Seq. No.	160352

Seq. ID	LIB3177-002-Q1-K1-B9
Method	BLASTX
NCBI GI	g3242075
BLAST score	505
E value	1.0e-51
Match length	99
% identity	100
NCBI Description	(Z97059) S-adenosyl-L-homocysteine hydrolase [Arabidopsis thaliana]

Seq. No.	160353
Seq. ID	LIB3177-002-Q1-K1-C10
Method	BLASTX
NCBI GI	g3063472
BLAST score	494
E value	3.0e-50
Match length	91
% identity	100
NCBI Description	(AC003981) F22O13.34 [Arabidopsis thaliana]

Seq. No.	160354
Seq. ID	LIB3177-002-Q1-K1-C11
Method	BLASTN
NCBI GI	g414549
BLAST score	249
E value	1.0e-138
Match length	269
% identity	99
NCBI Description	Arabidopsis thaliana Columbia cytosolic triose phosphate isomerase (Atctimc) mRNA, complete cds

Seq. No.	160355
Seq. ID	LIB3177-002-Q1-K1-C12
Method	BLASTX
NCBI GI	g3859600
BLAST score	197
E value	2.0e-15
Match length	83
% identity	19
NCBI Description	(AF104919) T15B16.6 gene product [Arabidopsis thaliana] >gi_4558545_gb_AAD22638.1_AC007138_2 (AC007138) putative CHP-rich zinc finger protein [Arabidopsis thaliana]

Seq. No.	160356
Seq. ID	LIB3177-002-Q1-K1-C2
Method	BLASTX
NCBI GI	g3688799
BLAST score	368
E value	2.0e-35
Match length	82
% identity	84
NCBI Description	(AF057137) gamma tonoplast intrinsic protein 2 [Arabidopsis thaliana]

Seq. No.	160357
Seq. ID	LIB3177-002-Q1-K1-C3
Method	BLASTX

NCBI GI	g421836
BLAST score	161
E value	3.0e-11
Match length	33
% identity	100
NCBI Description	G-box-binding factor GF14 - Arabidopsis thaliana >gi_553040 (M96855) GF14 [Arabidopsis thaliana]

Seq. No.	160358
Seq. ID	LIB3177-002-Q1-K1-C4
Method	BLASTX
NCBI GI	g1255951
BLAST score	436
E value	2.0e-43
Match length	97
% identity	80
NCBI Description	(X96932) PS60 [Nicotiana tabacum]

Seq. No.	160359
Seq. ID	LIB3177-002-Q1-K1-C5
Method	BLASTX
NCBI GI	g1363489
BLAST score	419
E value	2.0e-41
Match length	81
% identity	95
NCBI Description	thioglucosidase (EC 3.2.3.1) 3D precursor - Arabidopsis thaliana >gi_984052_emb_CAA61592_ (X89413) thioglucoside glucohydrolase [Arabidopsis thaliana]

Seq. No.	160360
Seq. ID	LIB3177-002-Q1-K1-C6
Method	BLASTX
NCBI GI	g1363489
BLAST score	424
E value	5.0e-42
Match length	77
% identity	99
NCBI Description	thioglucosidase (EC 3.2.3.1) 3D precursor - Arabidopsis thaliana >gi_984052_emb_CAA61592_ (X89413) thioglucoside glucohydrolase [Arabidopsis thaliana]

Seq. No.	160361
Seq. ID	LIB3177-002-Q1-K1-C8
Method	BLASTX
NCBI GI	g2119846
BLAST score	547
E value	2.0e-56
Match length	99
% identity	100
NCBI Description	chlorophyll a/b-binding protein type I precursor Lhb1B2 - Arabidopsis thaliana >gi_16364_emb_CAA45790_ (X64460) photosystem II type I chlorophyll a /b binding protein [Arabidopsis thaliana] >gi_3128230 (AC004077) photosystem II type I chlorophyll a/b binding protein [Arabidopsis thaliana] >gi_3337371 (AC004481) photosystem II type I chlorophyll a/b binding protein [Arabidopsis thaliana]

Seq. No.	160362
Seq. ID	LIB3177-002-Q1-K1-C9
Method	BLASTN
NCBI GI	g3510342
BLAST score	296
E value	1.0e-166
Match length	296
% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MGN6, complete sequence [Arabidopsis thaliana]

Seq. No.	160363
Seq. ID	LIB3177-002-Q1-K1-D1
Method	BLASTX
NCBI GI	g3851636
BLAST score	272
E value	3.0e-24
Match length	78
% identity	68
NCBI Description	(AF098519) unknown [Avicennia marina] >gi_4128206 (AF056316) 40S ribosome protein S7 [Avicennia marina]

Seq. No.	160364
Seq. ID	LIB3177-002-Q1-K1-D3
Method	BLASTN
NCBI GI	g4589443
BLAST score	73
E value	4.0e-33
Match length	133
% identity	94
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MVP7, complete sequence

Seq. No.	160365
Seq. ID	LIB3177-002-Q1-K1-D4
Method	BLASTX
NCBI GI	g113026
BLAST score	326
E value	1.0e-30
Match length	77
% identity	83
NCBI Description	ISOCITRATE LYASE (ISOCITRASE) (ISOCITRATASE) (ICL) >gi_68211_pir__WZRPI isocitrate lyase (EC 4.1.3.1) - rape >gi_255220_bbs_112862 isocitrate lyase, threo-D S-isocitrate glyoxylate-lyase, IL {EC 4.1.3.1} [Brassica napus, seedlings, Peptide, 576 aa] >gi_167144 (L08482) isocitrate lyase [Brassica napus] >gi_447142_prf__1913424A isocitrate lyase [Brassica napus]

Seq. No.	160366
Seq. ID	LIB3177-002-Q1-K1-D5
Method	BLASTX
NCBI GI	g120667
BLAST score	481
E value	1.0e-48
Match length	98

% identity	99
NCBI Description	GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE, CYTOSOLIC >gi_81622_pir__JQ1287 glyceraldehyde-3-phosphate dehydrogenase (EC 1.2.1.12), cytosolic - Arabidopsis thaliana >gi_166706 (M64116) cystolic glyceraldehyde-3-phosphate dehydrogenase [Arabidopsis thaliana] >gi_166710 (M64119) glyceraldehyde-3-phosphate dehydrogenase [Arabidopsis thaliana]

Seq. No.	160367
Seq. ID	LIB3177-002-Q1-K1-D6
Method	BLASTX
NCBI GI	g2062161
BLAST score	497
E value	1.0e-50
Match length	93
% identity	53
NCBI Description	(AC001645) jasmonate inducible protein isolog [Arabidopsis thaliana]

Seq. No.	160368
Seq. ID	LIB3177-002-Q1-K1-D7
Method	BLASTX
NCBI GI	g4666287
BLAST score	248
E value	2.0e-21
Match length	85
% identity	58
NCBI Description	(D85764) cytosolic monodehydroascorbate reductase [Oryza sativa]

Seq. No.	160369
Seq. ID	LIB3177-002-Q1-K1-D9
Method	BLASTX
NCBI GI	g4680713
BLAST score	234
E value	9.0e-20
Match length	94
% identity	50
NCBI Description	(AF132971) CGI-37 protein [Homo sapiens]

Seq. No.	160370
Seq. ID	LIB3177-002-Q1-K1-E1
Method	BLASTX
NCBI GI	g2983997
BLAST score	266
E value	2.0e-23
Match length	91
% identity	53
NCBI Description	(AE000749) hypothetical protein [Aquifex aeolicus]

Seq. No.	160371
Seq. ID	LIB3177-002-Q1-K1-E10
Method	BLASTX
NCBI GI	g402753
BLAST score	469
E value	2.0e-47

Match length	99
% identity	92
NCBI Description	(X71439) translation elongation factor EF-G [Glycine max]

Seq. No.	160372
Seq. ID	LIB3177-002-Q1-K1-E11
Method	BLASTN
NCBI GI	g4406752
BLAST score	162
E value	3.0e-86
Match length	224
% identity	99
NCBI Description	Arabidopsis thaliana chromosome II BAC F19B11 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	160373
Seq. ID	LIB3177-002-Q1-K1-E3
Method	BLASTX
NCBI GI	g1172872
BLAST score	400
E value	3.0e-39
Match length	98
% identity	81
NCBI Description	CYSTEINE PROTEINASE RD19A PRECURSOR >gi_541856_pir__JN0718 drought-inducible cysteine proteinase (EC 3.4.22.-) RD19A precursor - Arabidopsis thaliana >gi_435618_dbj_BAA02373_ (D13042) thiol protease [Arabidopsis thaliana] >gi_4539328_emb_CAB38829.1_ (AL035679) drought-inducible cysteine proteinase RD19A precursor [Arabidopsis thaliana]

Seq. No.	160374
Seq. ID	LIB3177-002-Q1-K1-E4
Method	BLASTX
NCBI GI	g2462929
BLAST score	303
E value	1.0e-38
Match length	87
% identity	99
NCBI Description	(Y12295) glutathione transferase [Arabidopsis thaliana]

Seq. No.	160375
Seq. ID	LIB3177-002-Q1-K1-E5
Method	BLASTN
NCBI GI	g3241924
BLAST score	161
E value	2.0e-85
Match length	300
% identity	99
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MNC6, complete sequence [Arabidopsis thaliana]

Seq. No.	160376
Seq. ID	LIB3177-002-Q1-K1-E7
Method	BLASTN
NCBI GI	g4589438
BLAST score	104
E value	7.0e-52

Match length	112
% identity	99
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MQJ2, complete sequence

Seq. No.	160377
Seq. ID	LIB3177-002-Q1-K1-E8
Method	BLASTX
NCBI GI	g2062161
BLAST score	334
E value	2.0e-31
Match length	98
% identity	68
NCBI Description	(AC001645) jasmonate inducible protein isolog [Arabidopsis thaliana]

Seq. No.	160378
Seq. ID	LIB3177-002-Q1-K1-E9
Method	BLASTX
NCBI GI	g126766
BLAST score	433
E value	4.0e-43
Match length	93
% identity	86
NCBI Description	MALATE SYNTHASE, GLYOXYSOMAL >gi_68216_pir__SYRPMA malate synthase (EC 4.1.3.2), glyoxysomal - rape >gi_167150 (J04468) malate synthase (EC 4.1.3.2) [Brassica napus]

Seq. No.	160379
Seq. ID	LIB3177-002-Q1-K1-F10
Method	BLASTN
NCBI GI	g3659491
BLAST score	259
E value	1.0e-144
Match length	289
% identity	98
NCBI Description	Sequence of BAC T22H22 from Arabidopsis thaliana chromosome 1, complete sequence [Arabidopsis thaliana]

Seq. No.	160380
Seq. ID	LIB3177-002-Q1-K1-F11
Method	BLASTN
NCBI GI	g16327
BLAST score	240
E value	1.0e-132
Match length	248
% identity	100
NCBI Description	A.thaliana homeobox gene Athb-1 mRNA

Seq. No.	160381
Seq. ID	LIB3177-002-Q1-K1-F12
Method	BLASTN
NCBI GI	g2980757
BLAST score	254
E value	1.0e-141
Match length	299
% identity	95

NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F6I18 (ESSAII project)
Seq. No.	160382
Seq. ID	LIB3177-002-Q1-K1-F2
Method	BLASTN
NCBI GI	g3608126
BLAST score	255
E value	1.0e-141
Match length	300
% identity	99
NCBI Description	Arabidopsis thaliana chromosome II BAC T32F12 genomic sequence, complete sequence [Arabidopsis thaliana]
Seq. No.	160383
Seq. ID	LIB3177-002-Q1-K1-F3
Method	BLASTX
NCBI GI	g2921209
BLAST score	191
E value	2.0e-31
Match length	98
% identity	72
NCBI Description	(AF026148) beta-ketoacyl-ACP synthase I [Perilla frutescens]
Seq. No.	160384
Seq. ID	LIB3177-002-Q1-K1-F4
Method	BLASTN
NCBI GI	g3355463
BLAST score	53
E value	5.0e-21
Match length	80
% identity	91
NCBI Description	Arabidopsis thaliana chromosome II BAC F12L6 genomic sequence, complete sequence [Arabidopsis thaliana]
Seq. No.	160385
Seq. ID	LIB3177-002-Q1-K1-F6
Method	BLASTX
NCBI GI	g3023848
BLAST score	432
E value	6.0e-43
Match length	85
% identity	37
NCBI Description	GUANINE NUCLEOTIDE-BINDING PROTEIN BETA SUBUNIT-LIKE PROTEIN (WD-40 REPEAT AUXIN-DEPENDENT PROTEIN ARCA) >gi_2289095 (U77381) WD-40 repeat protein [Arabidopsis thaliana]
Seq. No.	160386
Seq. ID	LIB3177-002-Q1-K1-F7
Method	BLASTX
NCBI GI	g1575327
BLAST score	491
E value	6.0e-50
Match length	98
% identity	98

NCBI Description	(U59738) ATP sulfurylase [Arabidopsis thaliana]

Seq. No.	160387
Seq. ID	LIB3177-002-Q1-K1-F8
Method	BLASTX
NCBI GI	g2286069
BLAST score	373
E value	4.0e-36
Match length	72
% identity	99
NCBI Description	(U72155) beta-glucosidase [Arabidopsis thaliana]

Seq. No.	160388
Seq. ID	LIB3177-002-Q1-K1-F9
Method	BLASTX
NCBI GI	g82512
BLAST score	408
E value	3.0e-40
Match length	82
% identity	41
NCBI Description	ubiquitin precursor - rice (fragment) >gi_218189_dbj_BAA02241_ (D12776) poly-ubiquitin [Oryza sativa]

Seq. No.	160389
Seq. ID	LIB3177-002-Q1-K1-G1
Method	BLASTN
NCBI GI	g3414927
BLAST score	296
E value	1.0e-166
Match length	296
% identity	100
NCBI Description	Arabidopsis thaliana PsbY precursor (psbY) mRNA, nuclear gene encoding chloroplast protein, complete cds

Seq. No.	160390
Seq. ID	LIB3177-002-Q1-K1-G10
Method	BLASTX
NCBI GI	g2347199
BLAST score	226
E value	8.0e-19
Match length	76
% identity	61
NCBI Description	(AC002338) protein kinase isolog [Arabidopsis thaliana]

Seq. No.	160391
Seq. ID	LIB3177-002-Q1-K1-G11
Method	BLASTX
NCBI GI	g3461837
BLAST score	384
E value	2.0e-37
Match length	74
% identity	100
NCBI Description	(AC005315) putative expansin [Arabidopsis thaliana] >gi_3927842 (AC005727) expansin AtEx6 [Arabidopsis thaliana]

Seq. No.	160392
Seq. ID	LIB3177-002-Q1-K1-G3
Method	BLASTX
NCBI GI	g4455192
BLAST score	456
E value	8.0e-46
Match length	100
% identity	95
NCBI Description	(AL035440) putative protein [Arabidopsis thaliana]

Seq. No.	160393
Seq. ID	LIB3177-002-Q1-K1-G4
Method	BLASTX
NCBI GI	g4538939
BLAST score	525
E value	7.0e-54
Match length	99
% identity	100
NCBI Description	(AL049483) Col-0 casein kinase I-like protein [Arabidopsis thaliana]

Seq. No.	160394
Seq. ID	LIB3177-002-Q1-K1-G5
Method	BLASTX
NCBI GI	g2160168
BLAST score	473
E value	8.0e-48
Match length	86
% identity	100
NCBI Description	(AC000132) Strong similarity to R. communis phosphoglycerate mutase (gb_X70652). ESTs gb_T41853,gb_T76648 come from this gene. [Arabidopsis thaliana]

Seq. No.	160395
Seq. ID	LIB3177-002-Q1-K1-G6
Method	BLASTX
NCBI GI	g1709970
BLAST score	374
E value	4.0e-36
Match length	90
% identity	83
NCBI Description	60S RIBOSOMAL PROTEIN L10A

Seq. No.	160396
Seq. ID	LIB3177-002-Q1-K1-G7
Method	BLASTX
NCBI GI	g1246019
BLAST score	47
E value	2.0e-11
Match length	85
% identity	44
NCBI Description	(S80554) chalcone synthase, CHS [Arabidopsis, Landsberg erecta, tt4, Peptide Mutant, 395 aa] [Arabidopsis]

Seq. No.	160397
Seq. ID	LIB3177-002-Q1-K1-G8

Method	BLASTX
NCBI GI	g3859600
BLAST score	202
E value	5.0e-16
Match length	83
% identity	19
NCBI Description	(AF104919) T15B16.6 gene product [Arabidopsis thaliana] >gi_4558545_gb_AAD22638.1_AC007138_2 (AC007138) putative CHP-rich zinc finger protein [Arabidopsis thaliana]

Seq. No.	160398
Seq. ID	LIB3177-002-Q1-K1-G9
Method	BLASTN
NCBI GI	g3779020
BLAST score	292
E value	1.0e-163
Match length	296
% identity	100
NCBI Description	Arabidopsis thaliana chromosome II BAC T4E14 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	160399
Seq. ID	LIB3177-002-Q1-K1-H10
Method	BLASTX
NCBI GI	g1361987
BLAST score	484
E value	4.0e-49
Match length	95
% identity	100
NCBI Description	GF14 protein chi chain - Arabidopsis thaliana

Seq. No.	160400
Seq. ID	LIB3177-002-Q1-K1-H12
Method	BLASTX
NCBI GI	g1076416
BLAST score	324
E value	2.0e-30
Match length	87
% identity	80
NCBI Description	sulfite reductase (ferredoxin) (EC 1.8.7.1) precursor - Arabidopsis thaliana >gi_2129745_pir__S71437 sulfite reductase (ferredoxin) (EC 1.8.7.1) precursor - Arabidopsis thaliana >gi_804953_emb_CAA89154_ (Z49217) sulfite reductase [Arabidopsis thaliana]

Seq. No.	160401
Seq. ID	LIB3177-002-Q1-K1-H2
Method	BLASTN
NCBI GI	g4580365
BLAST score	42
E value	2.0e-14
Match length	54
% identity	94
NCBI Description	Arabidopsis thaliana chromosome I BAC F3F20 genomic sequence, complete sequence

Seq. No.	160402

Seq. ID	LIB3177-002-Q1-K1-H3
Method	BLASTN
NCBI GI	g4678258
BLAST score	199
E value	1.0e-108
Match length	297
% identity	98
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F6I7 (ESSA project)

Seq. No.	160403
Seq. ID	LIB3177-002-Q1-K1-H4
Method	BLASTX
NCBI GI	g3377797
BLAST score	432
E value	6.0e-43
Match length	93
% identity	90
NCBI Description	(AF075597) Similar to 60S ribosome protein L19; coded for by A. thaliana cDNA T04719; coded for by A. thaliana cDNA H36046; coded for by A. thaliana cDNA T44067; coded for by A. thaliana cDNA T14056; coded for by A. thaliana cDNA R90691 [Ara

Seq. No.	160404
Seq. ID	LIB3177-002-Q1-K1-H5
Method	BLASTX
NCBI GI	g1363489
BLAST score	408
E value	4.0e-40
Match length	91
% identity	84
NCBI Description	thioglucosidase (EC 3.2.3.1) 3D precursor - Arabidopsis thaliana >gi_984052_emb_CAA61592_ (X89413) thioglucoside glucohydrolase [Arabidopsis thaliana]

Seq. No.	160405
Seq. ID	LIB3177-002-Q1-K1-H6
Method	BLASTN
NCBI GI	g4678258
BLAST score	90
E value	4.0e-43
Match length	288
% identity	100
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F6I7 (ESSA project)

Seq. No.	160406
Seq. ID	LIB3177-002-Q1-K1-H7
Method	BLASTX
NCBI GI	g3337356
BLAST score	499
E value	8.0e-51
Match length	99
% identity	98
NCBI Description	(AC004481) putative protein transport protein SEC61 alpha subunit [Arabidopsis thaliana]

Seq. No.	160407
Seq. ID	LIB3177-002-Q1-K1-H8
Method	BLASTX
NCBI GI	g3859609
BLAST score	385
E value	2.0e-37
Match length	79
% identity	100
NCBI Description	(AF104919) Arabidopsis thaliana ABC1 protein (GB:AJ001158) [Arabidopsis thaliana]

Seq. No.	160408
Seq. ID	LIB3177-002-Q1-K1-H9
Method	BLASTX
NCBI GI	g3953459
BLAST score	487
E value	2.0e-49
Match length	98
% identity	100
NCBI Description	(AC002328) F20N2.4 [Arabidopsis thaliana]

Seq. No.	160409
Seq. ID	LIB3177-003-P1-K1-A2
Method	BLASTN
NCBI GI	g4455321
BLAST score	81
E value	1.0e-37
Match length	127
% identity	46
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F4I10 (ESSAII project)

Seq. No.	160410
Seq. ID	LIB3177-003-P1-K1-A4
Method	BLASTX
NCBI GI	g1702986
BLAST score	288
E value	7.0e-26
Match length	92
% identity	70
NCBI Description	14-3-3-LIKE PROTEIN GF14 CHI >gi_1255987 (U09377) GF14chi isoform [Arabidopsis thaliana] >gi_1256534 (L09112) GF14 chi chain [Arabidopsis thaliana]

Seq. No.	160411
Seq. ID	LIB3177-003-P1-K1-B4
Method	BLASTN
NCBI GI	g2244950
BLAST score	73
E value	8.0e-33
Match length	340
% identity	83
NCBI Description	Arabidopsis thaliana DNA chromosome 4, ESSA I contig fragment No

Seq. No.	160412

Seq. ID	LIB3177-003-P1-K1-C1
Method	BLASTN
NCBI GI	g3510336
BLAST score	79
E value	1.0e-36
Match length	186
% identity	69
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K18J17, complete sequence [Arabidopsis thaliana]

Seq. No.	160413
Seq. ID	LIB3177-003-P1-K1-C2
Method	BLASTX
NCBI GI	g4585935
BLAST score	200
E value	1.0e-15
Match length	79
% identity	52
NCBI Description	(AC007211) putative chlorophyll A/B binding protein [Arabidopsis thaliana] >gi_4741946_gb_AAD28770.1_AF134123_1 (AF134123) Lhcb2 protein [Arabidopsis thaliana]

Seq. No.	160414
Seq. ID	LIB3177-003-P1-K1-D1
Method	BLASTN
NCBI GI	g4454022
BLAST score	49
E value	1.0e-18
Match length	85
% identity	49
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F9D16 (ESSAII project)

Seq. No.	160415
Seq. ID	LIB3177-003-P1-K1-D3
Method	BLASTX
NCBI GI	g1076416
BLAST score	154
E value	9.0e-11
Match length	62
% identity	55
NCBI Description	sulfite reductase (ferredoxin) (EC 1.8.7.1) precursor - Arabidopsis thaliana >gi_2129745_pir__S71437 sulfite reductase (ferredoxin) (EC 1.8.7.1) precursor - Arabidopsis thaliana >gi_804953_emb_CAA89154_ (Z49217) sulfite reductase [Arabidopsis thaliana]

Seq. No.	160416
Seq. ID	LIB3177-003-P1-K1-D8
Method	BLASTX
NCBI GI	g1732570
BLAST score	168
E value	1.0e-11
Match length	96
% identity	45
NCBI Description	(U72153) beta-glucosidase [Arabidopsis thaliana]

Seq. No.	160417
Seq. ID	LIB3177-003-P1-K1-D9
Method	BLASTX
NCBI GI	g4741954
BLAST score	303
E value	1.0e-27
Match length	124
% identity	54
NCBI Description	(AF134127) Lhcb4.2 protein [Arabidopsis thaliana]

Seq. No.	160418
Seq. ID	LIB3177-003-P1-K1-E2
Method	BLASTX
NCBI GI	g2129538
BLAST score	72
E value	6.0e-01
Match length	74
% identity	48
NCBI Description	AT103 protein - Arabidopsis thaliana >gi_1033195 (U38232) AT103 [Arabidopsis thaliana]

Seq. No.	160419
Seq. ID	LIB3177-003-P1-K1-E3
Method	BLASTX
NCBI GI	g4586047
BLAST score	217
E value	1.0e-17
Match length	106
% identity	44
NCBI Description	(AC007020) putative ferritin protein [Arabidopsis thaliana] >gi_4588004_gb_AAD25945.1_AF085279_18 (AF085279) hypothetical ferritin subunit [Arabidopsis thaliana]

Seq. No.	160420
Seq. ID	LIB3177-003-P1-K1-E4
Method	BLASTX
NCBI GI	g4468807
BLAST score	212
E value	4.0e-17
Match length	103
% identity	47
NCBI Description	(AL035601) cytochrome P450 monooxygenase-like protein [Arabidopsis thaliana]

Seq. No.	160421
Seq. ID	LIB3177-003-P1-K1-F1
Method	BLASTX
NCBI GI	g4741960
BLAST score	303
E value	1.0e-27
Match length	85
% identity	72
NCBI Description	(AF134130) Lhcb6 protein [Arabidopsis thaliana]

Seq. No.	160422
Seq. ID	LIB3177-003-P1-K1-F10
Method	BLASTN

NCBI GI	g4220635
BLAST score	33
E value	6.0e-09
Match length	113
% identity	87
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MDB19, complete sequence [Arabidopsis thaliana]

Seq. No.	160423
Seq. ID	LIB3177-003-P1-K1-F4
Method	BLASTX
NCBI GI	g4585882
BLAST score	369
E value	2.0e-35
Match length	132
% identity	60
NCBI Description	(AC005850) PSI type III chlorophyll a/b-binding protein [Arabidopsis thaliana]

Seq. No.	160424
Seq. ID	LIB3177-003-P1-K1-G3
Method	BLASTN
NCBI GI	g2564050
BLAST score	36
E value	1.0e-11
Match length	76
% identity	87
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MUA22, complete sequence [Arabidopsis thaliana]

Seq. No.	160425
Seq. ID	LIB3177-003-P1-K2-A2
Method	BLASTN
NCBI GI	g4455321
BLAST score	39
E value	5.0e-13
Match length	107
% identity	62
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F4I10 (ESSAII project)

Seq. No.	160426
Seq. ID	LIB3177-003-P1-K2-A4
Method	BLASTN
NCBI GI	g1255986
BLAST score	54
E value	7.0e-22
Match length	142
% identity	83
NCBI Description	Arabidopsis thaliana GF14chi isoform (GRF1) gene, complete cds

Seq. No.	160427
Seq. ID	LIB3177-003-P1-K2-A6
Method	BLASTX
NCBI GI	g3599491
BLAST score	142

E value	2.0e-09
Match length	61
% identity	51
NCBI Description	(AF085149) putative aminotransferase [Capsicum chinense]

Seq. No.	160428
Seq. ID	LIB3177-003-P1-K2-B4
Method	BLASTN
NCBI GI	g2244950
BLAST score	329
E value	0.0e+00
Match length	435
% identity	99
NCBI Description	Arabidopsis thaliana DNA chromosome 4, ESSA I contig fragment No

Seq. No.	160429
Seq. ID	LIB3177-003-P1-K2-B6
Method	BLASTN
NCBI GI	g3869075
BLAST score	39
E value	9.0e-13
Match length	91
% identity	87
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MXK3, complete sequence [Arabidopsis thaliana]

Seq. No.	160430
Seq. ID	LIB3177-003-P1-K2-C1
Method	BLASTN
NCBI GI	g3510336
BLAST score	43
E value	4.0e-15
Match length	79
% identity	95
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K18J17, complete sequence [Arabidopsis thaliana]

Seq. No.	160431
Seq. ID	LIB3177-003-P1-K2-C2
Method	BLASTN
NCBI GI	g4585918
BLAST score	33
E value	5.0e-09
Match length	55
% identity	91
NCBI Description	Arabidopsis thaliana chromosome II BAC F1O13 genomic sequence, complete sequence

Seq. No.	160432
Seq. ID	LIB3177-003-P1-K2-C4
Method	BLASTX
NCBI GI	g2062161
BLAST score	618
E value	2.0e-64
Match length	119
% identity	50

NCBI Description	(AC001645) jasmonate inducible protein isolog [Arabidopsis thaliana]

Seq. No.	160433
Seq. ID	LIB3177-003-P1-K2-D7
Method	BLASTN
NCBI GI	g984051
BLAST score	37
E value	2.0e-11
Match length	89
% identity	85
NCBI Description	A.thaliana mRNA for thioglucoside glucohydrolase

Seq. No.	160434
Seq. ID	LIB3177-003-P1-K2-E4
Method	BLASTX
NCBI GI	g4468807
BLAST score	565
E value	3.0e-58
Match length	150
% identity	76
NCBI Description	(AL035601) cytochrome P450 monooxygenase-like protein [Arabidopsis thaliana]

Seq. No.	160435
Seq. ID	LIB3177-003-P1-K2-F4
Method	BLASTX
NCBI GI	g4585882
BLAST score	594
E value	1.0e-61
Match length	124
% identity	95
NCBI Description	(AC005850) PSI type III chlorophyll a/b-binding protein [Arabidopsis thaliana]

Seq. No.	160436
Seq. ID	LIB3177-003-P1-K2-F7
Method	BLASTN
NCBI GI	g3785992
BLAST score	51
E value	9.0e-20
Match length	128
% identity	49
NCBI Description	Arabidopsis thaliana chromosome II BAC T6A23 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	160437
Seq. ID	LIB3177-003-P1-K2-G2
Method	BLASTX
NCBI GI	g4115381
BLAST score	406
E value	9.0e-40
Match length	120
% identity	64
NCBI Description	(AC005967) putative limonene cyclase [Arabidopsis thaliana]

Seq. No.	160438

Seq. ID	LIB3177-003-P1-K2-H4
Method	BLASTX
NCBI GI	g3892712
BLAST score	286
E value	1.0e-25
Match length	66
% identity	85
NCBI Description	(AL033545) adenine phosphoribosyltransferase (EC 2.4.2.7)-like protein [Arabidopsis thaliana]

Seq. No.	160439
Seq. ID	LIB3177-004-P1-K2-A4
Method	BLASTN
NCBI GI	g2351071
BLAST score	126
E value	1.0e-64
Match length	272
% identity	92
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MVA3, complete sequence [Arabidopsis thaliana]

Seq. No.	160440
Seq. ID	LIB3177-004-P1-K2-A8
Method	BLASTN
NCBI GI	g4589445
BLAST score	49
E value	9.0e-19
Match length	176
% identity	81
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MWL2, complete sequence

Seq. No.	160441
Seq. ID	LIB3177-004-P1-K2-B11
Method	BLASTX
NCBI GI	g2677828
BLAST score	141
E value	1.0e-08
Match length	83
% identity	39
NCBI Description	(U93166) cysteine protease [Prunus armeniaca]

Seq. No.	160442
Seq. ID	LIB3177-004-P1-K2-B2
Method	BLASTX
NCBI GI	g1169201
BLAST score	327
E value	2.0e-30
Match length	106
% identity	64
NCBI Description	DNA-DAMAGE-REPAIR/TOLERATION PROTEIN DRT112 PRECURSOR >gi_421830_pir__S33707 DRT112 protein - Arabidopsis thaliana >gi_166696 (M98456) DRT112 [Arabidopsis thaliana]

Seq. No.	160443
Seq. ID	LIB3177-004-P1-K2-B6
Method	BLASTX

NCBI GI	g132074
BLAST score	495
E value	3.0e-50
Match length	116
% identity	83
NCBI Description	RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN 1A PRECURSOR (RUBISCO SMALL SUBUNIT 1A) >gi_68063_pir__RKMUA1 ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain A1 precursor - Arabidopsis thaliana

Seq. No.	160444
Seq. ID	LIB3177-004-P1-K2-B7
Method	BLASTN
NCBI GI	g1142593
BLAST score	44
E value	3.0e-16
Match length	44
% identity	100
NCBI Description	Brassica oleracea chloroplast ATP synthase CF-0 subunit I (atpF) gene, partial cds

Seq. No.	160445
Seq. ID	LIB3177-004-P1-K2-C1
Method	BLASTX
NCBI GI	g266936
BLAST score	301
E value	2.0e-27
Match length	74
% identity	77
NCBI Description	50S RIBOSOMAL PROTEIN L27, CHLOROPLAST PRECURSOR (CL27) >gi_282960_pir__A42840 ribosomal protein L27 - common tobacco >gi_170306 (M98473) ribosomal protein L27 [Nicotiana tabacum] >gi_170326 (M75731) ribosomal protein L27 [Nicotiana tabacum]

Seq. No.	160446
Seq. ID	LIB3177-004-P1-K2-C2
Method	BLASTX
NCBI GI	g132110
BLAST score	360
E value	3.0e-34
Match length	79
% identity	86
NCBI Description	RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN 3B PRECURSOR (RUBISCO SMALL SUBUNIT 3B) >gi_68060_pir__RKMUB3 ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain B3 precursor - Arabidopsis thaliana >gi_16195_emb_CAA32702_ (X14564) ribulose bisphosphate carboxylase [Arabidopsis thaliana]

Seq. No.	160447
Seq. ID	LIB3177-004-P1-K2-C4
Method	BLASTX
NCBI GI	g2341034
BLAST score	349
E value	3.0e-33
Match length	77

% identity	94
NCBI Description	(AC000104) F19P19.13 [Arabidopsis thaliana]
Seq. No.	160448
Seq. ID	LIB3177-004-P1-K2-D1
Method	BLASTN
NCBI GI	g16206
BLAST score	99
E value	2.0e-48
Match length	225
% identity	86
NCBI Description	A.thaliana Cab mRNA for photossystem I chlorophyll A/B-binding protein
Seq. No.	160449
Seq. ID	LIB3177-004-P1-K2-D11
Method	BLASTN
NCBI GI	g3212846
BLAST score	89
E value	2.0e-42
Match length	131
% identity	92
NCBI Description	Arabidopsis thaliana chromosome II BAC F6E13 genomic sequence, complete sequence [Arabidopsis thaliana]
Seq. No.	160450
Seq. ID	LIB3177-004-P1-K2-D4
Method	BLASTN
NCBI GI	g1931636
BLAST score	112
E value	4.0e-56
Match length	345
% identity	96
NCBI Description	Arabidopsis thaliana BAC T19D16 genomic sequence
Seq. No.	160451
Seq. ID	LIB3177-004-P1-K2-D7
Method	BLASTX
NCBI GI	g132102
BLAST score	609
E value	2.0e-63
Match length	125
% identity	90
NCBI Description	RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN 2B PRECURSOR (RUBISCO SMALL SUBUNIT 2B) >gi_68061_pir__RKMUB2 ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain B2 precursor - Arabidopsis thaliana >gi_16194_emb_CAA32701_ (X14564) ribulose bisphosphate carboxylase [Arabidopsis thaliana]
Seq. No.	160452
Seq. ID	LIB3177-004-P1-K2-E10
Method	BLASTX
NCBI GI	g2828267
BLAST score	380
E value	1.0e-36
Match length	87

% identity	89
NCBI Description	(Y14044) geranylgeranyl reductase [Arabidopsis thaliana]

Seq. No.	160453
Seq. ID	LIB3177-004-P1-K2-E11
Method	BLASTX
NCBI GI	g1350720
BLAST score	324
E value	3.0e-30
Match length	91
% identity	70
NCBI Description	60S RIBOSOMAL PROTEIN L32

Seq. No.	160454
Seq. ID	LIB3177-004-P1-K2-E12
Method	BLASTN
NCBI GI	g643089
BLAST score	71
E value	1.0e-31
Match length	168
% identity	85
NCBI Description	A.thaliana mRNA for NADH:ubiquinone oxidoreductase (complex I)

Seq. No.	160455
Seq. ID	LIB3177-004-P1-K2-E7
Method	BLASTX
NCBI GI	g3738336
BLAST score	338
E value	1.0e-31
Match length	94
% identity	76
NCBI Description	(AC005170) unknown protein [Arabidopsis thaliana]

Seq. No.	160456
Seq. ID	LIB3177-004-P1-K2-E8
Method	BLASTX
NCBI GI	g2895510
BLAST score	617
E value	2.0e-64
Match length	123
% identity	97
NCBI Description	(AF033204) putative pectin methylesterase [Arabidopsis thaliana]

Seq. No.	160457
Seq. ID	LIB3177-004-P1-K2-E9
Method	BLASTX
NCBI GI	g548653
BLAST score	49
E value	1.0e-29
Match length	81
% identity	93
NCBI Description	50S RIBOSOMAL PROTEIN L12-A, CHLOROPLAST PRECURSOR (CL12-A) >gi_541895_pir__A53394 ribosomal protein L12.A, chloroplast - Arabidopsis thaliana >gi_468771_emb_CAA48181_ (X68046) ribosomal protein L12 [Arabidopsis thaliana]

Seq. No.	160458
Seq. ID	LIB3177-004-P1-K2-F1
Method	BLASTX
NCBI GI	g548653
BLAST score	322
E value	4.0e-30
Match length	96
% identity	72
NCBI Description	50S RIBOSOMAL PROTEIN L12-A, CHLOROPLAST PRECURSOR (CL12-A) >gi_541895_pir__A53394 ribosomal protein L12.A, chloroplast - Arabidopsis thaliana >gi_468771_emb_CAA48181_ (X68046) ribosomal protein L12 [Arabidopsis thaliana]

Seq. No.	160459
Seq. ID	LIB3177-004-P1-K2-F3
Method	BLASTX
NCBI GI	g115783
BLAST score	637
E value	9.0e-67
Match length	122
% identity	99
NCBI Description	CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR (CAB-140) (LHCP) >gi_16376_emb_CAA27543_ (X03909) chlorophyll a/b binding protein (LHCP AB 140) [Arabidopsis thaliana]

Seq. No.	160460
Seq. ID	LIB3177-004-P1-K2-F5
Method	BLASTN
NCBI GI	g3510247
BLAST score	122
E value	5.0e-62
Match length	388
% identity	98
NCBI Description	Arabidopsis thaliana chromosome II BAC F19D11 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	160461
Seq. ID	LIB3177-004-P1-K2-F8
Method	BLASTX
NCBI GI	g4455223
BLAST score	306
E value	6.0e-28
Match length	99
% identity	39
NCBI Description	(AL035440) putative DNA binding protein [Arabidopsis thaliana]

Seq. No.	160462
Seq. ID	LIB3177-004-P1-K2-G1
Method	BLASTX
NCBI GI	g1352056
BLAST score	455
E value	2.0e-45
Match length	86
% identity	97

NCBI Description	AUXIN-RESPONSIVE PROTEIN IAA2 >gi_454283 (L15449) auxin-responsive protein [Arabidopsis thaliana]

Seq. No.	160463
Seq. ID	LIB3177-004-P1-K2-G2
Method	BLASTX
NCBI GI	g4585882
BLAST score	528
E value	5.0e-54
Match length	115
% identity	93
NCBI Description	(AC005850) PSI type III chlorophyll a/b-binding protein [Arabidopsis thaliana]

Seq. No.	160464
Seq. ID	LIB3177-004-P1-K2-G7
Method	BLASTN
NCBI GI	g2351071
BLAST score	219
E value	1.0e-120
Match length	317
% identity	91
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MVA3, complete sequence [Arabidopsis thaliana]

Seq. No.	160465
Seq. ID	LIB3177-004-P1-K2-G8
Method	BLASTX
NCBI GI	g3402716
BLAST score	193
E value	1.0e-14
Match length	99
% identity	48
NCBI Description	(AC004261) unknown protein [Arabidopsis thaliana]

Seq. No.	160466
Seq. ID	LIB3177-004-P1-K2-H11
Method	BLASTN
NCBI GI	g972918
BLAST score	139
E value	1.0e-72
Match length	169
% identity	95
NCBI Description	Arabidopsis thaliana IAA8 (IAA8) gene complete cds

Seq. No.	160467
Seq. ID	LIB3177-004-P1-K2-H2
Method	BLASTN
NCBI GI	g166745
BLAST score	122
E value	5.0e-62
Match length	187
% identity	81
NCBI Description	A.thaliana plasma membrane proton ATPase (PMA) mRNA, complete cds

Seq. No.	160468

Seq. ID	LIB3177-004-P1-K2-H4
Method	BLASTN
NCBI GI	g14342
BLAST score	55
E value	2.0e-22
Match length	109
% identity	87
NCBI Description	A.thaliana mRNA for carbonic anhydrase

Seq. No.	160469
Seq. ID	LIB3177-004-P1-K2-H8
Method	BLASTN
NCBI GI	g14342
BLAST score	40
E value	1.0e-13
Match length	125
% identity	81
NCBI Description	A.thaliana mRNA for carbonic anhydrase

Seq. No.	160470
Seq. ID	LIB3177-005-P1-K1-A1
Method	BLASTX
NCBI GI	g136739
BLAST score	196
E value	4.0e-15
Match length	82
% identity	56
NCBI Description	UTP--GLUCOSE-1-PHOSPHATE URIDYLYLTRANSFERASE (UDP-GLUCOSE PYROPHOSPHORYLASE) (UDPGP) >gi_67061_pir__XNPOU UTP--glucose-1-phosphate uridylyltransferase (EC 2.7.7.9) - potato >gi_218001_dbj_BAA00570_ (D00667) UDP-glucose pyrophosphorylase precursor [Solanum tuberosum]

Seq. No.	160471
Seq. ID	LIB3177-005-P1-K1-A2
Method	BLASTX
NCBI GI	g1483150
BLAST score	58
E value	8.0e-12
Match length	72
% identity	58
NCBI Description	(D84417) monodehydroascorbate reductase [Arabidopsis thaliana]

Seq. No.	160472
Seq. ID	LIB3177-005-P1-K1-A3
Method	BLASTX
NCBI GI	g2583125
BLAST score	375
E value	4.0e-36
Match length	122
% identity	64
NCBI Description	(AC002387) putative transketolase precursor [Arabidopsis thaliana]

Seq. No.	160473
Seq. ID	LIB3177-005-P1-K1-A4

Method	BLASTX
NCBI GI	g4262174
BLAST score	487
E value	4.0e-49
Match length	137
% identity	66
NCBI Description	(AC005508) 9058 [Arabidopsis thaliana]

Seq. No.	160474
Seq. ID	LIB3177-005-P1-K1-A8
Method	BLASTX
NCBI GI	g4587542
BLAST score	319
E value	2.0e-29
Match length	111
% identity	60
NCBI Description	(AC006577) Belongs to the PF_00657 Lipase/Acylhydrolase with GDSL-motif family. ESTs gb_T45815, gb_T45130 and gb_Z38046 come from this gene. [Arabidopsis thaliana]

Seq. No.	160475
Seq. ID	LIB3177-005-P1-K1-B2
Method	BLASTX
NCBI GI	g2982301
BLAST score	177
E value	6.0e-13
Match length	103
% identity	45
NCBI Description	(AF051235) YGL010w-like protein [Picea mariana]

Seq. No.	160476
Seq. ID	LIB3177-005-P1-K1-B3
Method	BLASTN
NCBI GI	g4589409
BLAST score	74
E value	2.0e-33
Match length	409
% identity	81
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: F17P19, complete sequence

Seq. No.	160477
Seq. ID	LIB3177-005-P1-K1-B6
Method	BLASTX
NCBI GI	g4191778
BLAST score	258
E value	1.0e-22
Match length	86
% identity	62
NCBI Description	(AC005917) putative nucleosome assembly protein I [Arabidopsis thaliana]

Seq. No.	160478
Seq. ID	LIB3177-005-P1-K1-B8
Method	BLASTX
NCBI GI	g4335763
BLAST score	196

E value	3.0e-15
Match length	75
% identity	59
NCBI Description	(AC006284) unknown protein [Arabidopsis thaliana]

Seq. No.	160479
Seq. ID	LIB3177-005-P1-K1-C1
Method	BLASTX
NCBI GI	g3153205
BLAST score	237
E value	7.0e-20
Match length	68
% identity	66
NCBI Description	(U80922) serine/threonine protein phosphatase type one [Arabidopsis thaliana]

Seq. No.	160480
Seq. ID	LIB3177-005-P1-K1-C3
Method	BLASTN
NCBI GI	g4519194
BLAST score	100
E value	6.0e-49
Match length	329
% identity	86
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MHM17, complete sequence

Seq. No.	160481
Seq. ID	LIB3177-005-P1-K1-D1
Method	BLASTN
NCBI GI	g1022779
BLAST score	47
E value	3.0e-17
Match length	167
% identity	82
NCBI Description	Arabidopsis thaliana GF14 Kappa isoform mRNA, complete cds

Seq. No.	160482
Seq. ID	LIB3177-005-P1-K1-D2
Method	BLASTN
NCBI GI	g2754815
BLAST score	129
E value	3.0e-66
Match length	301
% identity	86
NCBI Description	Arabidopsis thaliana non-race specific disease resistance protein (NDR1) gene, complete cds

Seq. No.	160483
Seq. ID	LIB3177-005-P1-K1-D4
Method	BLASTX
NCBI GI	g1946690
BLAST score	216
E value	2.0e-17
Match length	78
% identity	58
NCBI Description	(U94495) glutathione peroxidase [Arabidopsis thaliana]

>gi_4582452_gb_AAD24836.1_AC007071_8 (AC007071) putative glutathione peroxidase [Arabidopsis thaliana]

Seq. No.	160484
Seq. ID	LIB3177-005-P1-K1-D7
Method	BLASTX
NCBI GI	g4585925
BLAST score	280
E value	4.0e-25
Match length	86
% identity	69
NCBI Description	(AC007211) unknown protein [Arabidopsis thaliana]

Seq. No.	160485
Seq. ID	LIB3177-005-P1-K1-E10
Method	BLASTN
NCBI GI	g4538949
BLAST score	39
E value	1.0e-12
Match length	63
% identity	90
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F24G24 (ESSA project)

Seq. No.	160486
Seq. ID	LIB3177-005-P1-K1-E2
Method	BLASTN
NCBI GI	g4662640
BLAST score	101
E value	1.0e-49
Match length	209
% identity	37
NCBI Description	Arabidopsis thaliana chromosome II BAC F15K19 genomic sequence, complete sequence

Seq. No.	160487
Seq. ID	LIB3177-005-P1-K1-E3
Method	BLASTX
NCBI GI	g3157944
BLAST score	143
E value	4.0e-09
Match length	59
% identity	56
NCBI Description	(AC002131) Very strong similarity to aminomethyltransferase precursor gb_U79769 from Mesembryanthemum crystallinum. ESTs gb_T43167, gb_T21076, gb_H36999, gb_T22773, gb_N38038, gb_T13742, gb_Z26545, gb_T20753 and gb_W43123 come from this ge

Seq. No.	160488
Seq. ID	LIB3177-005-P1-K1-E5
Method	BLASTX
NCBI GI	g115470
BLAST score	362
E value	1.0e-34
Match length	133
% identity	59

NCBI Description	CARBONIC ANHYDRASE, CHLOROPLAST PRECURSOR (CARBONATE DEHYDRATASE) >gi_320554_pir__S28412 carbonate dehydratase (EC 4.2.1.1) precursor - Arabidopsis thaliana >gi_14343_emb_CAA46508_ (X65541) carbonic anhydrase [Arabidopsis thaliana]
Seq. No.	160489
Seq. ID	LIB3177-005-P1-K1-E7
Method	BLASTX
NCBI GI	g464662
BLAST score	218
E value	1.0e-17
Match length	127
% identity	45
NCBI Description	CHLOROPLAST 31 KD RIBONUCLEOPROTEIN PRECURSOR (RNA-BINDING PROTEIN RNP-T) (RNA-BINDING PROTEIN 1) >gi_282884_pir__S28057 RNA-binding protein RNP-T - Arabidopsis thaliana >gi_16490_emb_CAA46347_ (X65255) RNA-binding protein [Arabidopsis thaliana] >gi_387569 (M94554) 31 kDa RNA binding protein [Arabidopsis thaliana] >gi_475718 (U08467) RNA-binding protein 1 [Arabidopsis thaliana] >gi_4220513_emb_CAA22986_ (AL035356) RNA-binding protein RNP-T precursor [Arabidopsis thaliana] >gi_737169_prf__1921382A RNA-binding protein [Arabidopsis thaliana]
Seq. No.	160490
Seq. ID	LIB3177-005-P1-K1-F10
Method	BLASTX
NCBI GI	g1175011
BLAST score	211
E value	6.0e-17
Match length	77
% identity	57
NCBI Description	PLASMA MEMBRANE INTRINSIC PROTEIN 1B (TRANSMEMBRANE PROTEIN A) (TMP-A) >gi_296085_emb_CAA48356_ (X68293) transmembrane protein [Arabidopsis thaliana] >gi_3386599 (AC004665) plasma membrane intrinsic protein 1B [Arabidopsis thaliana]
Seq. No.	160491
Seq. ID	LIB3177-005-P1-K1-F3
Method	BLASTX
NCBI GI	g3914863
BLAST score	224
E value	2.0e-18
Match length	88
% identity	59
NCBI Description	CHLOROPLAST 30S RIBOSOMAL PROTEIN S4 >gi_2293074_emb_CAA92560_ (Z68262) ribosomal protein S4 [Sisyrinchium sp. 'Lejeune 1997'] >gi_2293081_emb_CAA92561_ (Z68263) ribosomal protein S4 [Sisyrinchium striatum]
Seq. No.	160492
Seq. ID	LIB3177-005-P1-K1-F4
Method	BLASTX
NCBI GI	g4583542
BLAST score	144

E value	4.0e-09
Match length	61
% identity	59
NCBI Description	(Y16847) 16 kDa polypeptide of oxygen-evolving complex [Arabidopsis thaliana]

Seq. No.	160493
Seq. ID	LIB3177-005-P1-K1-F6
Method	BLASTN
NCBI GI	g2252848
BLAST score	72
E value	4.0e-32
Match length	332
% identity	80
NCBI Description	Arabidopsis thaliana BAC TM018A10

Seq. No.	160494
Seq. ID	LIB3177-005-P1-K1-F7
Method	BLASTX
NCBI GI	g4263525
BLAST score	279
E value	6.0e-25
Match length	96
% identity	64
NCBI Description	(AC004044) putative photosystem I reaction center subunit II precursor [Arabidopsis thaliana]

Seq. No.	160495
Seq. ID	LIB3177-005-P1-K1-G2
Method	BLASTX
NCBI GI	g2781354
BLAST score	214
E value	3.0e-17
Match length	103
% identity	49
NCBI Description	(AC003113) F24O1.10 [Arabidopsis thaliana]

Seq. No.	160496
Seq. ID	LIB3177-005-P1-K1-G3
Method	BLASTX
NCBI GI	g3386613
BLAST score	356
E value	7.0e-34
Match length	101
% identity	70
NCBI Description	(AC004665) putative ATP-dependent RNA helicase [Arabidopsis thaliana]

Seq. No.	160497
Seq. ID	LIB3177-005-P1-K1-G5
Method	BLASTX
NCBI GI	g4432839
BLAST score	255
E value	5.0e-22
Match length	127
% identity	47
NCBI Description	(AC006283) unknown protein [Arabidopsis thaliana]

Seq. No.	160498
Seq. ID	LIB3177-005-P1-K1-G7
Method	BLASTN
NCBI GI	g2656031
BLAST score	50
E value	5.0e-19
Match length	201
% identity	82
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MXC20

Seq. No.	160499
Seq. ID	LIB3177-005-P1-K1-H12
Method	BLASTX
NCBI GI	g3123188
BLAST score	308
E value	3.0e-28
Match length	117
% identity	56
NCBI Description	CATALASE 3 >gi_2347178 (U43147) catalase 3 [Arabidopsis thaliana] >gi_2511726 (AF021937) catalase 3 [Arabidopsis thaliana]

Seq. No.	160500
Seq. ID	LIB3177-005-P1-K1-H2
Method	BLASTN
NCBI GI	g2791999
BLAST score	60
E value	3.0e-25
Match length	192
% identity	88
NCBI Description	Arabidopsis thaliana mRNA for ribosomal protein L4

Seq. No.	160501
Seq. ID	LIB3177-005-P1-K1-H4
Method	BLASTX
NCBI GI	g1732570
BLAST score	186
E value	6.0e-14
Match length	76
% identity	51
NCBI Description	(U72153) beta-glucosidase [Arabidopsis thaliana]

Seq. No.	160502
Seq. ID	LIB3177-005-P1-K1-H8
Method	BLASTX
NCBI GI	g1710780
BLAST score	158
E value	7.0e-11
Match length	75
% identity	43
NCBI Description	40S RIBOSOMAL PROTEIN S9 (S7) >gi_1321917_emb_CAA65433_ (X96613) cytoplasmic ribosomal protein S7 [Podospora anserina]

Seq. No.	160503

Seq. ID	LIB3177-005-P1-K1-H9
Method	BLASTX
NCBI GI	g2244740
BLAST score	200
E value	2.0e-15
Match length	142
% identity	36
NCBI Description	(D88417) endo-1,4-beta-glucanase [Gossypium hirsutum]

Seq. No.	160504
Seq. ID	LIB3177-005-P1-K2-A1
Method	BLASTX
NCBI GI	g136739
BLAST score	289
E value	5.0e-26
Match length	97
% identity	59
NCBI Description	UTP--GLUCOSE-1-PHOSPHATE URIDYLYLTRANSFERASE (UDP-GLUCOSE PYROPHOSPHORYLASE) (UDPGP) >gi_67061_pir__XNPOU UTP--glucose-1-phosphate uridylyltransferase (EC 2.7.7.9) - potato >gi_218001_dbj_BAA00570_ (D00667) UDP-glucose pyrophosphorylase precursor [Solanum tuberosum]

Seq. No.	160505
Seq. ID	LIB3177-005-P1-K2-A2
Method	BLASTX
NCBI GI	g4704613
BLAST score	567
E value	1.0e-58
Match length	120
% identity	92
NCBI Description	(AF109695) monodehydroascorbate reductase [Brassica juncea]

Seq. No.	160506
Seq. ID	LIB3177-005-P1-K2-A3
Method	BLASTX
NCBI GI	g2583125
BLAST score	694
E value	2.0e-73
Match length	144
% identity	92
NCBI Description	(AC002387) putative transketolase precursor [Arabidopsis thaliana]

Seq. No.	160507
Seq. ID	LIB3177-005-P1-K2-A4
Method	BLASTX
NCBI GI	g4262174
BLAST score	783
E value	7.0e-84
Match length	142
% identity	100
NCBI Description	(AC005508) 9058 [Arabidopsis thaliana]

Seq. No.	160508
Seq. ID	LIB3177-005-P1-K2-A8
Method	BLASTX

NCBI GI	g4587542
BLAST score	456
E value	1.0e-45
Match length	108
% identity	83
NCBI Description	(AC006577) Belongs to the PF_00657 Lipase/Acylhydrolase with GDSL-motif family. ESTs gb_T45815, gb_T45130 and gb_Z38046 come from this gene. [Arabidopsis thaliana]

Seq. No.	160509
Seq. ID	LIB3177-005-P1-K2-B1
Method	BLASTX
NCBI GI	g4650842
BLAST score	153
E value	3.0e-10
Match length	36
% identity	86
NCBI Description	(AB026185) elongation factor 2 [Lithospermum erythrorhizon]

Seq. No.	160510
Seq. ID	LIB3177-005-P1-K2-B2
Method	BLASTX
NCBI GI	g2982301
BLAST score	317
E value	2.0e-29
Match length	93
% identity	63
NCBI Description	(AF051235) YGL010w-like protein [Picea mariana]

Seq. No.	160511
Seq. ID	LIB3177-005-P1-K2-B3
Method	BLASTX
NCBI GI	g4559358
BLAST score	191
E value	2.0e-14
Match length	61
% identity	57
NCBI Description	(AC006585) putative steroid binding protein [Arabidopsis thaliana]

Seq. No.	160512
Seq. ID	LIB3177-005-P1-K2-B4
Method	BLASTN
NCBI GI	g4757401
BLAST score	230
E value	1.0e-126
Match length	410
% identity	91
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MGH6, complete sequence

Seq. No.	160513
Seq. ID	LIB3177-005-P1-K2-B6
Method	BLASTX
NCBI GI	g4191778
BLAST score	616
E value	3.0e-64

Match length	140
% identity	88
NCBI Description	(AC005917) putative nucleosome assembly protein I [Arabidopsis thaliana]

Seq. No.	160514
Seq. ID	LIB3177-005-P1-K2-B8
Method	BLASTN
NCBI GI	g4335744
BLAST score	164
E value	4.0e-87
Match length	393
% identity	97
NCBI Description	Arabidopsis thaliana chromosome II BAC T4M8 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	160515
Seq. ID	LIB3177-005-P1-K2-C1
Method	BLASTX
NCBI GI	g3153205
BLAST score	362
E value	1.0e-34
Match length	74
% identity	96
NCBI Description	(U80922) serine/threonine protein phosphatase type one [Arabidopsis thaliana]

Seq. No.	160516
Seq. ID	LIB3177-005-P1-K2-C2
Method	BLASTX
NCBI GI	g548605
BLAST score	175
E value	1.0e-12
Match length	53
% identity	74
NCBI Description	PHOTOSYSTEM I REACTION CENTRE SUBUNIT X PRECURSOR (LIGHT-HARVESTING COMPLEX I 7 KD PROTEIN) (PSI-K) >gi_539055_pir__A48527 photosystem I protein psaK precursor - barley >gi_304220 (L12707) photosystem I PSI-K subunit [Hordeum vulgare]

Seq. No.	160517
Seq. ID	LIB3177-005-P1-K2-C3
Method	BLASTX
NCBI GI	g3212870
BLAST score	255
E value	6.0e-22
Match length	71
% identity	75
NCBI Description	(AC004005) putative N-myristoyltransferase [Arabidopsis thaliana]

Seq. No.	160518
Seq. ID	LIB3177-005-P1-K2-C8
Method	BLASTN
NCBI GI	g4519194
BLAST score	85

E value	4.0e-40
Match length	252
% identity	83
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MHM17, complete sequence

Seq. No.	160519
Seq. ID	LIB3177-005-P1-K2-D1
Method	BLASTN
NCBI GI	g1022779
BLAST score	221
E value	1.0e-121
Match length	279
% identity	94
NCBI Description	Arabidopsis thaliana GF14 Kappa isoform mRNA, complete cds

Seq. No.	160520
Seq. ID	LIB3177-005-P1-K2-D10
Method	BLASTX
NCBI GI	g404670
BLAST score	68
E value	3.0e-13
Match length	56
% identity	80
NCBI Description	(L21154) phytochrome A [Arabidopsis thaliana] >gi_3482934 (AC003970) phytochrome A [Arabidopsis thaliana]

Seq. No.	160521
Seq. ID	LIB3177-005-P1-K2-D2
Method	BLASTN
NCBI GI	g2754815
BLAST score	221
E value	1.0e-121
Match length	257
% identity	96
NCBI Description	Arabidopsis thaliana non-race specific disease resistance protein (NDR1) gene, complete cds

Seq. No.	160522
Seq. ID	LIB3177-005-P1-K2-D3
Method	BLASTX
NCBI GI	g1938549
BLAST score	154
E value	4.0e-10
Match length	51
% identity	57
NCBI Description	(U97016) similar to drosophila Rlc1 gene product (NID:g563361) and S. cerevisiae mitochondrial 60S ribosomal protein L4 (YML4) (NID:g459259) [Caenorhabditis elegans]

Seq. No.	160523
Seq. ID	LIB3177-005-P1-K2-D4
Method	BLASTX
NCBI GI	g1946690
BLAST score	388
E value	1.0e-37
Match length	83

% identity	92
NCBI Description	(U94495) glutathione peroxidase [Arabidopsis thaliana] >gi_4582452_gb_AAD24836.1_AC007071_8 (AC007071) putative glutathione peroxidase [Arabidopsis thaliana]

Seq. No.	160524
Seq. ID	LIB3177-005-P1-K2-D7
Method	BLASTX
NCBI GI	g4585925
BLAST score	88
E value	7.0e-70
Match length	140
% identity	98
NCBI Description	(AC007211) unknown protein [Arabidopsis thaliana]

Seq. No.	160525
Seq. ID	LIB3177-005-P1-K2-E1
Method	BLASTX
NCBI GI	g401621
BLAST score	201
E value	1.0e-15
Match length	129
% identity	39
NCBI Description	HYPOTHETICAL 20.4 KD PROTEIN IN TNAB-BGLB INTERGENIC REGION >gi_290561 (L10328) o188 [Escherichia coli] >gi_1790149 (AE000448) orf, hypothetical protein [Escherichia coli]

Seq. No.	160526
Seq. ID	LIB3177-005-P1-K2-E2
Method	BLASTN
NCBI GI	g4662640
BLAST score	328
E value	0.0e+00
Match length	373
% identity	97
NCBI Description	Arabidopsis thaliana chromosome II BAC F15K19 genomic sequence, complete sequence

Seq. No.	160527
Seq. ID	LIB3177-005-P1-K2-E3
Method	BLASTX
NCBI GI	g3157944
BLAST score	570
E value	6.0e-59
Match length	113
% identity	96
NCBI Description	(AC002131) Very strong similarity to aminomethyltransferase precursor gb_U79769 from Mesembryanthemum crystallinum. ESTs gb_T43167, gb_T21076, gb_H36999, gb_T22773, gb_N38038, gb_T13742, gb_Z26545, gb_T20753 and gb_W43123 come from this ge

Seq. No.	160528
Seq. ID	LIB3177-005-P1-K2-E5
Method	BLASTX
NCBI GI	g115470
BLAST score	489

E value	2.0e-64
Match length	143
% identity	91
NCBI Description	CARBONIC ANHYDRASE, CHLOROPLAST PRECURSOR (CARBONATE DEHYDRATASE) >gi_320554_pir__S28412 carbonate dehydratase (EC 4.2.1.1) precursor - Arabidopsis thaliana >gi_14343_emb_CAA46508_ (X65541) carbonic anhydrase [Arabidopsis thaliana]

Seq. No.	160529
Seq. ID	LIB3177-005-P1-K2-E7
Method	BLASTX
NCBI GI	g464662
BLAST score	191
E value	2.0e-14
Match length	143
% identity	34
NCBI Description	CHLOROPLAST 31 KD RIBONUCLEOPROTEIN PRECURSOR (RNA-BINDING PROTEIN RNP-T) (RNA-BINDING PROTEIN 1) >gi_282884_pir__S28057 RNA-binding protein RNP-T - Arabidopsis thaliana >gi_16490_emb_CAA46347_ (X65255) RNA-binding protein [Arabidopsis thaliana] >gi_387569 (M94554) 31 kDa RNA binding protein [Arabidopsis thaliana] >gi_475718 (U08467) RNA-binding protein 1 [Arabidopsis thaliana] >gi_4220513_emb_CAA22986_ (AL035356) RNA-binding protein RNP-T precursor [Arabidopsis thaliana] >gi_737169_prf__1921382A RNA-binding protein [Arabidopsis thaliana]

Seq. No.	160530
Seq. ID	LIB3177-005-P1-K2-E9
Method	BLASTN
NCBI GI	g3643588
BLAST score	381
E value	0.0e+00
Match length	389
% identity	99
NCBI Description	Arabidopsis thaliana chromosome II BAC F17H15 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	160531
Seq. ID	LIB3177-005-P1-K2-F1
Method	BLASTN
NCBI GI	g3860243
BLAST score	173
E value	2.0e-92
Match length	445
% identity	98
NCBI Description	Arabidopsis thaliana chromosome II BAC F15K20 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	160532
Seq. ID	LIB3177-005-P1-K2-F10
Method	BLASTX
NCBI GI	g1175011
BLAST score	120
E value	1.0e-65

Match length	143
% identity	94
NCBI Description	PLASMA MEMBRANE INTRINSIC PROTEIN 1B (TRANSMEMBRANE PROTEIN A) (TMP-A) >gi_296085_emb_CAA48356_ (X68293) transmembrane protein [Arabidopsis thaliana] >gi_3386599 (AC004665) plasma membrane intrinsic protein 1B [Arabidopsis thaliana]
Seq. No.	160533
Seq. ID	LIB3177-005-P1-K2-F2
Method	BLASTN
NCBI GI	g3309276
BLAST score	166
E value	1.0e-88
Match length	174
% identity	99
NCBI Description	Arabidopsis thaliana BAC T26N6 from chromosome IV at 19.3 cM, complete sequence
Seq. No.	160534
Seq. ID	LIB3177-005-P1-K2-F3
Method	BLASTX
NCBI GI	g133960
BLAST score	471
E value	2.0e-47
Match length	112
% identity	84
NCBI Description	CHLOROPLAST 30S RIBOSOMAL PROTEIN S4 >gi_70876_pir__R3NT4 ribosomal protein S4 - common tobacco chloroplast >gi_11834_emb_CAA77354_ (Z00044) ribosomal protein S4 [Nicotiana tabacum] >gi_225202_prf__1211235AG ribosomal protein S4 [Nicotiana tabacum]
Seq. No.	160535
Seq. ID	LIB3177-005-P1-K2-F4
Method	BLASTX
NCBI GI	g131397
BLAST score	124
E value	3.0e-29
Match length	130
% identity	69
NCBI Description	OXYGEN-EVOLVING ENHANCER PROTEIN 3 PRECURSOR (OEE3) (16 KD SUBUNIT OF OXYGEN-EVOLVING SYSTEM OF PHOTOSYSTEM II) >gi_81480_pir__S00008 photosystem II oxygen-evolving complex protein 3 precursor - spinach >gi_755802_emb_CAA29056_ (X05512) 16 kDa protein of the photosynthetic oxygen- evolving protein (OEC) [Spinacia oleracea] >gi_225597_prf__1307179B luminal protein 16kD [Spinacia oleracea]
Seq. No.	160536
Seq. ID	LIB3177-005-P1-K2-F5
Method	BLASTN
NCBI GI	g3869075
BLAST score	36
E value	9.0e-11
Match length	142
% identity	86

NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MXK3, complete sequence [Arabidopsis thaliana]
Seq. No.	160537
Seq. ID	LIB3177-005-P1-K2-F6
Method	BLASTN
NCBI GI	g2252848
BLAST score	173
E value	2.0e-92
Match length	301
% identity	97
NCBI Description	Arabidopsis thaliana BAC TM018A10
Seq. No.	160538
Seq. ID	LIB3177-005-P1-K2-F7
Method	BLASTX
NCBI GI	g4263525
BLAST score	469
E value	4.0e-47
Match length	121
% identity	76
NCBI Description	(AC004044) putative photosystem I reaction center subunit II precursor [Arabidopsis thaliana]
Seq. No.	160539
Seq. ID	LIB3177-005-P1-K2-F8
Method	BLASTN
NCBI GI	g3241922
BLAST score	53
E value	7.0e-21
Match length	207
% identity	89
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MLM24, complete sequence [Arabidopsis thaliana]
Seq. No.	160540
Seq. ID	LIB3177-005-P1-K2-G1
Method	BLASTX
NCBI GI	g136242
BLAST score	150
E value	1.0e-09
Match length	118
% identity	35
NCBI Description	N2,N2-DIMETHYLGUANOSINE TRNA METHYLTRANSFERASE PRECURSOR >gi_83343_pir__A28323 N2,N2-dimethylguanine tRNA methyltransferase - yeast (Saccharomyces cerevisiae) >gi_172940 (M17193) tRNA dimethyltransferase [Saccharomyces cerevisiae] >gi_747894_emb_CAA88673_ (Z48758) Trm1p [Saccharomyces cerevisiae]
Seq. No.	160541
Seq. ID	LIB3177-005-P1-K2-G2
Method	BLASTX
NCBI GI	g2781354
BLAST score	50
E value	2.0e-34
Match length	104

% identity	75
NCBI Description	(AC003113) F24O1.10 [Arabidopsis thaliana]
Seq. No.	160542
Seq. ID	LIB3177-005-P1-K2-G3
Method	BLASTX
NCBI GI	g3386613
BLAST score	637
E value	9.0e-67
Match length	123
% identity	98
NCBI Description	(AC004665) putative ATP-dependent RNA helicase [Arabidopsis thaliana]
Seq. No.	160543
Seq. ID	LIB3177-005-P1-K2-G7
Method	BLASTN
NCBI GI	g2656031
BLAST score	314
E value	1.0e-176
Match length	355
% identity	97
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MXC20
Seq. No.	160544
Seq. ID	LIB3177-005-P1-K2-G9
Method	BLASTN
NCBI GI	g2564048
BLAST score	115
E value	3.0e-58
Match length	173
% identity	80
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MKD15, complete sequence [Arabidopsis thaliana]
Seq. No.	160545
Seq. ID	LIB3177-005-P1-K2-H12
Method	BLASTX
NCBI GI	g3123188
BLAST score	353
E value	1.0e-33
Match length	82
% identity	84
NCBI Description	CATALASE 3 >gi_2347178 (U43147) catalase 3 [Arabidopsis thaliana] >gi_2511726 (AF021937) catalase 3 [Arabidopsis thaliana]
Seq. No.	160546
Seq. ID	LIB3177-005-P1-K2-H2
Method	BLASTX
NCBI GI	g3914666
BLAST score	596
E value	6.0e-62
Match length	134
% identity	90
NCBI Description	CHLOROPLAST 50S RIBOSOMAL PROTEIN L4 PRECURSOR

	>gi_2791998_emb_CAA74895_ (Y14566) ribosomal protein L4 [Arabidopsis thaliana] >gi_2792000_emb_CAA74894_ (Y14565) ribosomal protein L4 [Arabidopsis thaliana]
Seq. No.	160547
Seq. ID	LIB3177-005-P1-K2-H4
Method	BLASTX
NCBI GI	g1732570
BLAST score	394
E value	3.0e-38
Match length	97
% identity	87
NCBI Description	(U72153) beta-glucosidase [Arabidopsis thaliana]
Seq. No.	160548
Seq. ID	LIB3177-005-P1-K2-H5
Method	BLASTX
NCBI GI	g4583542
BLAST score	179
E value	3.0e-13
Match length	73
% identity	58
NCBI Description	(Y16847) 16 kDa polypeptide of oxygen-evolving complex [Arabidopsis thaliana]
Seq. No.	160549
Seq. ID	LIB3177-005-P1-K2-H6
Method	BLASTX
NCBI GI	g3123188
BLAST score	568
E value	8.0e-59
Match length	114
% identity	91
NCBI Description	CATALASE 3 >gi_2347178 (U43147) catalase 3 [Arabidopsis thaliana] >gi_2511726 (AF021937) catalase 3 [Arabidopsis thaliana]
Seq. No.	160550
Seq. ID	LIB3177-005-P1-K2-H8
Method	BLASTX
NCBI GI	g1710780
BLAST score	473
E value	2.0e-47
Match length	125
% identity	74
NCBI Description	40S RIBOSOMAL PROTEIN S9 (S7) >gi_1321917_emb_CAA65433_ (X96613) cytoplasmic ribosomal protein S7 [Podospora anserina]
Seq. No.	160551
Seq. ID	LIB3177-005-P1-K2-H9
Method	BLASTX
NCBI GI	g2244740
BLAST score	91
E value	1.0e-34
Match length	135
% identity	60

NCBI Description	(D88417) endo-1,4-beta-glucanase [Gossypium hirsutum]

Seq. No.	160552
Seq. ID	LIB3177-006-P1-K1-A4
Method	BLASTX
NCBI GI	g132074
BLAST score	289
E value	3.0e-26
Match length	89
% identity	67
NCBI Description	RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN 1A PRECURSOR (RUBISCO SMALL SUBUNIT 1A) >gi_68063_pir__RKMUA1 ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain A1 precursor - Arabidopsis thaliana

Seq. No.	160553
Seq. ID	LIB3177-006-P1-K1-A5
Method	BLASTX
NCBI GI	g445612
BLAST score	199
E value	1.0e-15
Match length	102
% identity	44
NCBI Description	ribosomal protein S19 [Solanum tuberosum]

Seq. No.	160554
Seq. ID	LIB3177-006-P1-K1-B1
Method	BLASTN
NCBI GI	g3046851
BLAST score	106
E value	2.0e-52
Match length	342
% identity	83
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MIJ24, complete sequence [Arabidopsis thaliana]

Seq. No.	160555
Seq. ID	LIB3177-006-P1-K1-B2
Method	BLASTX
NCBI GI	g115385
BLAST score	185
E value	8.0e-14
Match length	106
% identity	61
NCBI Description	CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR (CAB-4) (LHCP) >gi_166646 (M63931) light-harvesting chlorophyll a/b binding protein [Arabidopsis thaliana]

Seq. No.	160556
Seq. ID	LIB3177-006-P1-K1-B3
Method	BLASTX
NCBI GI	g3859606
BLAST score	237
E value	6.0e-20
Match length	81
% identity	54
NCBI Description	(AF104919) contains similarity to cysteine proteases (Pfam:

PF00112, E=1.3e-79, N=1) [Arabidopsis thaliana]

Seq. No.	160557
Seq. ID	LIB3177-006-P1-K1-B4
Method	BLASTN
NCBI GI	g4567259
BLAST score	35
E value	2.0e-10
Match length	100
% identity	90
NCBI Description	Arabidopsis thaliana chromosome II BAC F3K23 genomic sequence, complete sequence

Seq. No.	160558
Seq. ID	LIB3177-006-P1-K1-B6
Method	BLASTX
NCBI GI	g4240116
BLAST score	222
E value	4.0e-18
Match length	84
% identity	56
NCBI Description	(AB007799) NADH-cytochrome b5 reductase [Arabidopsis thaliana] >gi_4240118_dbj_BAA74838_ (AB007800) NADH-cytochrome b5 reductase [Arabidopsis thaliana]

Seq. No.	160559
Seq. ID	LIB3177-006-P1-K1-B8
Method	BLASTN
NCBI GI	g4220633
BLAST score	176
E value	3.0e-94
Match length	345
% identity	87
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K7J8, complete sequence [Arabidopsis thaliana]

Seq. No.	160560
Seq. ID	LIB3177-006-P1-K1-C1
Method	BLASTN
NCBI GI	g166707
BLAST score	49
E value	2.0e-18
Match length	180
% identity	85
NCBI Description	Arabidopsis thaliana glyceraldehyde-3-phosphate dehydrogenase (GapB) gene, exons 1-9, complete cds

Seq. No.	160561
Seq. ID	LIB3177-006-P1-K1-C4
Method	BLASTX
NCBI GI	g115783
BLAST score	420
E value	2.0e-41
Match length	119
% identity	73
NCBI Description	CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR (CAB-140) (LHCP) >gi_16376_emb_CAA27543_ (X03909)

chlorophyll a/b binding protein (LHCP AB 140) [Arabidopsis thaliana]

Seq. No.	160562
Seq. ID	LIB3177-006-P1-K1-C7
Method	BLASTN
NCBI GI	g4490734
BLAST score	43
E value	7.0e-15
Match length	239
% identity	79
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone (ESSA project)

Seq. No.	160563
Seq. ID	LIB3177-006-P1-K1-D1
Method	BLASTX
NCBI GI	g2829899
BLAST score	284
E value	2.0e-25
Match length	110
% identity	50
NCBI Description	(AC002311) similar to ripening-induced protein, gp_AJ001449_2465015 and major#latex protein, gp_X91961_1107495 [Arabidopsis thaliana]

Seq. No.	160564
Seq. ID	LIB3177-006-P1-K1-D3
Method	BLASTX
NCBI GI	g2497733
BLAST score	343
E value	2.0e-32
Match length	101
% identity	71
NCBI Description	NONSPECIFIC LIPID-TRANSFER PROTEIN 1 PRECURSOR (LTP 1) >gi_1177796 (M80567) non-specific lipid transfer protein [Arabidopsis thaliana] >gi_3786018 (AC005499) unknown protein [Arabidopsis thaliana]

Seq. No.	160565
Seq. ID	LIB3177-006-P1-K1-D7
Method	BLASTN
NCBI GI	g2583106
BLAST score	44
E value	7.0e-16
Match length	112
% identity	85
NCBI Description	Arabidopsis thaliana chromosome II BAC F4L23 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	160566
Seq. ID	LIB3177-006-P1-K1-E1
Method	BLASTN
NCBI GI	g3047100
BLAST score	52
E value	2.0e-20
Match length	249

% identity	83
NCBI Description	Arabidopsis thaliana BAC F6N23

Seq. No.	160567
Seq. ID	LIB3177-006-P1-K1-E10
Method	BLASTX
NCBI GI	g4585935
BLAST score	105
E value	3.0e-28
Match length	108
% identity	60
NCBI Description	(AC007211) putative chlorophyll A/B binding protein [Arabidopsis thaliana] >gi_4741946_gb_AAD28770.1_AF134123_1 (AF134123) Lhcb2 protein [Arabidopsis thaliana]

Seq. No.	160568
Seq. ID	LIB3177-006-P1-K1-E2
Method	BLASTX
NCBI GI	g1732570
BLAST score	242
E value	2.0e-20
Match length	96
% identity	54
NCBI Description	(U72153) beta-glucosidase [Arabidopsis thaliana]

Seq. No.	160569
Seq. ID	LIB3177-006-P1-K1-E3
Method	BLASTX
NCBI GI	g99696
BLAST score	245
E value	8.0e-29
Match length	115
% identity	65
NCBI Description	glutamate--ammonia ligase (EC 6.3.1.2) precursor, chloroplast (clone lambdaAtgsl1) - Arabidopsis thaliana >gi_240070_bbs_69728 (S69727) light-regulated glutamine synthetase isoenzyme [Arabidopsis thaliana, Peptide, 430 aa] [Arabidopsis thaliana] >gi_228453_prf__1804333A Gln synthetase [Arabidopsis thaliana]

Seq. No.	160570
Seq. ID	LIB3177-006-P1-K1-E7
Method	BLASTN
NCBI GI	g4519183
BLAST score	91
E value	1.0e-43
Match length	155
% identity	90
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K15C23, complete sequence

Seq. No.	160571
Seq. ID	LIB3177-006-P1-K1-F10
Method	BLASTX
NCBI GI	g2062161
BLAST score	228
E value	6.0e-19

Match length	74
% identity	40
NCBI Description	(AC001645) jasmonate inducible protein isolog [Arabidopsis thaliana]

Seq. No.	160572
Seq. ID	LIB3177-006-P1-K1-F2
Method	BLASTX
NCBI GI	g2645971
BLAST score	506
E value	2.0e-51
Match length	141
% identity	72
NCBI Description	(AF034255) reversibly glycosylated polypeptide-3 [Arabidopsis thaliana]

Seq. No.	160573
Seq. ID	LIB3177-006-P1-K1-F6
Method	BLASTX
NCBI GI	g477819
BLAST score	144
E value	8.0e-13
Match length	94
% identity	48
NCBI Description	mitochondrial processing peptidase (EC 3.4.99.41) beta chain precursor - potato >gi_410634_bbs_136741 cytochrome c reductase-processing peptidase subunit II, MPP subunit II, P53 [potatoes, var. Marfona, tuber, Peptide Mitochondrial, 530 aa]

Seq. No.	160574
Seq. ID	LIB3177-006-P1-K1-F8
Method	BLASTX
NCBI GI	g2738248
BLAST score	455
E value	2.0e-45
Match length	138
% identity	67
NCBI Description	(U97200) cobalamin-independent methionine synthase [Arabidopsis thaliana]

Seq. No.	160575
Seq. ID	LIB3177-006-P1-K1-G1
Method	BLASTX
NCBI GI	g2119846
BLAST score	227
E value	4.0e-19
Match length	67
% identity	67
NCBI Description	chlorophyll a/b-binding protein type I precursor Lhb1B2 - Arabidopsis thaliana >gi_16364_emb_CAA45790_ (X64460) photosystem II type I chlorophyll a /b binding protein [Arabidopsis thaliana] >gi_3128230 (AC004077) photosystem II type I chlorophyll a/b binding protein [Arabidopsis thaliana] >gi_3337371 (AC004481) photosystem II type I chlorophyll a/b binding protein [Arabidopsis thaliana]

Seq. No.	160576
Seq. ID	LIB3177-006-P1-K1-G2
Method	BLASTX
NCBI GI	g1490554
BLAST score	242
E value	2.0e-20
Match length	122
% identity	52
NCBI Description	(U63633) S-adenosylmethionine decarboxylase [Arabidopsis thaliana]

Seq. No.	160577
Seq. ID	LIB3177-006-P1-K1-G3
Method	BLASTX
NCBI GI	g1710581
BLAST score	269
E value	8.0e-24
Match length	85
% identity	67
NCBI Description	60S RIBOSOMAL PROTEIN L9 >gi_2129720_pir__S71255 ribosomal protein L9 - Arabidopsis thaliana >gi_1107489_emb_CAA63024_ (X91958) 60S ribosomal protein L9 [Arabidopsis thaliana]

Seq. No.	160578
Seq. ID	LIB3177-006-P1-K1-H6
Method	BLASTX
NCBI GI	g2623962
BLAST score	193
E value	9.0e-15
Match length	87
% identity	52
NCBI Description	(Y12540) isocitrate dehydrogenase (NADP+) [Apium graveolens]

Seq. No.	160579
Seq. ID	LIB3177-006-P1-K2-A2
Method	BLASTX
NCBI GI	g2623962
BLAST score	309
E value	2.0e-28
Match length	63
% identity	94
NCBI Description	(Y12540) isocitrate dehydrogenase (NADP+) [Apium graveolens]

Seq. No.	160580
Seq. ID	LIB3177-006-P1-K2-A3
Method	BLASTN
NCBI GI	g4585952
BLAST score	87
E value	2.0e-41
Match length	178
% identity	92
NCBI Description	Genomic sequence for Arabidopsis thaliana BAC F26F24, complete sequence

Seq. No. 160581

Seq. ID	LIB3177-006-P1-K2-A4
Method	BLASTN
NCBI GI	g4455348
BLAST score	390
E value	0.0e+00
Match length	429
% identity	98
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone T13J8 (ESSAII project)

Seq. No.	160582
Seq. ID	LIB3177-006-P1-K2-A5
Method	BLASTX
NCBI GI	g126766
BLAST score	501
E value	5.0e-51
Match length	105
% identity	90
NCBI Description	MALATE SYNTHASE, GLYOXYSOMAL >gi_68216_pir__SYRPMA malate synthase (EC 4.1.3.2), glyoxysomal - rape >gi_167150 (J04468) malate synthase (EC 4.1.3.2) [Brassica napus]

Seq. No.	160583
Seq. ID	LIB3177-006-P1-K2-A9
Method	BLASTN
NCBI GI	g2264320
BLAST score	41
E value	7.0e-14
Match length	93
% identity	34
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MXI10, complete sequence [Arabidopsis thaliana]

Seq. No.	160584
Seq. ID	LIB3177-006-P1-K2-B1
Method	BLASTN
NCBI GI	g1149572
BLAST score	189
E value	1.0e-102
Match length	245
% identity	94
NCBI Description	A.thaliana rpl21 mRNA for chloroplast ribosomal large subunit protein L21

Seq. No.	160585
Seq. ID	LIB3177-006-P1-K2-B4
Method	BLASTX
NCBI GI	g1710581
BLAST score	239
E value	2.0e-20
Match length	73
% identity	73
NCBI Description	60S RIBOSOMAL PROTEIN L9 >gi_2129720_pir__S71255 ribosomal protein L9 - Arabidopsis thaliana >gi_1107489_emb_CAA63024_ (X91958) 60S ribosomal protein L9 [Arabidopsis thaliana]

Seq. No.	160586

Seq. ID	LIB3177-006-P1-K2-B5
Method	BLASTX
NCBI GI	g1490554
BLAST score	365
E value	4.0e-35
Match length	97
% identity	76
NCBI Description	(U63633) S-adenosylmethionine decarboxylase [Arabidopsis thaliana]

Seq. No.	160587
Seq. ID	LIB3177-006-P1-K2-B6
Method	BLASTX
NCBI GI	g115767
BLAST score	268
E value	3.0e-42
Match length	92
% identity	89
NCBI Description	CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR (CAB-165/180) (LHCP) >gi_81603_pir__A29280 chlorophyll a/b-binding protein ab165 - Arabidopsis thaliana >gi_16368_emb_CAA27540_ (X03907) chlorophyll a/b binding protein (LHCP AB 65) [Arabidopsis thaliana] >gi_16372_emb_CAA27541_ (X03908) chlorophyll a/b binding protein (LHCP AB 180) [Arabidopsis thaliana]

Seq. No.	160588
Seq. ID	LIB3177-006-P1-K2-C2
Method	BLASTX
NCBI GI	g477819
BLAST score	346
E value	1.0e-32
Match length	127
% identity	56
NCBI Description	mitochondrial processing peptidase (EC 3.4.99.41) beta chain precursor - potato >gi_410634_bbs_136741 cytochrome c reductase-processing peptidase subunit II, MPP subunit II, P53 [potatoes, var. Marfona, tuber, Peptide Mitochondrial, 530 aa]

Seq. No.	160589
Seq. ID	LIB3177-006-P1-K2-C5
Method	BLASTX
NCBI GI	g2317731
BLAST score	709
E value	3.0e-75
Match length	133
% identity	99
NCBI Description	(AF013628) reversibly glycosylated polypeptide-2 [Arabidopsis thaliana]

Seq. No.	160590
Seq. ID	LIB3177-006-P1-K2-C9
Method	BLASTX
NCBI GI	g2062161
BLAST score	123
E value	1.0e-06

Match length	82
% identity	18
NCBI Description	(AC001645) jasmonate inducible protein isolog [Arabidopsis thaliana]

Seq. No.	160591
Seq. ID	LIB3177-006-P1-K2-D10
Method	BLASTN
NCBI GI	g2121272
BLAST score	122
E value	4.0e-62
Match length	250
% identity	88
NCBI Description	Arabidopsis thaliana dihydroorotase (pyr4) mRNA, complete cds

Seq. No.	160592
Seq. ID	LIB3177-006-P1-K2-D11
Method	BLASTN
NCBI GI	g4519183
BLAST score	224
E value	1.0e-123
Match length	323
% identity	92
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K15C23, complete sequence

Seq. No.	160593
Seq. ID	LIB3177-006-P1-K2-D4
Method	BLASTX
NCBI GI	g99696
BLAST score	412
E value	2.0e-40
Match length	96
% identity	86
NCBI Description	glutamate--ammonia ligase (EC 6.3.1.2) precursor, chloroplast (clone lambdaAtgsl1) - Arabidopsis thaliana >gi_240070_bbs_69728 (S69727) light-regulated glutamine synthetase isoenzyme [Arabidopsis thaliana, Peptide, 430 aa] [Arabidopsis thaliana] >gi_228453_prf__1804333A Gln synthetase [Arabidopsis thaliana]

Seq. No.	160594
Seq. ID	LIB3177-006-P1-K2-D5
Method	BLASTX
NCBI GI	g1363489
BLAST score	691
E value	4.0e-73
Match length	136
% identity	94
NCBI Description	thioglucosidase (EC 3.2.3.1) 3D precursor - Arabidopsis thaliana >gi_984052_emb_CAA61592_ (X89413) thioglucoside glucohydrolase [Arabidopsis thaliana]

Seq. No.	160595
Seq. ID	LIB3177-006-P1-K2-D6
Method	BLASTN

NCBI GI	g3047100
BLAST score	190
E value	1.0e-102
Match length	414
% identity	96
NCBI Description	Arabidopsis thaliana BAC F6N23

Seq. No.	160596
Seq. ID	LIB3177-006-P1-K2-D7
Method	BLASTX
NCBI GI	g4689386
BLAST score	287
E value	9.0e-26
Match length	123
% identity	52
NCBI Description	(AF139468) photosystem I reaction center subunit III [Vigna radiata]

Seq. No.	160597
Seq. ID	LIB3177-006-P1-K2-D9
Method	BLASTX
NCBI GI	g4585935
BLAST score	640
E value	4.0e-67
Match length	124
% identity	98
NCBI Description	(AC007211) putative chlorophyll A/B binding protein [Arabidopsis thaliana] >gi_4741946_gb_AAD28770.1_AF134123_1 (AF134123) Lhcb2 protein [Arabidopsis thaliana]

Seq. No.	160598
Seq. ID	LIB3177-006-P1-K2-E1
Method	BLASTX
NCBI GI	g4006856
BLAST score	78
E value	3.0e-18
Match length	99
% identity	65
NCBI Description	(Z99707) receptor kinase-like protein [Arabidopsis thaliana]

Seq. No.	160599
Seq. ID	LIB3177-006-P1-K2-E10
Method	BLASTX
NCBI GI	g1592672
BLAST score	446
E value	2.0e-44
Match length	111
% identity	79
NCBI Description	(X91921) germin1 [Arabidopsis thaliana]

Seq. No.	160600
Seq. ID	LIB3177-006-P1-K2-E4
Method	BLASTX
NCBI GI	g2497733
BLAST score	580
E value	4.0e-60

Match length	118
% identity	96
NCBI Description	NONSPECIFIC LIPID-TRANSFER PROTEIN 1 PRECURSOR (LTP 1) >gi_1177796 (M80567) non-specific lipid transfer protein [Arabidopsis thaliana] >gi_3786018 (AC005499) unknown protein [Arabidopsis thaliana]

Seq. No.	160601
Seq. ID	LIB3177-006-P1-K2-E6
Method	BLASTX
NCBI GI	g2829899
BLAST score	345
E value	2.0e-32
Match length	110
% identity	60
NCBI Description	(AC002311) similar to ripening-induced protein, gp_AJ001449_2465015 and major#latex protein, gp_X91961_1107495 [Arabidopsis thaliana]

Seq. No.	160602
Seq. ID	LIB3177-006-P1-K2-F11
Method	BLASTN
NCBI GI	g4490734
BLAST score	211
E value	1.0e-115
Match length	247
% identity	96
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone (ESSA project)

Seq. No.	160603
Seq. ID	LIB3177-006-P1-K2-F3
Method	BLASTX
NCBI GI	g115783
BLAST score	594
E value	9.0e-62
Match length	117
% identity	97
NCBI Description	CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR (CAB-140) (LHCP) >gi_16376_emb_CAA27543_ (X03909) chlorophyll a/b binding protein (LHCP AB 140) [Arabidopsis thaliana]

Seq. No.	160604
Seq. ID	LIB3177-006-P1-K2-F6
Method	BLASTX
NCBI GI	g166708
BLAST score	266
E value	1.0e-23
Match length	49
% identity	98
NCBI Description	(M64118) glyceraldehyde-3-phosphate dehydrogenase [Arabidopsis thaliana]

Seq. No.	160605
Seq. ID	LIB3177-006-P1-K2-G1
Method	BLASTX

NCBI GI	g4240116
BLAST score	311
E value	1.0e-28
Match length	84
% identity	76
NCBI Description	(AB007799) NADH-cytochrome b5 reductase [Arabidopsis thaliana] >gi_4240118_dbj_BAA74838_ (AB007800) NADH-cytochrome b5 reductase [Arabidopsis thaliana]

Seq. No.	160606
Seq. ID	LIB3177-006-P1-K2-G10
Method	BLASTN
NCBI GI	g4220633
BLAST score	302
E value	1.0e-169
Match length	302
% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K7J8, complete sequence [Arabidopsis thaliana]

Seq. No.	160607
Seq. ID	LIB3177-006-P1-K2-G12
Method	BLASTX
NCBI GI	g4587542
BLAST score	291
E value	2.0e-26
Match length	75
% identity	75
NCBI Description	(AC006577) Belongs to the PF_00657 Lipase/Acylhydrolase with GDSL-motif family. ESTs gb_T45815, gb_T45130 and gb_Z38046 come from this gene. [Arabidopsis thaliana]

Seq. No.	160608
Seq. ID	LIB3177-006-P1-K2-G3
Method	BLASTN
NCBI GI	g4567259
BLAST score	61
E value	8.0e-26
Match length	224
% identity	96
NCBI Description	Arabidopsis thaliana chromosome II BAC F3K23 genomic sequence, complete sequence

Seq. No.	160609
Seq. ID	LIB3177-006-P1-K2-G4
Method	BLASTX
NCBI GI	g3859606
BLAST score	546
E value	3.0e-56
Match length	111
% identity	88
NCBI Description	(AF104919) contains similarity to cysteine proteases (Pfam: PF00112, E=1.3e-79, N=1) [Arabidopsis thaliana]

Seq. No.	160610
Seq. ID	LIB3177-006-P1-K2-G5
Method	BLASTX

NCBI GI	g115385
BLAST score	588
E value	5.0e-61
Match length	113
% identity	100
NCBI Description	CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR (CAB-4) (LHCP) >gi_166646 (M63931) light-harvesting chlorophyll a/b binding protein [Arabidopsis thaliana]

Seq. No.	160611
Seq. ID	LIB3177-006-P1-K2-G6
Method	BLASTN
NCBI GI	g3046851
BLAST score	296
E value	1.0e-166
Match length	408
% identity	93
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MIJ24, complete sequence [Arabidopsis thaliana]

Seq. No.	160612
Seq. ID	LIB3177-006-P1-K2-H1
Method	BLASTN
NCBI GI	g4406752
BLAST score	95
E value	4.0e-46
Match length	255
% identity	88
NCBI Description	Arabidopsis thaliana chromosome II BAC F19B11 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	160613
Seq. ID	LIB3177-006-P1-K2-H10
Method	BLASTX
NCBI GI	g132074
BLAST score	705
E value	9.0e-75
Match length	140
% identity	92
NCBI Description	RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN 1A PRECURSOR (RUBISCO SMALL SUBUNIT 1A) >gi_68063_pir__RKMUA1 ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain A1 precursor - Arabidopsis thaliana

Seq. No.	160614
Seq. ID	LIB3177-006-P1-K2-H11
Method	BLASTX
NCBI GI	g1350965
BLAST score	313
E value	5.0e-29
Match length	65
% identity	92
NCBI Description	40S RIBOSOMAL PROTEIN S23 (S12)

Seq. No.	160615
Seq. ID	LIB3177-006-P1-K2-H2
Method	BLASTX

NCBI GI	g445612
BLAST score	52
E value	3.0e-19
Match length	61
% identity	89
NCBI Description	ribosomal protein S19 [Solanum tuberosum]

Seq. No.	160616
Seq. ID	LIB3177-006-P1-K2-H3
Method	BLASTX
NCBI GI	g132074
BLAST score	639
E value	5.0e-67
Match length	116
% identity	100
NCBI Description	RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN 1A PRECURSOR (RUBISCO SMALL SUBUNIT 1A) >gi_68063_pir__RKMUA1 ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain A1 precursor - Arabidopsis thaliana

Seq. No.	160617
Seq. ID	LIB3177-006-P1-K2-H4
Method	BLASTX
NCBI GI	g4582430
BLAST score	627
E value	1.0e-65
Match length	122
% identity	98
NCBI Description	(AC007196) nonsense-mediated mRNA decay protein [Arabidopsis thaliana]

Seq. No.	160618
Seq. ID	LIB3177-006-P1-K2-H5
Method	BLASTX
NCBI GI	g3377797
BLAST score	247
E value	2.0e-21
Match length	78
% identity	63
NCBI Description	(AF075597) Similar to 60S ribosome protein L19; coded for by A. thaliana cDNA T04719; coded for by A. thaliana cDNA H36046; coded for by A. thaliana cDNA T44067; coded for by A. thaliana cDNA T14056; coded for by A. thaliana cDNA R90691 [Ara

Seq. No.	160619
Seq. ID	LIB3177-006-P1-K2-H6
Method	BLASTN
NCBI GI	g3046849
BLAST score	88
E value	7.0e-42
Match length	168
% identity	88
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K18L3, complete sequence [Arabidopsis thaliana]

Seq. No. 160620

Seq. ID	LIB3177-007-P1-K1-A1
Method	BLASTX
NCBI GI	g2119846
BLAST score	440
E value	1.0e-43
Match length	116
% identity	74
NCBI Description	chlorophyll a/b-binding protein type I precursor Lhb1B2 - Arabidopsis thaliana >gi_16364_emb_CAA45790_ (X64460) photosystem II type I chlorophyll a /b binding protein [Arabidopsis thaliana] >gi_3128230 (AC004077) photosystem II type I chlorophyll a/b binding protein [Arabidopsis thaliana] >gi_3337371 (AC004481) photosystem II type I chlorophyll a/b binding protein [Arabidopsis thaliana]

Seq. No.	160621
Seq. ID	LIB3177-007-P1-K1-A2
Method	BLASTX
NCBI GI	g115385
BLAST score	379
E value	2.0e-36
Match length	116
% identity	66
NCBI Description	CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR (CAB-4) (LHCP) >gi_166646 (M63931) light-harvesting chlorophyll a/b binding protein [Arabidopsis thaliana]

Seq. No.	160622
Seq. ID	LIB3177-007-P1-K1-A3
Method	BLASTX
NCBI GI	g1363489
BLAST score	335
E value	2.0e-31
Match length	107
% identity	57
NCBI Description	thioglucosidase (EC 3.2.3.1) 3D precursor - Arabidopsis thaliana >gi_984052_emb_CAA61592_ (X89413) thioglucoside glucohydrolase [Arabidopsis thaliana]

Seq. No.	160623
Seq. ID	LIB3177-007-P1-K1-B1
Method	BLASTX
NCBI GI	g3184281
BLAST score	317
E value	3.0e-29
Match length	131
% identity	55
NCBI Description	(AC004136) putative cytochrome P450 [Arabidopsis thaliana]

Seq. No.	160624
Seq. ID	LIB3177-007-P1-K1-B11
Method	BLASTX
NCBI GI	g1208408
BLAST score	238
E value	6.0e-20
Match length	133
% identity	44

NCBI Description	(D14824) nitrite reductase [Arabidopsis thaliana] >gi_2289780_dbj_BAA21672_ (AB006032) nitrite reductase [Arabidopsis thaliana] >gi_4335728_gb_AAD17406_ (AC006248) nitrate reductase [Arabidopsis thaliana]
Seq. No.	160625
Seq. ID	LIB3177-007-P1-K1-B3
Method	BLASTX
NCBI GI	g2119846
BLAST score	255
E value	6.0e-22
Match length	109
% identity	45
NCBI Description	chlorophyll a/b-binding protein type I precursor Lhb1B2 - Arabidopsis thaliana >gi_16364_emb_CAA45790_ (X64460) photosystem II type I chlorophyll a /b binding protein [Arabidopsis thaliana] >gi_3128230 (AC004077) photosystem II type I chlorophyll a/b binding protein [Arabidopsis thaliana] >gi_3337371 (AC004481) photosystem II type I chlorophyll a/b binding protein [Arabidopsis thaliana]
Seq. No.	160626
Seq. ID	LIB3177-007-P1-K1-C2
Method	BLASTX
NCBI GI	g1170028
BLAST score	352
E value	3.0e-33
Match length	129
% identity	59
NCBI Description	GLUTAMATE-1-SEMIALDEHYDE 2,1-AMINOMUTASE 1 PRECURSOR (GSA 1) (GLUTAMATE-1-SEMIALDEHYDE AMINOTRANSFERASE 1) (GSA-AT 1) >gi_454357 (U03773) glutamate-1-semialdehyde-2,1-aminomutase [Arabidopsis thaliana]
Seq. No.	160627
Seq. ID	LIB3177-007-P1-K1-C3
Method	BLASTX
NCBI GI	g4204274
BLAST score	71
E value	2.2e+00
Match length	134
% identity	59
NCBI Description	(AC004146) ribulose bisphosphate carboxylase, small subunit [Arabidopsis thaliana]
Seq. No.	160628
Seq. ID	LIB3177-007-P1-K1-E2
Method	BLASTN
NCBI GI	g3927822
BLAST score	109
E value	2.0e-54
Match length	277
% identity	85
NCBI Description	Arabidopsis thaliana chromosome II BAC F8N16 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	160629
Seq. ID	LIB3177-007-P1-K1-E3
Method	BLASTX
NCBI GI	g2511594
BLAST score	377
E value	2.0e-36
Match length	106
% identity	71
NCBI Description	(Y13694) multicatalytic endopeptidase complex, proteasome precursor, beta subunit [Arabidopsis thaliana] >gi_2827525_emb_CAA16533_ (AL021633) multicatalytic endopeptidase complex, proteasome precursor, beta subunit [Arabidopsis thaliana] >gi_3421099 (AF043529) 20S proteasome subunit PBA1 [Arabidopsis thaliana]

Seq. No.	160630
Seq. ID	LIB3177-007-P1-K1-E5
Method	BLASTX
NCBI GI	g2119848
BLAST score	329
E value	8.0e-31
Match length	89
% identity	75
NCBI Description	chlorophyll a/b-binding protein type I precursor Lhb1B1 - Arabidopsis thaliana >gi_16366_emb_CAA45789_ (X64459) photosystem II type I chlorophyll a /b binding protein [Arabidopsis thaliana] >gi_3128229 (AC004077) putative photosystem II type I chlorophyll a/b binding protein [Arabidopsis thaliana] >gi_3337372 (AC004481) putative photosystem II type I chlorophyll a/b binding protein [Arabidopsis thaliana]

Seq. No.	160631
Seq. ID	LIB3177-007-P1-K1-E7
Method	BLASTX
NCBI GI	g4191778
BLAST score	271
E value	5.0e-24
Match length	87
% identity	63
NCBI Description	(AC005917) putative nucleosome assembly protein I [Arabidopsis thaliana]

Seq. No.	160632
Seq. ID	LIB3177-007-P1-K1-F1
Method	BLASTX
NCBI GI	g4467128
BLAST score	279
E value	5.0e-25
Match length	75
% identity	73
NCBI Description	(AL035538) putative protein [Arabidopsis thaliana]

Seq. No.	160633
Seq. ID	LIB3177-007-P1-K1-F12
Method	BLASTX
NCBI GI	g282865

BLAST score	248
E value	3.0e-21
Match length	95
% identity	56
NCBI Description	chlorophyll a/b-binding protein - Arabidopsis thaliana >gi_16207_emb_CAA39534.1_ (X56062) chlorophyll A/B-binding protein [Arabidopsis thaliana] >gi_166644 (M85150) chlorophyll a/b-binding protein [Arabidopsis thaliana] >gi_4678304_emb_CAB41095.1_ (AL049655) chlorophyll a/b-binding protein [Arabidopsis thaliana]

Seq. No.	160634
Seq. ID	LIB3177-007-P1-K1-F2
Method	BLASTX
NCBI GI	g3219858
BLAST score	331
E value	7.0e-31
Match length	116
% identity	61
NCBI Description	DNA-DIRECTED RNA POLYMERASE II 13.6 KD POLYPEPTIDE >gi_2129724_pir__S71204 RNA polymerase II 13.6 kDa chain - Arabidopsis thaliana >gi_881501 (U28048) RNA polymerase II 13.6 kDa subunit [Arabidopsis thaliana] >gi_4678938_emb_CAB41329.1_ (AL049711) DNA-directed RNA polymerase II 13.6K chain [Arabidopsis thaliana]

Seq. No.	160635
Seq. ID	LIB3177-007-P1-K1-F3
Method	BLASTX
NCBI GI	g4056479
BLAST score	351
E value	3.0e-33
Match length	114
% identity	68
NCBI Description	(AC005896) unknown protein [Arabidopsis thaliana]

Seq. No.	160636
Seq. ID	LIB3177-007-P1-K1-F4
Method	BLASTX
NCBI GI	g2062167
BLAST score	193
E value	9.0e-15
Match length	85
% identity	49
NCBI Description	(AC001645) Proline-rich protein APG isolog [Arabidopsis thaliana]

Seq. No.	160637
Seq. ID	LIB3177-007-P1-K1-F6
Method	BLASTX
NCBI GI	g1199503
BLAST score	335
E value	2.0e-31
Match length	104
% identity	65
NCBI Description	(X95640) transmembrane channel protein [Brassica oleracea]

Seq. No.	160638
Seq. ID	LIB3177-007-P1-K1-F8
Method	BLASTX
NCBI GI	g515616
BLAST score	363
E value	1.0e-34
Match length	106
% identity	70
NCBI Description	(X61608) LHC II Type III chlorophyll a /b binding protein [Brassica napus]

Seq. No.	160639
Seq. ID	LIB3177-007-P1-K1-G1
Method	BLASTX
NCBI GI	g3193303
BLAST score	316
E value	3.0e-29
Match length	116
% identity	57
NCBI Description	(AF069298) similar to several proteins containing a tandem repeat region such as Plasmodium falciparum GGM tandem repeat protein (GB:U27807); partial CDS [Arabidopsis thaliana]

Seq. No.	160640
Seq. ID	LIB3177-007-P1-K1-G11
Method	BLASTX
NCBI GI	g4218123
BLAST score	208
E value	1.0e-16
Match length	103
% identity	48
NCBI Description	(AL035353) photosystem I subunit PSI-E-like protein [Arabidopsis thaliana]

Seq. No.	160641
Seq. ID	LIB3177-007-P1-K1-G5
Method	BLASTN
NCBI GI	g1149572
BLAST score	90
E value	5.0e-43
Match length	210
% identity	86
NCBI Description	A.thaliana rpl21 mRNA for chloroplast ribosomal large subunit protein L21

Seq. No.	160642
Seq. ID	LIB3177-007-P1-K1-G6
Method	BLASTX
NCBI GI	g4240116
BLAST score	296
E value	6.0e-27
Match length	101
% identity	59
NCBI Description	(AB007799) NADH-cytochrome b5 reductase [Arabidopsis thaliana] >gi_4240118_dbj_BAA74838_ (AB007800) NADH-cytochrome b5 reductase [Arabidopsis thaliana]

Seq. No.	160643
Seq. ID	LIB3177-007-P1-K1-H12
Method	BLASTX
NCBI GI	g2252830
BLAST score	304
E value	1.0e-27
Match length	125
% identity	57
NCBI Description	(AF013293) weak similarity to receptor protein kinase [Arabidopsis thaliana]

Seq. No.	160644
Seq. ID	LIB3177-007-P1-K1-H4
Method	BLASTX
NCBI GI	g132110
BLAST score	176
E value	7.0e-13
Match length	70
% identity	56
NCBI Description	RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN 3B PRECURSOR (RUBISCO SMALL SUBUNIT 3B) >gi_68060_pir__RKMUB3 ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain B3 precursor - Arabidopsis thaliana >gi_16195_emb_CAA32702_ (X14564) ribulose bisphosphate carboxylase [Arabidopsis thaliana]

Seq. No.	160645
Seq. ID	LIB3177-007-P1-K2-A11
Method	BLASTX
NCBI GI	g4105798
BLAST score	393
E value	1.0e-38
Match length	84
% identity	73
NCBI Description	(AF049930) PGP237-11 [Petunia x hybrida]

Seq. No.	160646
Seq. ID	LIB3177-007-P1-K2-A12
Method	BLASTX
NCBI GI	g4467126
BLAST score	265
E value	4.0e-23
Match length	142
% identity	35
NCBI Description	(AL035538) guanine nucleotide-exchange protein-like [Arabidopsis thaliana]

Seq. No.	160647
Seq. ID	LIB3177-007-P1-K2-A2
Method	BLASTX
NCBI GI	g115385
BLAST score	623
E value	4.0e-65
Match length	123
% identity	98
NCBI Description	CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR

	(CAB-4) (LHCP) >gi_166646 (M63931) light-harvesting chlorophyll a/b binding protein [Arabidopsis thaliana]
Seq. No.	160648
Seq. ID	LIB3177-007-P1-K2-A3
Method	BLASTX
NCBI GI	g1363489
BLAST score	618
E value	1.0e-64
Match length	114
% identity	99
NCBI Description	thioglucosidase (EC 3.2.3.1) 3D precursor - Arabidopsis thaliana >gi_984052_emb_CAA61592_ (X89413) thioglucoside glucohydrolase [Arabidopsis thaliana]
Seq. No.	160649
Seq. ID	LIB3177-007-P1-K2-A4
Method	BLASTX
NCBI GI	g131360
BLAST score	241
E value	2.0e-20
Match length	61
% identity	80
NCBI Description	PHOTOSYSTEM II 4 KD REACTION CENTRE PROTEIN PRECURSOR >gi_81727_pir__S02115 photosystem II protein psbK precursor - white mustard chloroplast >gi_12209_emb_CAA31909_ (X13558) K preprotein (AA -24 to 37) [Sinapis alba]
Seq. No.	160650
Seq. ID	LIB3177-007-P1-K2-A5
Method	BLASTN
NCBI GI	g12208
BLAST score	126
E value	2.0e-64
Match length	235
% identity	91
NCBI Description	Sinapis alba plastid trnQ and psbK genes for tRNA-Glu and K proteiH of photosystem II
Seq. No.	160651
Seq. ID	LIB3177-007-P1-K2-A9
Method	BLASTX
NCBI GI	g3184281
BLAST score	387
E value	1.0e-37
Match length	100
% identity	77
NCBI Description	(AC004136) putative cytochrome P450 [Arabidopsis thaliana]
Seq. No.	160652
Seq. ID	LIB3177-007-P1-K2-B1
Method	BLASTX
NCBI GI	g3184281
BLAST score	588
E value	5.0e-61
Match length	140
% identity	79

NCBI Description	(AC004136) putative cytochrome P450 [Arabidopsis thaliana]

Seq. No.	160653
Seq. ID	LIB3177-007-P1-K2-B11
Method	BLASTX
NCBI GI	g1208408
BLAST score	672
E value	6.0e-71
Match length	130
% identity	99
NCBI Description	(D14824) nitrite reductase [Arabidopsis thaliana] >gi_2289780_dbj_BAA21672_ (AB006032) nitrite reductase [Arabidopsis thaliana] >gi_4335728_gb_AAD17406_ (AC006248) nitrate reductase [Arabidopsis thaliana]

Seq. No.	160654
Seq. ID	LIB3177-007-P1-K2-B12
Method	BLASTX
NCBI GI	g1208408
BLAST score	298
E value	2.0e-27
Match length	80
% identity	78
NCBI Description	(D14824) nitrite reductase [Arabidopsis thaliana] >gi_2289780_dbj_BAA21672_ (AB006032) nitrite reductase [Arabidopsis thaliana] >gi_4335728_gb_AAD17406_ (AC006248) nitrate reductase [Arabidopsis thaliana]

Seq. No.	160655
Seq. ID	LIB3177-007-P1-K2-B2
Method	BLASTN
NCBI GI	g4584351
BLAST score	418
E value	0.0e+00
Match length	428
% identity	99
NCBI Description	Arabidopsis thaliana chromosome II BAC T12H3 genomic sequence, complete sequence

Seq. No.	160656
Seq. ID	LIB3177-007-P1-K2-B3
Method	BLASTX
NCBI GI	g2119846
BLAST score	693
E value	2.0e-73
Match length	131
% identity	99
NCBI Description	chlorophyll a/b-binding protein type I precursor Lhb1B2 - Arabidopsis thaliana >gi_16364_emb_CAA45790_ (X64460) photosystem II type I chlorophyll a /b binding protein [Arabidopsis thaliana] >gi_3128230 (AC004077) photosystem II type I chlorophyll a/b binding protein [Arabidopsis thaliana] >gi_3337371 (AC004481) photosystem II type I chlorophyll a/b binding protein [Arabidopsis thaliana]

Seq. No.	160657
Seq. ID	LIB3177-007-P1-K2-B4

Method	BLASTN
NCBI GI	g1033194
BLAST score	108
E value	5.0e-54
Match length	199
% identity	88
NCBI Description	Arabidopsis thaliana AT103 mRNA, complete cds

Seq. No.	160658
Seq. ID	LIB3177-007-P1-K2-B5
Method	BLASTX
NCBI GI	g132102
BLAST score	692
E value	3.0e-73
Match length	132
% identity	98
NCBI Description	RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN 2B PRECURSOR (RUBISCO SMALL SUBUNIT 2B) >gi_68061_pir__RKMUB2 ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain B2 precursor - Arabidopsis thaliana >gi_16194_emb_CAA32701_ (X14564) ribulose bisphosphate carboxylase [Arabidopsis thaliana]

Seq. No.	160659
Seq. ID	LIB3177-007-P1-K2-B6
Method	BLASTX
NCBI GI	g132090
BLAST score	150
E value	5.0e-10
Match length	58
% identity	59
NCBI Description	RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN 1B PRECURSOR (RUBISCO SMALL SUBUNIT 1B) >gi_68062_pir__RKMUB1 ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain B1 precursor - Arabidopsis thaliana >gi_16193_emb_CAA32700_ (X14564) ribulose bisphosphate carboxylase [Arabidopsis thaliana]

Seq. No.	160660
Seq. ID	LIB3177-007-P1-K2-B7
Method	BLASTN
NCBI GI	g4220634
BLAST score	237
E value	1.0e-130
Match length	261
% identity	98
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K9H21, complete sequence [Arabidopsis thaliana]

Seq. No.	160661
Seq. ID	LIB3177-007-P1-K2-B8
Method	BLASTN
NCBI GI	g2244901
BLAST score	193
E value	1.0e-104
Match length	193
% identity	100

NCBI Description	Arabidopsis thaliana DNA chromosome 4, ESSA I contig fragment No
Seq. No.	160662
Seq. ID	LIB3177-007-P1-K2-C1
Method	BLASTX
NCBI GI	g1345841
BLAST score	357
E value	4.0e-34
Match length	85
% identity	78
NCBI Description	CRUCIFERIN BNC2 PRECURSOR (11S GLOBULIN) (12S STORAGE PROTEIN) >gi_762920_emb_CAA41985_ (X59295) cruciferin storage protein [Brassica napus]
Seq. No.	160663
Seq. ID	LIB3177-007-P1-K2-C2
Method	BLASTX
NCBI GI	g1170028
BLAST score	585
E value	1.0e-60
Match length	131
% identity	88
NCBI Description	GLUTAMATE-1-SEMIALDEHYDE 2,1-AMINOMUTASE 1 PRECURSOR (GSA 1) (GLUTAMATE-1-SEMIALDEHYDE AMINOTRANSFERASE 1; (GSA-AT 1) >gi_454357 (U03773) glutamate-1-semialdehyde-2,1-aminomutase [Arabidopsis thaliana]
Seq. No.	160664
Seq. ID	LIB3177-007-P1-K2-C6
Method	BLASTN
NCBI GI	g4741961
BLAST score	75
E value	4.0e-34
Match length	167
% identity	87
NCBI Description	Arabidopsis thaliana PsbS protein (PsbS) mRNA, complete cds
Seq. No.	160665
Seq. ID	LIB3177-007-P1-K2-C7
Method	BLASTX
NCBI GI	g1213594
BLAST score	625
E value	2.0e-65
Match length	128
% identity	95
NCBI Description	(X93080) responsible for fatty acid elo[illegible]on from C28 to C30 [Arabidopsis thaliana] >gi_165[illegible]J40849) CER2 gene product [Arabidopsis thaliana] >gi[illegible]20539_emb_CAA23012_ (AL035356) CER2 [Arabidopsis thaliana]
Seq. No.	160666
Seq. ID	LIB3177-007-P1-K2-C9
Method	BLASTN
NCBI GI	g4220636
BLAST score	50

E value	2.0e-19
Match length	163
% identity	83
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MFB16, complete sequence [Arabidopsis thaliana]

Seq. No.	160667
Seq. ID	LIB3177-007-P1-K2-D1
Method	BLASTX
NCBI GI	g4741966
BLAST score	211
E value	3.0e-17
Match length	80
% identity	60
NCBI Description	(AF134133) Lil3 protein [Arabidopsis thaliana]

Seq. No.	160668
Seq. ID	LIB3177-007-P1-K2-D11
Method	BLASTX
NCBI GI	g2832674
BLAST score	513
E value	4.0e-59
Match length	134
% identity	94
NCBI Description	(AL021712) fibrillin precursor-like protein [Arabidopsis thaliana]

Seq. No.	160669
Seq. ID	LIB3177-007-P1-K2-D12
Method	BLASTN
NCBI GI	g4757402
BLAST score	392
E value	0.0e+00
Match length	428
% identity	98
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MIG5, complete sequence

Seq. No.	160670
Seq. ID	LIB3177-007-P1-K2-D2
Method	BLASTX
NCBI GI	g1765899
BLAST score	582
E value	2.0e-60
Match length	110
% identity	100
NCBI Description	(Y07917) Spot 3 protein [Arabidopsis thaliana] >gi_1839244 (U86700) EGF receptor like protein [Arabidopsis thaliana]

Seq. No.	160671
Seq. ID	LIB3177-007-P1-K2-D3
Method	BLASTN
NCBI GI	g4519195
BLAST score	155
E value	7.0e-82
Match length	266
% identity	95

NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MQC12, complete sequence
Seq. No.	160672
Seq. ID	LIB3177-007-P1-K2-D4
Method	BLASTX
NCBI GI	g4337175
BLAST score	560
E value	1.0e-57
Match length	131
% identity	85
NCBI Description	(AC006416) ESTs gb_T20589, gb_T04648, gb_AA597906, gb_T04111, gb_R84180, gb_R65428, gb_T44439, gb_T76570, gb_R90004, gb_T45020, gb_T42457, gb_T20921, gb_AA042762 and gb_AA720210 come from this gene. [Arabidopsis thaliana]
Seq. No.	160673
Seq. ID	LIB3177-007-P1-K2-D6
Method	BLASTX
NCBI GI	g4741962
BLAST score	465
E value	1.0e-46
Match length	134
% identity	54
NCBI Description	(AF134131) PsbS protein [Arabidopsis thaliana]
Seq. No.	160674
Seq. ID	LIB3177-007-P1-K2-D7
Method	BLASTN
NCBI GI	g4741961
BLAST score	54
E value	1.0e-21
Match length	130
% identity	85
NCBI Description	Arabidopsis thaliana PsbS protein (PsbS) mRNA, complete cds
Seq. No.	160675
Seq. ID	LIB3177-007-P1-K2-E10
Method	BLASTN
NCBI GI	g2182286
BLAST score	254
E value	1.0e-141
Match length	282
% identity	98
NCBI Description	Sequence of BAC F20P5 from Arabidopsis thaliana chromosome 1, complete sequence [Arabidopsis thaliana]
Seq. No.	160676
Seq. ID	LIB3177-007-P1-K2-E12
Method	BLASTN
NCBI GI	g2264320
BLAST score	37
E value	1.0e-11
Match length	145
% identity	27
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MXI10, complete sequence [Arabidopsis thaliana]

Seq. No.	160677
Seq. ID	LIB3177-007-P1-K2-E2
Method	BLASTN
NCBI GI	g3927822
BLAST score	58
E value	2.0e-24
Match length	118
% identity	94
NCBI Description	Arabidopsis thaliana chromosome II BAC F8N16 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	160678
Seq. ID	LIB3177-007-P1-K2-E3
Method	BLASTN
NCBI GI	g1694707
BLAST score	113
E value	5.0e-57
Match length	137
% identity	96
NCBI Description	A.thaliana mRNA, expressed sequence tag, 946 bp >gi_2511593_emb_Y13694.1_ATY13694 Arabidopsis thaliana mRNA for proteasome subunit prcd

Seq. No.	160679
Seq. ID	LIB3177-007-P1-K2-E4
Method	BLASTX
NCBI GI	g115385
BLAST score	303
E value	5.0e-28
Match length	72
% identity	79
NCBI Description	CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR (CAB-4) (LHCP) >gi_166646 (M63931) light-harvesting chlorophyll a/b binding protein [Arabidopsis thaliana]

Seq. No.	160680
Seq. ID	LIB3177-007-P1-K2-E5
Method	BLASTX
NCBI GI	g2119848
BLAST score	639
E value	6.0e-67
Match length	118
% identity	100
NCBI Description	chlorophyll a/b-binding protein type I precursor Lhb1B1 - Arabidopsis thaliana >gi_16366_emb_CAA45789_ (X64459) photosystem II type I chlorophyll a /b binding protein [Arabidopsis thaliana] >gi_3128229 (AC004077) putative photosystem II type I chlorophyll a/b binding protein [Arabidopsis thaliana] >gi_3337372 (AC004481) putative photosystem II type I chlorophyll a/b binding protein [Arabidopsis thaliana]

Seq. No.	160681
Seq. ID	LIB3177-007-P1-K2-E7
Method	BLASTX
NCBI GI	g4191778

BLAST score	563
E value	4.0e-58
Match length	128
% identity	88
NCBI Description	(AC005917) putative nucleosome assembly protein I [Arabidopsis thaliana]

Seq. No.	160682
Seq. ID	LIB3177-007-P1-K2-F1
Method	BLASTN
NCBI GI	g4467094
BLAST score	209
E value	1.0e-114
Match length	217
% identity	99
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F20D10 (ESSA project)

Seq. No.	160683
Seq. ID	LIB3177-007-P1-K2-F12
Method	BLASTX
NCBI GI	g282865
BLAST score	275
E value	1.0e-24
Match length	68
% identity	79
NCBI Description	chlorophyll a/b-binding protein - Arabidopsis thaliana >gi_16207_emb_CAA39534_ (X56062) chlorophyll A/B-binding protein [Arabidopsis thaliana] >gi_166644 (M85150) chlorophyll a/b-binding protein [Arabidopsis thaliana] >gi_4678304_emb_CAB41095.1_ (AL049655) chlorophyll a/b-binding protein [Arabidopsis thaliana]

Seq. No.	160684
Seq. ID	LIB3177-007-P1-K2-F2
Method	BLASTX
NCBI GI	g3219858
BLAST score	447
E value	1.0e-44
Match length	87
% identity	99
NCBI Description	DNA-DIRECTED RNA POLYMERASE II 13.6 KD POLYPEPTIDE >gi_2129724_pir__S71204 RNA polymerase II 13.6 kDa chain - Arabidopsis thaliana >gi_881501 (U28048) RNA polymerase II 13.6 kDa subunit [Arabidopsis thaliana] >gi_4678938_emb_CAB41329.1_ (AL049711) DNA-directed RNA polymerase II 13.6K chain [Arabidopsis thaliana]

Seq. No.	160685
Seq. ID	LIB3177-007-P1-K2-F3
Method	BLASTN
NCBI GI	g4056476
BLAST score	144
E value	4.0e-75
Match length	417
% identity	100
NCBI Description	Arabidopsis thaliana chromosome II BAC F3G5 genomic

sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	160686
Seq. ID	LIB3177-007-P1-K2-F4
Method	BLASTX
NCBI GI	g2062167
BLAST score	313
E value	1.0e-28
Match length	90
% identity	63
NCBI Description	(AC001645) Proline-rich protein APG isolog [Arabidopsis thaliana]

Seq. No.	160687
Seq. ID	LIB3177-007-P1-K2-F5
Method	BLASTN
NCBI GI	g3241917
BLAST score	120
E value	7.0e-61
Match length	368
% identity	95
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K19B1, complete sequence [Arabidopsis thaliana]

Seq. No.	160688
Seq. ID	LIB3177-007-P1-K2-F6
Method	BLASTX
NCBI GI	g2199574
BLAST score	382
E value	3.0e-37
Match length	76
% identity	96
NCBI Description	(AF004293) aquaporin [Brassica rapa]

Seq. No.	160689
Seq. ID	LIB3177-007-P1-K2-F9
Method	BLASTX
NCBI GI	g3522956
BLAST score	339
E value	5.0e-32
Match length	98
% identity	69
NCBI Description	(AC004411) putative pectinacetylesterase precursor [Arabidopsis thaliana]

Seq. No.	160690
Seq. ID	LIB3177-007-P1-K2-G11
Method	BLASTX
NCBI GI	g4218123
BLAST score	450
E value	8.0e-45
Match length	142
% identity	67
NCBI Description	(AL035353) photosystem I subunit PSI-E-like protein [Arabidopsis thaliana]

Seq. No.	160691

Seq. ID	LIB3177-007-P1-K2-G12
Method	BLASTN
NCBI GI	g3341671
BLAST score	198
E value	1.0e-107
Match length	363
% identity	93
NCBI Description	Arabidopsis thaliana chromosome II BAC F16B22 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	160692
Seq. ID	LIB3177-007-P1-K2-G2
Method	BLASTX
NCBI GI	g2746335
BLAST score	180
E value	3.0e-13
Match length	52
% identity	58
NCBI Description	(AF037205) RING zinc finger protein [Mus musculus]

Seq. No.	160693
Seq. ID	LIB3177-007-P1-K2-G3
Method	BLASTX
NCBI GI	g2911085
BLAST score	560
E value	1.0e-57
Match length	143
% identity	85
NCBI Description	(AL021960) photosystem II oxygen-evolving complex protein 3-like [Arabidopsis thaliana] >gi_3402748_emb_CAA20194.1_ (AL031187) photosystem II oxygen-evolving complex protein 3 - like [Arabidopsis thaliana]

Seq. No.	160694
Seq. ID	LIB3177-007-P1-K2-G4
Method	BLASTX
NCBI GI	g2911085
BLAST score	526
E value	1.0e-53
Match length	144
% identity	80
NCBI Description	(AL021960) photosystem II oxygen-evolving complex protein 3-like [Arabidopsis thaliana] >gi_3402748_emb_CAA20194.1_ (AL031187) photosystem II oxygen-evolving complex protein 3 - like [Arabidopsis thaliana]

Seq. No.	160695
Seq. ID	LIB3177-007-P1-K2-G5
Method	BLASTX
NCBI GI	g1710424
BLAST score	663
E value	9.0e-70
Match length	149
% identity	90
NCBI Description	50S RIBOSOMAL PROTEIN L21, CHLOROPLAST PRECURSOR (CL21) >gi_2129718_pir__S71282 ribosomal protein L21 - Arabidopsis thaliana >gi_1149573_emb_CAA89887_ (Z49787) chloroplast

ribosomal large subunit protein L21 [Arabidopsis thaliana]

Seq. No.	160696
Seq. ID	LIB3177-007-P1-K2-G6
Method	BLASTN
NCBI GI	g4240115
BLAST score	154
E value	1.0e-81
Match length	170
% identity	98
NCBI Description	Arabidopsis thaliana mRNA for NADH-cytochrome b5 reductase, complete cds

Seq. No.	160697
Seq. ID	LIB3177-007-P1-K2-G7
Method	BLASTN
NCBI GI	g1149572
BLAST score	103
E value	7.0e-51
Match length	163
% identity	91
NCBI Description	A.thaliana rpl21 mRNA for chloroplast ribosomal large subunit protein L21

Seq. No.	160698
Seq. ID	LIB3177-007-P1-K2-G9
Method	BLASTX
NCBI GI	g4741962
BLAST score	503
E value	5.0e-51
Match length	141
% identity	56
NCBI Description	(AF134131) PsbS protein [Arabidopsis thaliana]

Seq. No.	160699
Seq. ID	LIB3177-007-P1-K2-H1
Method	BLASTX
NCBI GI	g4538963
BLAST score	516
E value	1.0e-52
Match length	129
% identity	61
NCBI Description	(AL049488) chlorophyll a/b-binding protein-like [Arabidopsis thaliana] >gi_4741958_gb_AAD28776.1_AF134129_1 (AF134129) Lhcb5 protein [Arabidopsis thaliana]

Seq. No.	160700
Seq. ID	LIB3177-007-P1-K2-H10
Method	BLASTX
NCBI GI	g4455235
BLAST score	215
E value	1.0e-17
Match length	64
% identity	70
NCBI Description	(AL035523) PROTEIN TRANSPORT PROTEIN SEC61 GAMMA SUBUNIT-like [Arabidopsis thaliana]

Seq. No.	160701
Seq. ID	LIB3177-007-P1-K2-H2
Method	BLASTX
NCBI GI	g99681
BLAST score	184
E value	7.0e-14
Match length	52
% identity	39
NCBI Description	cold-regulated protein cor47 - Arabidopsis thaliana (fragment) >gi_388259_emb_CAA42483_ (X59814) Cold and ABA regulated gene [Arabidopsis thaliana]

Seq. No.	160702
Seq. ID	LIB3177-007-P1-K2-H4
Method	BLASTX
NCBI GI	g132110
BLAST score	689
E value	7.0e-73
Match length	133
% identity	97
NCBI Description	RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN 3B PRECURSOR (RUBISCO SMALL SUBUNIT 3B) >gi_68060_pir__RKMUB3 ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain B3 precursor - Arabidopsis thaliana >gi_16195_emb_CAA32702_ (X14564) ribulose bisphosphate carboxylase [Arabidopsis thaliana]

Seq. No.	160703
Seq. ID	LIB3177-008-P1-K1-B1
Method	BLASTN
NCBI GI	g4538918
BLAST score	105
E value	6.0e-52
Match length	349
% identity	82
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F20B18 (ESSA project)

Seq. No.	160704
Seq. ID	LIB3177-008-P1-K1-B10
Method	BLASTX
NCBI GI	g2062164
BLAST score	172
E value	3.0e-12
Match length	81
% identity	51
NCBI Description	(AC001645) jasmonate inducible protein isolog [Arabidopsis thaliana]

Seq. No.	160705
Seq. ID	LIB3177-008-P1-K1-B11
Method	BLASTX
NCBI GI	g548355
BLAST score	316
E value	2.0e-29
Match length	97
% identity	67

NCBI Description	NITRATE REDUCTASE 1 (NR1) >gi_486751_pir__S35228 nitrate reductase (NADH) (EC 1.6.6.1) 1 - Arabidopsis thaliana >gi_22757_emb_CAA79494_ (Z19050) nitrate reductase [Arabidopsis thaliana] >gi_448286_prf__1916406A nitrate reductase [Arabidopsis thaliana]
Seq. No.	160706
Seq. ID	LIB3177-008-P1-K1-B2
Method	BLASTX
NCBI GI	g115783
BLAST score	311
E value	1.0e-28
Match length	111
% identity	62
NCBI Description	CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR (CAB-140) (LHCP) >gi_16376_emb_CAA27543_ (X03909) chlorophyll a/b binding protein (LHCP AB 140) [Arabidopsis thaliana]
Seq. No.	160707
Seq. ID	LIB3177-008-P1-K1-B8
Method	BLASTX
NCBI GI	g1769905
BLAST score	187
E value	4.0e-14
Match length	85
% identity	51
NCBI Description	(X98108) 23 kDa polypeptide of oxygen-evolving comlex (OEC) [Arabidopsis thaliana]
Seq. No.	160708
Seq. ID	LIB3177-008-P1-K1-C1
Method	BLASTX
NCBI GI	g2506443
BLAST score	250
E value	2.0e-21
Match length	121
% identity	51
NCBI Description	GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE A PRECURSOR, CHLOROPLAST >gi_2117520_pir__JQ1285 glyceraldehyde-3-phosphate dehydrogenase (NADP+) (phosphorylating) (EC 1.2.1.13) A precursor, chloroplast - Arabidopsis thaliana >gi_166704 (M64117) glyceraldehyde 3-phosphate dehydrogenase [Arabidopsis thaliana] >gi_1402885_emb_CAA66816_ (X98130) glyceraldehyde-3-phosphate dehydrogenase (NADP+) (phosphorylating) [Arabidopsis thaliana]
Seq. No.	160709
Seq. ID	LIB3177-008-P1-K1-C2
Method	BLASTX
NCBI GI	g1420852
BLAST score	389
E value	1.0e-37
Match length	138
% identity	58
NCBI Description	(X98877) CP47 [Spinacia oleracea]

Seq. No.	160710
Seq. ID	LIB3177-008-P1-K1-D1
Method	BLASTN
NCBI GI	g2281081
BLAST score	78
E value	7.0e-36
Match length	202
% identity	85
NCBI Description	Arabidopsis thaliana chromosome II BAC F18O19 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	160711
Seq. ID	LIB3177-008-P1-K1-D2
Method	BLASTN
NCBI GI	g3882354
BLAST score	133
E value	1.0e-68
Match length	293
% identity	86
NCBI Description	Arabidopsis thaliana 12-oxophytodienoate reductase OPR1 and 12-oxophytodienoate reductase OPR2 genes, complete cds

Seq. No.	160712
Seq. ID	LIB3177-008-P1-K1-D4
Method	BLASTX
NCBI GI	g4539292
BLAST score	362
E value	1.0e-34
Match length	92
% identity	74
NCBI Description	(AL049480) putative ribosomal protein S10 [Arabidopsis thaliana]

Seq. No.	160713
Seq. ID	LIB3177-008-P1-K1-D7
Method	BLASTX
NCBI GI	g4455152
BLAST score	255
E value	3.0e-22
Match length	67
% identity	79
NCBI Description	(AL022140) putative protein (fragment) [Arabidopsis thaliana]

Seq. No.	160714
Seq. ID	LIB3177-008-P1-K1-E2
Method	BLASTN
NCBI GI	g2062153
BLAST score	53
E value	6.0e-21
Match length	212
% identity	75
NCBI Description	Arabidopsis thaliana chromosome III BAC T02O04 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	160715

Seq. ID	LIB3177-008-P1-K1-E3
Method	BLASTN
NCBI GI	g3873174
BLAST score	68
E value	8.0e-30
Match length	296
% identity	81
NCBI Description	Genomic sequence for Arabidopsis thaliana BAC F14N23, complete sequence [Arabidopsis thaliana]

Seq. No.	160716
Seq. ID	LIB3177-008-P1-K1-E4
Method	BLASTX
NCBI GI	g3367517
BLAST score	180
E value	4.0e-13
Match length	91
% identity	45
NCBI Description	(AC004392) Similar to F4I1.26 putative beta-glucosidase gi_3128187 from A. thaliana BAC gb_AC004521. ESTs gb_N97083, gb_F19868 and gb_F15482 come from this gene. [Arabidopsis thaliana]

Seq. No.	160717
Seq. ID	LIB3177-008-P1-K1-E5
Method	BLASTX
NCBI GI	g1790922
BLAST score	148
E value	1.0e-09
Match length	88
% identity	45
NCBI Description	(U76670) AtDMC1 [Arabidopsis thaliana]

Seq. No.	160718
Seq. ID	LIB3177-008-P1-K1-E6
Method	BLASTX
NCBI GI	g3219164
BLAST score	177
E value	4.0e-13
Match length	76
% identity	61
NCBI Description	(AB006210) glutamine amidotransferase/cyclase [Arabidopsis thaliana]

Seq. No.	160719
Seq. ID	LIB3177-008-P1-K1-F1
Method	BLASTX
NCBI GI	g124224
BLAST score	295
E value	1.0e-26
Match length	87
% identity	68
NCBI Description	INITIATION FACTOR 5A-1 (EIF-5A) (EIF-4D) >gi_100345_pir__S21060 translation initiation factor eIF-5A - common tobacco >gi_19887_emb_CAA45105_ (X63543) eukaryotic initiatin factor 5A (3) [Nicotiana tabacum]

Seq. No.	160720
Seq. ID	LIB3177-008-P1-K1-F10
Method	BLASTX
NCBI GI	g2583125
BLAST score	203
E value	6.0e-16
Match length	115
% identity	37
NCBI Description	(AC002387) putative transketolase precursor [Arabidopsis thaliana]

Seq. No.	160721
Seq. ID	LIB3177-008-P1-K1-F3
Method	BLASTX
NCBI GI	g4585873
BLAST score	201
E value	1.0e-15
Match length	98
% identity	50
NCBI Description	(AC005850) Putative protein kinase [Arabidopsis thaliana]

Seq. No.	160722
Seq. ID	LIB3177-008-P1-K1-F4
Method	BLASTX
NCBI GI	g115767
BLAST score	269
E value	1.0e-23
Match length	134
% identity	48
NCBI Description	CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR (CAB-165/180) (LHCP) >gi_81603_pir__A29280 chlorophyll a/b-binding protein ab165 - Arabidopsis thaliana >gi_16368_emb_CAA27540_ (X03907) chlorophyll a/b binding protein (LHCP AB 65) [Arabidopsis thaliana] >gi_16372_emb_CAA27541_ (X03908) chlorophyll a/b binding protein (LHCP AB 180) [Arabidopsis thaliana]

Seq. No.	160723
Seq. ID	LIB3177-008-P1-K1-F5
Method	BLASTN
NCBI GI	g4371278
BLAST score	102
E value	5.0e-50
Match length	320
% identity	87
NCBI Description	Arabidopsis thaliana chromosome II BAC T2N18 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	160724
Seq. ID	LIB3177-008-P1-K1-F7
Method	BLASTX
NCBI GI	g1350956
BLAST score	248
E value	4.0e-21
Match length	97
% identity	55
NCBI Description	40S RIBOSOMAL PROTEIN S20 (S22)

Seq. No.	160725
Seq. ID	LIB3177-008-P1-K1-F8
Method	BLASTX
NCBI GI	g2129672
BLAST score	200
E value	1.0e-15
Match length	80
% identity	54
NCBI Description	photosystem II reaction center protein, 6.1K - Arabidopsis thaliana >gi_950023_emb_CAA62296_ (X90769) component of 6.1 kDa polypeptide of photosystem II reaction center [Arabidopsis thaliana]

Seq. No.	160726
Seq. ID	LIB3177-008-P1-K1-G10
Method	BLASTX
NCBI GI	g99735
BLAST score	241
E value	3.0e-20
Match length	124
% identity	42
NCBI Description	L-ascorbate peroxidase (EC 1.11.1.11) precursor - Arabidopsis thaliana (fragment)

Seq. No.	160727
Seq. ID	LIB3177-008-P1-K1-G2
Method	BLASTX
NCBI GI	g3914658
BLAST score	218
E value	9.0e-18
Match length	98
% identity	37
NCBI Description	50S RIBOSOMAL PROTEIN L24, CHLOROPLAST PRECURSOR >gi_1694974_emb_CAA70851_ (Y09635) plastid ribosomal protein [Arabidopsis thaliana]

Seq. No.	160728
Seq. ID	LIB3177-008-P1-K1-G3
Method	BLASTX
NCBI GI	g4210334
BLAST score	363
E value	1.0e-34
Match length	124
% identity	64
NCBI Description	(AJ223804) 2-oxoglutarate dehydrogenase, E3 subunit [Arabidopsis thaliana]

Seq. No.	160729
Seq. ID	LIB3177-008-P1-K1-G7
Method	BLASTX
NCBI GI	g4008010
BLAST score	305
E value	8.0e-28
Match length	104
% identity	65
NCBI Description	(AF084036) receptor-like protein kinase [Arabidopsis

thaliana]

Seq. No.	160730
Seq. ID	LIB3177-008-P1-K1-H2
Method	BLASTN
NCBI GI	g2924729
BLAST score	49
E value	2.0e-18
Match length	117
% identity	85
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MNA5, complete sequence [Arabidopsis thaliana]

Seq. No.	160731
Seq. ID	LIB3177-008-P1-K2-A3
Method	BLASTX
NCBI GI	g3953473
BLAST score	656
E value	6.0e-69
Match length	134
% identity	99
NCBI Description	(AC002328) F22O2.18 [Arabidopsis thaliana]

Seq. No.	160732
Seq. ID	LIB3177-008-P1-K2-A4
Method	BLASTN
NCBI GI	g2924729
BLAST score	110
E value	4.0e-55
Match length	202
% identity	72
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MNA5, complete sequence [Arabidopsis thaliana]

Seq. No.	160733
Seq. ID	LIB3177-008-P1-K2-A7
Method	BLASTX
NCBI GI	g4741952
BLAST score	566
E value	2.0e-58
Match length	113
% identity	70
NCBI Description	(AF134126) Lhcb3 protein [Arabidopsis thaliana]

Seq. No.	160734
Seq. ID	LIB3177-008-P1-K2-B1
Method	BLASTX
NCBI GI	g4538930
BLAST score	627
E value	1.0e-65
Match length	139
% identity	90
NCBI Description	(AL049483) putative peroxidase [Arabidopsis thaliana]

Seq. No.	160735
Seq. ID	LIB3177-008-P1-K2-B11
Method	BLASTX

NCBI GI	g548355
BLAST score	136
E value	2.0e-76
Match length	147
% identity	100
NCBI Description	NITRATE REDUCTASE 1 (NR1) >gi_486751_pir__S35228 nitrate reductase (NADH) (EC 1.6.6.1) 1 - Arabidopsis thaliana >gi_22757_emb_CAA79494_ (Z19050) nitrate reductase [Arabidopsis thaliana] >gi_448286_prf__1916406A nitrate reductase [Arabidopsis thaliana]

Seq. No.	160736
Seq. ID	LIB3177-008-P1-K2-B12
Method	BLASTN
NCBI GI	g3449330
BLAST score	98
E value	1.0e-47
Match length	253
% identity	88
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MDJ14, complete sequence [Arabidopsis thaliana]

Seq. No.	160737
Seq. ID	LIB3177-008-P1-K2-B3
Method	BLASTX
NCBI GI	g1710585
BLAST score	103
E value	3.0e-13
Match length	74
% identity	56
NCBI Description	60S ACIDIC RIBOSOMAL PROTEIN P0 >gi_1143507_emb_CAA63786_ (X93587) P0 ribosomal protein [Lupinus luteus]

Seq. No.	160738
Seq. ID	LIB3177-008-P1-K2-B4
Method	BLASTX
NCBI GI	g4585900
BLAST score	464
E value	2.0e-46
Match length	125
% identity	76
NCBI Description	(AC007133) putative histone H2A [Arabidopsis thaliana]

Seq. No.	160739
Seq. ID	LIB3177-008-P1-K2-B5
Method	BLASTX
NCBI GI	g136636
BLAST score	330
E value	9.0e-31
Match length	62
% identity	98
NCBI Description	UBIQUITIN-CONJUGATING ENZYME E2-17 KD 1 (UBIQUITIN-PROTEIN LIGASE 1) (UBIQUITIN CARRIER PROTEIN 1) >gi_1076424_pir__S43781 ubiquitin-conjugating enzyme UBC1 - Arabidopsis thaliana >gi_442594_pdb_1AAK_ Ubiquitin Conjugating Enzyme (E.C.6.3.2.19) >gi_2981894_pdb_2AAK_ Ubiquitin Conjugating Enzyme From Arabidopsis Thaliana

>gi_166924 (M62721) ubiquitin carrier protein [Arabidopsis thaliana] >gi_431260 (L19351) ubiquitin conjugating enzyme [Arabidopsis thaliana]

Seq. No.	160740
Seq. ID	LIB3177-008-P1-K2-B6
Method	BLASTX
NCBI GI	g1769905
BLAST score	812
E value	3.0e-87
Match length	153
% identity	100
NCBI Description	(X98108) 23 kDa polypeptide of oxygen-evolving comlex (OEC) [Arabidopsis thaliana]

Seq. No.	160741
Seq. ID	LIB3177-008-P1-K2-B8
Method	BLASTX
NCBI GI	g1769905
BLAST score	469
E value	5.0e-47
Match length	134
% identity	69
NCBI Description	(X98108) 23 kDa polypeptide of oxygen-evolving comlex (OEC) [Arabidopsis thaliana]

Seq. No.	160742
Seq. ID	LIB3177-008-P1-K2-C1
Method	BLASTX
NCBI GI	g2506443
BLAST score	754
E value	2.0e-80
Match length	148
% identity	100
NCBI Description	GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE A PRECURSOR, CHLOROPLAST >gi_2117520_pir__JQ1285 glyceraldehyde-3-phosphate dehydrogenase (NADP+) (phosphorylating) (EC 1.2.1.13) A precursor, chloroplast - Arabidopsis thaliana >gi_166704 (M64117) glyceraldehyde 3-phosphate dehydrogenase [Arabidopsis thaliana] >gi_1402885_emb_CAA66816_ (X98130) glyceraldehyde-3-phosphate dehydrogenase (NADP+) (phosphorylating) [Arabidopsis thaliana]

Seq. No.	160743
Seq. ID	LIB3177-008-P1-K2-C2
Method	BLASTX
NCBI GI	g131276
BLAST score	783
E value	7.0e-84
Match length	150
% identity	99
NCBI Description	PHOTOSYSTEM II P680 CHLOROPHYLL A APOPROTEIN (CP-47 PROTEIN) >gi_72704_pir__QJNT6A photosystem II chlorophyll a-binding protein psbB - common tobacco chloroplast >gi_11856_emb_CAA77373_ (Z00044) PSII 47kD protein [Nicotiana tabacum] >gi_225224_prf__1211235BF photosystem

II P680 apoprotein [Nicotiana tabacum]

Seq. No.	160744
Seq. ID	LIB3177-008-P1-K2-C6
Method	BLASTX
NCBI GI	g115767
BLAST score	52
E value	2.0e-44
Match length	106
% identity	90
NCBI Description	CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR (CAB-165/180) (LHCP) >gi_81603_pir__A29280 chlorophyll a/b-binding protein ab165 - Arabidopsis thaliana >gi_16368_emb_CAA27540_ (X03907) chlorophyll a/b binding protein (LHCP AB 65) [Arabidopsis thaliana] >gi_16372_emb_CAA27541_ (X03908) chlorophyll a/b binding protein (LHCP AB 180) [Arabidopsis thaliana]

Seq. No.	160745
Seq. ID	LIB3177-008-P1-K2-C9
Method	BLASTX
NCBI GI	g3789911
BLAST score	291
E value	4.0e-26
Match length	114
% identity	49
NCBI Description	(AF081802) developmental protein DG1118 [Dictyostelium discoideum]

Seq. No.	160746
Seq. ID	LIB3177-008-P1-K2-D11
Method	BLASTN
NCBI GI	g4335744
BLAST score	69
E value	2.0e-30
Match length	208
% identity	86
NCBI Description	Arabidopsis thaliana chromosome II BAC T4M8 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	160747
Seq. ID	LIB3177-008-P1-K2-D12
Method	BLASTX
NCBI GI	g2129558
BLAST score	140
E value	4.0e-09
Match length	28
% identity	96
NCBI Description	calmodulin isoform 4 - Arabidopsis thaliana (fragment)

Seq. No.	160748
Seq. ID	LIB3177-008-P1-K2-D2
Method	BLASTN
NCBI GI	g3882354
BLAST score	396
E value	0.0e+00
Match length	440

% identity	99
NCBI Description	Arabidopsis thaliana 12-oxophytodienoate reductase OPR1 and 12-oxophytodienoate reductase OPR2 genes, complete cds

Seq. No.	160749
Seq. ID	LIB3177-008-P1-K2-D4
Method	BLASTX
NCBI GI	g4539292
BLAST score	510
E value	8.0e-52
Match length	96
% identity	99
NCBI Description	(AL049480) putative ribosomal protein S10 [Arabidopsis thaliana]

Seq. No.	160750
Seq. ID	LIB3177-008-P1-K2-D6
Method	BLASTX
NCBI GI	g3123271
BLAST score	461
E value	3.0e-46
Match length	122
% identity	76
NCBI Description	40S RIBOSOMAL PROTEIN S6 >gi_2224751_emb_CAA74381_ (Y14052) ribosomal protein S6 [Arabidopsis thaliana]

Seq. No.	160751
Seq. ID	LIB3177-008-P1-K2-D7
Method	BLASTX
NCBI GI	g4455152
BLAST score	602
E value	1.0e-62
Match length	122
% identity	99
NCBI Description	(AL022140) putative protein (fragment) [Arabidopsis thaliana]

Seq. No.	160752
Seq. ID	LIB3177-008-P1-K2-E1
Method	BLASTN
NCBI GI	g2564046
BLAST score	167
E value	7.0e-89
Match length	448
% identity	98
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MGI19, complete sequence [Arabidopsis thaliana]

Seq. No.	160753
Seq. ID	LIB3177-008-P1-K2-E10
Method	BLASTX
NCBI GI	g3264757
BLAST score	414
E value	1.0e-40
Match length	124
% identity	62
NCBI Description	(AF071888) zeaxanthin epoxidase [Prunus armeniaca]

Seq. No.	160754
Seq. ID	LIB3177-008-P1-K2-E11
Method	BLASTN
NCBI GI	g4220627
BLAST score	47
E value	3.0e-17
Match length	286
% identity	4
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K20J1, complete sequence [Arabidopsis thaliana]

Seq. No.	160755
Seq. ID	LIB3177-008-P1-K2-E2
Method	BLASTX
NCBI GI	g2062161
BLAST score	354
E value	1.0e-57
Match length	117
% identity	53
NCBI Description	(AC001645) jasmonate inducible protein isolog [Arabidopsis thaliana]

Seq. No.	160756
Seq. ID	LIB3177-008-P1-K2-E3
Method	BLASTX
NCBI GI	g2982262
BLAST score	387
E value	2.0e-37
Match length	124
% identity	57
NCBI Description	(AF051214) probable glutathione S-transferase [Picea mariana]

Seq. No.	160757
Seq. ID	LIB3177-008-P1-K2-E5
Method	BLASTX
NCBI GI	g1790922
BLAST score	95
E value	4.0e-54
Match length	122
% identity	94
NCBI Description	(U76670) AtDMC1 [Arabidopsis thaliana]

Seq. No.	160758
Seq. ID	LIB3177-008-P1-K2-E8
Method	BLASTX
NCBI GI	g399013
BLAST score	498
E value	2.0e-50
Match length	105
% identity	95
NCBI Description	ADP,ATP CARRIER PROTEIN 1 PRECURSOR (ADP/ATP TRANSLOCASE 1) (ADENINE NUCLEOTIDE TRANSLOCATOR 1) (ANT 1) >gi_99658_pir__S21313 ADP,ATP carrier protein - Arabidopsis thaliana (fragment) >gi_16175_emb_CAA46518_ (X65549) adenylate translocator [Arabidopsis thaliana]

>gi_445607_prf__1909354A adenylate translocator [Arabidopsis thaliana]

Seq. No.	160759
Seq. ID	LIB3177-008-P1-K2-E9
Method	BLASTX
NCBI GI	g3763918
BLAST score	722
E value	1.0e-76
Match length	145
% identity	96
NCBI Description	(AC004450) putative isopropylmalate dehydratase [Arabidopsis thaliana]

Seq. No.	160760
Seq. ID	LIB3177-008-P1-K2-F1
Method	BLASTX
NCBI GI	g3024022
BLAST score	578
E value	8.0e-60
Match length	126
% identity	86
NCBI Description	INITIATION FACTOR 5A-5 (EIF-5A) (EIF-4D) >gi_2225885_dbj_BAA20879_ (AB004826) eukaryotic initiation factor 5A5 [Solanum tuberosum]

Seq. No.	160761
Seq. ID	LIB3177-008-P1-K2-F10
Method	BLASTX
NCBI GI	g2583125
BLAST score	733
E value	6.0e-78
Match length	152
% identity	89
NCBI Description	(AC002387) putative transketolase precursor [Arabidopsis thaliana]

Seq. No.	160762
Seq. ID	LIB3177-008-P1-K2-F11
Method	BLASTN
NCBI GI	g16470
BLAST score	59
E value	2.0e-24
Match length	103
% identity	89
NCBI Description	Arabidopsis thaliana mRNA for rubisco activase

Seq. No.	160763
Seq. ID	LIB3177-008-P1-K2-F12
Method	BLASTX
NCBI GI	g4741954
BLAST score	384
E value	2.0e-37
Match length	86
% identity	86
NCBI Description	(AF134127) Lhcb4.2 protein [Arabidopsis thaliana]

Seq. No.	160764
Seq. ID	LIB3177-008-P1-K2-F2
Method	BLASTX
NCBI GI	g416681
BLAST score	163
E value	4.0e-11
Match length	122
% identity	35
NCBI Description	ATP SYNTHASE DELTA CHAIN, CHLOROPLAST PRECURSOR >gi_280404_pir__S26198 H+-transporting ATP synthase (EC 3.6.1.34) delta chain precursor, chloroplast - common tobacco >gi_19787_emb_CAA45153_ (X63607) chloroplast ATP synthase (delta subunit) [Nicotiana tabacum]

Seq. No.	160765
Seq. ID	LIB3177-008-P1-K2-F3
Method	BLASTN
NCBI GI	g4235150
BLAST score	187
E value	1.0e-101
Match length	219
% identity	96
NCBI Description	Arabidopsis thaliana chromosome I BAC T25B24 genomic sequence, complete sequence

Seq. No.	160766
Seq. ID	LIB3177-008-P1-K2-F4
Method	BLASTX
NCBI GI	g115767
BLAST score	677
E value	2.0e-71
Match length	129
% identity	100
NCBI Description	CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR (CAB-165/180) (LHCP) >gi_81603_pir__A29280 chlorophyll a/b-binding protein ab165 - Arabidopsis thaliana >gi_16368_emb_CAA27540_ (X03907) chlorophyll a/b binding protein (LHCP AB 65) [Arabidopsis thaliana] >gi_16372_emb_CAA27541_ (X03908) chlorophyll a/b binding protein (LHCP AB 180) [Arabidopsis thaliana]

Seq. No.	160767
Seq. ID	LIB3177-008-P1-K2-F5
Method	BLASTN
NCBI GI	g4371278
BLAST score	342
E value	0.0e+00
Match length	446
% identity	99
NCBI Description	Arabidopsis thaliana chromosome II BAC T2N18 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	160768
Seq. ID	LIB3177-008-P1-K2-F6
Method	BLASTX
NCBI GI	g2062167
BLAST score	523

E value	2.0e-53
Match length	99
% identity	99
NCBI Description	(AC001645) Proline-rich protein APG isolog [Arabidopsis thaliana]

Seq. No.	160769
Seq. ID	LIB3177-008-P1-K2-F7
Method	BLASTX
NCBI GI	g1350956
BLAST score	351
E value	3.0e-39
Match length	113
% identity	81
NCBI Description	40S RIBOSOMAL PROTEIN S20 (S22)

Seq. No.	160770
Seq. ID	LIB3177-008-P1-K2-F8
Method	BLASTX
NCBI GI	g1946362
BLAST score	381
E value	1.0e-36
Match length	120
% identity	66
NCBI Description	(U93215) photosystem II reaction center 6.1KD protein [Arabidopsis thaliana]

Seq. No.	160771
Seq. ID	LIB3177-008-P1-K2-F9
Method	BLASTN
NCBI GI	g2264310
BLAST score	167
E value	7.0e-89
Match length	412
% identity	97
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MKP11, complete sequence [Arabidopsis thaliana]

Seq. No.	160772
Seq. ID	LIB3177-008-P1-K2-G10
Method	BLASTX
NCBI GI	g99735
BLAST score	652
E value	2.0e-68
Match length	124
% identity	100
NCBI Description	L-ascorbate peroxidase (EC 1.11.1.11) precursor - Arabidopsis thaliana (fragment)

Seq. No.	160773
Seq. ID	LIB3177-008-P1-K2-G11
Method	BLASTX
NCBI GI	g99735
BLAST score	120
E value	5.0e-13
Match length	51
% identity	69

NCBI Description	L-ascorbate peroxidase (EC 1.11.1.11) precursor - Arabidopsis thaliana (fragment)

Seq. No.	160774
Seq. ID	LIB3177-008-P1-K2-G3
Method	BLASTX
NCBI GI	g4210334
BLAST score	648
E value	5.0e-68
Match length	148
% identity	86
NCBI Description	(AJ223804) 2-oxoglutarate dehydrogenase, E3 subunit [Arabidopsis thaliana]

Seq. No.	160775
Seq. ID	LIB3177-008-P1-K2-G4
Method	BLASTX
NCBI GI	g285317
BLAST score	125
E value	7.0e-09
Match length	70
% identity	56
NCBI Description	dihydrolipoamide dehydrogenase (EC 1.8.1.4) - garden pea

Seq. No.	160776
Seq. ID	LIB3177-008-P1-K2-G7
Method	BLASTX
NCBI GI	g4008010
BLAST score	718
E value	3.0e-76
Match length	145
% identity	99
NCBI Description	(AF084036) receptor-like protein kinase [Arabidopsis thaliana]

Seq. No.	160777
Seq. ID	LIB3177-008-P1-K2-G8
Method	BLASTX
NCBI GI	g421826
BLAST score	507
E value	1.0e-51
Match length	135
% identity	76
NCBI Description	chlorophyll a/b-binding protein CP29 - Arabidopsis thaliana >gi_298036_emb_CAA50712_ (X71878) CP29 [Arabidopsis thaliana]

Seq. No.	160778
Seq. ID	LIB3177-008-P1-K2-H11
Method	BLASTN
NCBI GI	g4220640
BLAST score	128
E value	8.0e-66
Match length	199
% identity	90
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MPE11, complete sequence [Arabidopsis thaliana]

Seq. No.	160779
Seq. ID	LIB3177-008-P1-K2-H2
Method	BLASTN
NCBI GI	g2924729
BLAST score	297
E value	1.0e-166
Match length	354
% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MNA5, complete sequence [Arabidopsis thaliana]

Seq. No.	160780
Seq. ID	LIB3177-008-P1-K2-H3
Method	BLASTN
NCBI GI	g2924729
BLAST score	131
E value	1.0e-67
Match length	180
% identity	98
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MNA5, complete sequence [Arabidopsis thaliana]

Seq. No.	160781
Seq. ID	LIB3177-008-P1-K2-H4
Method	BLASTN
NCBI GI	g4586241
BLAST score	35
E value	5.0e-11
Match length	63
% identity	90
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone T20K18 (ESSA project)

Seq. No.	160782
Seq. ID	LIB3177-008-P1-K2-H5
Method	BLASTN
NCBI GI	g4490324
BLAST score	209
E value	1.0e-114
Match length	345
% identity	98
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone T9A14 (ESSA project)

Seq. No.	160783
Seq. ID	LIB3177-008-P1-K2-H6
Method	BLASTN
NCBI GI	g4159709
BLAST score	373
E value	0.0e+00
Match length	414
% identity	99
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MLN21, complete sequence

Seq. No.	160784

Seq. ID	LIB3177-008-P1-K2-H7
Method	BLASTN
NCBI GI	g166829
BLAST score	214
E value	1.0e-117
Match length	294
% identity	93
NCBI Description	Arabidopsis thaliana proteasome (PSM30) gene, complete cds

Seq. No.	160785
Seq. ID	LIB3177-008-P1-K2-H9
Method	BLASTX
NCBI GI	g4538928
BLAST score	162
E value	5.0e-11
Match length	42
% identity	79
NCBI Description	(AL049483) putative protein [Arabidopsis thaliana]

Seq. No.	160786
Seq. ID	LIB3177-009-P1-K2-A1
Method	BLASTX
NCBI GI	g2119846
BLAST score	442
E value	3.0e-44
Match length	83
% identity	100
NCBI Description	chlorophyll a/b-binding protein type I precursor Lhb1B2 - Arabidopsis thaliana >gi_16364_emb_CAA45790_ (X64460) photosystem II type I chlorophyll a /b binding protein [Arabidopsis thaliana] >gi_3128230 (AC004077) photosystem II type I chlorophyll a/b binding protein [Arabidopsis thaliana] >gi_3337371 (AC004481) photosystem II type I chlorophyll a/b binding protein [Arabidopsis thaliana]

Seq. No.	160787
Seq. ID	LIB3177-009-P1-K2-A2
Method	BLASTX
NCBI GI	g115767
BLAST score	488
E value	2.0e-49
Match length	93
% identity	100
NCBI Description	CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR (CAB-165/180) (LHCP) >gi_81603_pir__A29280 chlorophyll a/b-binding protein ab165 - Arabidopsis thaliana >gi_16368_emb_CAA27540_ (X03907) chlorophyll a/b binding protein (LHCP AB 65) [Arabidopsis thaliana] >gi_16372_emb_CAA27541_ (X03908) chlorophyll a/b binding protein (LHCP AB 180) [Arabidopsis thaliana]

Seq. No.	160788
Seq. ID	LIB3177-009-P1-K2-A4
Method	BLASTX
NCBI GI	g3702332
BLAST score	239
E value	3.0e-20

Match length	89
% identity	56
NCBI Description	(AC005397) unknown protein [Arabidopsis thaliana]

Seq. No.	160789
Seq. ID	LIB3177-009-P1-K2-A6
Method	BLASTN
NCBI GI	g3478699
BLAST score	79
E value	1.0e-36
Match length	123
% identity	92
NCBI Description	Arabidopsis thaliana AFT protein (AFT) mRNA, complete cds

Seq. No.	160790
Seq. ID	LIB3177-009-P1-K2-B1
Method	BLASTN
NCBI GI	g2351061
BLAST score	75
E value	1.0e-34
Match length	115
% identity	91
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MAF19, complete sequence [Arabidopsis thaliana]

Seq. No.	160791
Seq. ID	LIB3177-009-P1-K2-B2
Method	BLASTX
NCBI GI	g4454036
BLAST score	695
E value	1.0e-73
Match length	127
% identity	100
NCBI Description	(AL035394) putative major latex protein [Arabidopsis thaliana]

Seq. No.	160792
Seq. ID	LIB3177-009-P1-K2-B5
Method	BLASTX
NCBI GI	g2795806
BLAST score	415
E value	7.0e-41
Match length	104
% identity	82
NCBI Description	(AC003674) unknown protein [Arabidopsis thaliana]

Seq. No.	160793
Seq. ID	LIB3177-009-P1-K2-B7
Method	BLASTN
NCBI GI	g3426033
BLAST score	57
E value	1.0e-23
Match length	73
% identity	95
NCBI Description	Arabidopsis thaliana chromosome II BAC F12C20 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	160794
Seq. ID	LIB3177-009-P1-K2-C1
Method	BLASTX
NCBI GI	g4539389
BLAST score	706
E value	7.0e-75
Match length	135
% identity	96
NCBI Description	(AL035526) putative protein kinase [Arabidopsis thaliana]

Seq. No.	160795
Seq. ID	LIB3177-009-P1-K2-C3
Method	BLASTX
NCBI GI	g1706368
BLAST score	113
E value	1.0e-60
Match length	131
% identity	82
NCBI Description	DIHYDROFLAVONOL-4-REDUCTASE (DFR) (DIHYDROKAEMPFEROL 4-REDUCTASE) >gi_320557_pir__JQ1688 dihydrokaempferol 4-reductase (EC 1.1.1.219) - Arabidopsis thaliana >gi_166686 (M86359) dihydroflavonol 4-reductase [Arabidopsis thaliana]

Seq. No.	160796
Seq. ID	LIB3177-009-P1-K2-C4
Method	BLASTN
NCBI GI	g4079614
BLAST score	36
E value	6.0e-11
Match length	194
% identity	82
NCBI Description	Arabidopsis thaliana chromosome I BAC F21M11 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	160797
Seq. ID	LIB3177-009-P1-K2-D11
Method	BLASTX
NCBI GI	g2119846
BLAST score	205
E value	5.0e-16
Match length	42
% identity	95
NCBI Description	chlorophyll a/b-binding protein type I precursor Lhb1B2 - Arabidopsis thaliana >gi_16364_emb_CAA45790_ (X64460) photosystem II type I chlorophyll a /b binding protein [Arabidopsis thaliana] >gi_3128230 (AC004077) photosystem II type I chlorophyll a/b binding protein [Arabidopsis thaliana] >gi_3337371 (AC004481) photosystem II type I chlorophyll a/b binding protein [Arabidopsis thaliana]

Seq. No.	160798
Seq. ID	LIB3177-009-P1-K2-D2
Method	BLASTX
NCBI GI	g2851508
BLAST score	514
E value	2.0e-52

Match length	98
% identity	99
NCBI Description	60S RIBOSOMAL PROTEIN L21 >gi_2160162 (AC000132) Similar to ribosomal protein L21 (gb_L38826). ESTs gb_AA395597,gb_ATTS5197 come from this gene. [Arabidopsis thaliana] >gi_3482935 (AC003970) Putative ribosomal protein L21 [Arabidopsis thaliana]
Seq. No.	160799
Seq. ID	LIB3177-009-P1-K2-D3
Method	BLASTX
NCBI GI	g4490329
BLAST score	291
E value	8.0e-27
Match length	57
% identity	95
NCBI Description	(AL035656) extensin-like protein [Arabidopsis thaliana]
Seq. No.	160800
Seq. ID	LIB3177-009-P1-K2-D4
Method	BLASTX
NCBI GI	g2829899
BLAST score	250
E value	2.0e-21
Match length	76
% identity	61
NCBI Description	(AC002311) similar to ripening-induced protein, gp_AJ001449_2465015 and major#latex protein, gp_X91961_1107495 [Arabidopsis thaliana]
Seq. No.	160801
Seq. ID	LIB3177-009-P1-K2-E10
Method	BLASTX
NCBI GI	g1345592
BLAST score	264
E value	2.0e-23
Match length	57
% identity	93
NCBI Description	14-3-3-LIKE PROTEIN GF14 EPSILON >gi_1022778 (U36446) GF14 epsilon isoform [Arabidopsis thaliana]
Seq. No.	160802
Seq. ID	LIB3177-009-P1-K2-E2
Method	BLASTN
NCBI GI	g4454004
BLAST score	62
E value	2.0e-26
Match length	117
% identity	96
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F24A6 (ESSAII project)
Seq. No.	160803
Seq. ID	LIB3177-009-P1-K2-E3
Method	BLASTN
NCBI GI	g2244991
BLAST score	242

E value	1.0e-134
Match length	270
% identity	97
NCBI Description	Arabidopsis thaliana DNA chromosome 4, ESSA I contig fragment No

Seq. No.	160804
Seq. ID	LIB3177-009-P1-K2-E5
Method	BLASTX
NCBI GI	g872116
BLAST score	580
E value	4.0e-60
Match length	138
% identity	36
NCBI Description	(X79770) sti (stress inducible protein) [Glycine max]

Seq. No.	160805
Seq. ID	LIB3177-009-P1-K2-E6
Method	BLASTN
NCBI GI	g3046851
BLAST score	128
E value	6.0e-66
Match length	203
% identity	90
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MIJ24, complete sequence [Arabidopsis thaliana]

Seq. No.	160806
Seq. ID	LIB3177-009-P1-K2-E7
Method	BLASTX
NCBI GI	g2062161
BLAST score	198
E value	7.0e-16
Match length	42
% identity	88
NCBI Description	(AC001645) jasmonate inducible protein isolog [Arabidopsis thaliana]

Seq. No.	160807
Seq. ID	LIB3177-009-P1-K2-E8
Method	BLASTX
NCBI GI	g127045
BLAST score	300
E value	1.0e-27
Match length	65
% identity	86
NCBI Description	S-ADENOSYLMETHIONINE SYNTHETASE 2 (METHIONINE ADENOSYLTRANSFERASE 2) (ADOMET SYNTHETASE 2) >gi_99756_pir__JQ0410 methionine adenosyltransferase (EC 2.5.1.6) 2 - Arabidopsis thaliana >gi_166874 (M33217) S-adenosylmethionine synthetase (sam-2) [Arabidopsis thaliana] >gi_4558554_gb_AAD22647.1_AC007138_11 (AC007138) S-adenosylmethionine synthase 2 [Arabidopsis thaliana]

Seq. No.	160808
Seq. ID	LIB3177-009-P1-K2-F10
Method	BLASTX

NCBI GI	g1708420
BLAST score	358
E value	2.0e-34
Match length	94
% identity	79
NCBI Description	ISOFLAVONE REDUCTASE HOMOLOG P3 >gi_1361992_pir__S57613 isoflavonoid reductase homolog - Arabidopsis thaliana >gi_886432_emb_CAA89859_ (Z49777) isoflavonoid reductase homologue [Arabidopsis thaliana]

Seq. No.	160809
Seq. ID	LIB3177-009-P1-K2-F3
Method	BLASTX
NCBI GI	g2982303
BLAST score	580
E value	4.0e-60
Match length	133
% identity	83
NCBI Description	(AF051236) hypothetical protein [Picea mariana]

Seq. No.	160810
Seq. ID	LIB3177-009-P1-K2-F4
Method	BLASTX
NCBI GI	g3885511
BLAST score	420
E value	3.0e-41
Match length	103
% identity	82
NCBI Description	(AF084200) similar to PSI-K subunit of photosystem I from barley [Medicago sativa]

Seq. No.	160811
Seq. ID	LIB3177-009-P1-K2-F5
Method	BLASTN
NCBI GI	g3643588
BLAST score	80
E value	3.0e-37
Match length	136
% identity	90
NCBI Description	Arabidopsis thaliana chromosome II BAC F17H15 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	160812
Seq. ID	LIB3177-009-P1-K2-F8
Method	BLASTN
NCBI GI	g2358139
BLAST score	192
E value	1.0e-104
Match length	263
% identity	94
NCBI Description	Arabidopsis thaliana chromosome 1 YAC yUP8H12 complete sequence [Arabidopsis thaliana]

Seq. No.	160813
Seq. ID	LIB3177-009-P1-K2-F9
Method	BLASTX
NCBI GI	g1946362

BLAST score	297
E value	5.0e-27
Match length	96
% identity	65
NCBI Description	(U93215) photosystem II reaction center 6.1KD protein [Arabidopsis thaliana]

Seq. No.	160814
Seq. ID	LIB3177-009-P1-K2-G4
Method	BLASTN
NCBI GI	g2564050
BLAST score	282
E value	1.0e-157
Match length	286
% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MUA22, complete sequence [Arabidopsis thaliana]

Seq. No.	160815
Seq. ID	LIB3177-009-P1-K2-G6
Method	BLASTX
NCBI GI	g4538963
BLAST score	262
E value	4.0e-23
Match length	92
% identity	58
NCBI Description	(AL049488) chlorophyll a/b-binding protein-like [Arabidopsis thaliana] >gi_4741958_gb_AAD28776.1_AF134129_1 (AF134129) Lhcb5 protein [Arabidopsis thaliana]

Seq. No.	160816
Seq. ID	LIB3177-009-P1-K2-G8
Method	BLASTX
NCBI GI	g1172872
BLAST score	336
E value	4.0e-32
Match length	67
% identity	93
NCBI Description	CYSTEINE PROTEINASE RD19A PRECURSOR >gi_541856_pir__JN0718 drought-inducible cysteine proteinase (EC 3.4.22.-) RD19A precursor - Arabidopsis thaliana >gi_435618_dbj_BAA02373_ (D13042) thiol protease [Arabidopsis thaliana] >gi_4539328_emb_CAB38829.1_ (AL035679) drought-inducible cysteine proteinase RD19A precursor [Arabidopsis thaliana]

Seq. No.	160817
Seq. ID	LIB3177-009-P1-K2-H4
Method	BLASTX
NCBI GI	g1769905
BLAST score	452
E value	4.0e-45
Match length	126
% identity	70
NCBI Description	(X98108) 23 kDa polypeptide of oxygen-evolving comlex (OEC) [Arabidopsis thaliana]

Seq. No.	160818

Seq. ID	LIB3177-009-P1-K2-H7
Method	BLASTN
NCBI GI	g4691223
BLAST score	121
E value	1.0e-61
Match length	217
% identity	92
NCBI Description	Arabidopsis thaliana DNA chromosome 3, BAC clone F4F15 (ESSA project)

Seq. No.	160819
Seq. ID	LIB3177-010-P1-K1-A11
Method	BLASTN
NCBI GI	g4406776
BLAST score	105
E value	7.0e-52
Match length	308
% identity	83
NCBI Description	Arabidopsis thaliana chromosome II BAC F14H20 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	160820
Seq. ID	LIB3177-010-P1-K1-A12
Method	BLASTX
NCBI GI	g2911073
BLAST score	263
E value	7.0e-23
Match length	114
% identity	53
NCBI Description	(AL021960) putative protein [Arabidopsis thaliana]

Seq. No.	160821
Seq. ID	LIB3177-010-P1-K1-A2
Method	BLASTX
NCBI GI	g4262232
BLAST score	191
E value	4.0e-15
Match length	54
% identity	72
NCBI Description	(AC006200) putative ribosomal protein L7 [Arabidopsis thaliana]

Seq. No.	160822
Seq. ID	LIB3177-010-P1-K1-A6
Method	BLASTX
NCBI GI	g2129550
BLAST score	249
E value	1.0e-21
Match length	85
% identity	65
NCBI Description	calcium-dependent protein kinase (EC 2.7.1.-) CDPK6 - Arabidopsis thaliana >gi_2129554_pir__S71901 calcium-dependent protein kinase 6 - Arabidopsis thaliana >gi_836940 (U20623) calcium-dependent protein kinase [Arabidopsis thaliana] >gi_836944 (U20625) calcium-dependent protein kinase [Arabidopsis thaliana] >gi_4454034_emb_CAA23031.1_ (AL035394) calcium-dependent

protein kinase (CDPK6) [Arabidopsis thaliana]

Seq. No.	160823
Seq. ID	LIB3177-010-P1-K1-B1
Method	BLASTX
NCBI GI	g1946369
BLAST score	155
E value	7.0e-11
Match length	76
% identity	47
NCBI Description	(U93215) unknown protein [Arabidopsis thaliana]

Seq. No.	160824
Seq. ID	LIB3177-010-P1-K1-B4
Method	BLASTX
NCBI GI	g2160189
BLAST score	270
E value	9.0e-24
Match length	116
% identity	19
NCBI Description	(AC000132) Similar to A. thaliana receptor-like protein kinase (gb_RLK5_ARATH). ESTs gb_ATTS0475,gb_ATTS4362 come from this gene. [Arabidopsis thaliana]

Seq. No.	160825
Seq. ID	LIB3177-010-P1-K1-B8
Method	BLASTN
NCBI GI	g4454447
BLAST score	60
E value	3.0e-25
Match length	198
% identity	84
NCBI Description	Arabidopsis thaliana chromosome II BAC F5H14 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	160826
Seq. ID	LIB3177-010-P1-K1-C1
Method	BLASTX
NCBI GI	g115783
BLAST score	150
E value	3.0e-10
Match length	39
% identity	79
NCBI Description	CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR (CAB-140) (LHCP) >gi_16376_emb_CAA27543_ (X03909) chlorophyll a/b binding protein (LHCP AB 140) [Arabidopsis thaliana]

Seq. No.	160827
Seq. ID	LIB3177-010-P1-K1-C2
Method	BLASTN
NCBI GI	g4756963
BLAST score	58
E value	6.0e-24
Match length	209
% identity	83
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F10M23

(ESSA project)

Seq. No.	160828
Seq. ID	LIB3177-010-P1-K1-C3
Method	BLASTX
NCBI GI	g2244892
BLAST score	161
E value	4.0e-13
Match length	77
% identity	55
NCBI Description	(Z97338) similarity to cycloartenol synthase [Arabidopsis thaliana]

Seq. No.	160829
Seq. ID	LIB3177-010-P1-K1-F11
Method	BLASTX
NCBI GI	g3273743
BLAST score	219
E value	6.0e-18
Match length	91
% identity	53
NCBI Description	(AF057357) lipid transfer protein 2 precursor [Arabidopsis thaliana] >gi_3786019 (AC005499) unknown protein [Arabidopsis thaliana]

Seq. No.	160830
Seq. ID	LIB3177-010-P1-K1-G5
Method	BLASTN
NCBI GI	g3492855
BLAST score	48
E value	6.0e-18
Match length	136
% identity	84
NCBI Description	Genomic sequence for Arabidopsis thaliana BAC F20N2, complete sequence [Arabidopsis thaliana]

Seq. No.	160831
Seq. ID	LIB3177-010-P1-K1-H1
Method	BLASTX
NCBI GI	g4205079
BLAST score	203
E value	5.0e-16
Match length	92
% identity	50
NCBI Description	(U70425) ankyrin repeat-containing protein 2 [Arabidopsis thaliana]

Seq. No.	160832
Seq. ID	LIB3177-010-P1-K2-A11
Method	BLASTN
NCBI GI	g4406776
BLAST score	459
E value	0.0e+00
Match length	463
% identity	100
NCBI Description	Arabidopsis thaliana chromosome II BAC F14H20 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	160833
Seq. ID	LIB3177-010-P1-K2-A12
Method	BLASTN
NCBI GI	g4406776
BLAST score	149
E value	3.0e-78
Match length	289
% identity	88
NCBI Description	Arabidopsis thaliana chromosome II BAC F14H20 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	160834
Seq. ID	LIB3177-010-P1-K2-A2
Method	BLASTX
NCBI GI	g4262232
BLAST score	543
E value	9.0e-56
Match length	132
% identity	86
NCBI Description	(AC006200) putative ribosomal protein L7 [Arabidopsis thaliana]

Seq. No.	160835
Seq. ID	LIB3177-010-P1-K2-A3
Method	BLASTX
NCBI GI	g4586256
BLAST score	380
E value	7.0e-37
Match length	77
% identity	96
NCBI Description	(AL049640) probable photosystem I chain XI precursor [Arabidopsis thaliana]

Seq. No.	160836
Seq. ID	LIB3177-010-P1-K2-A4
Method	BLASTN
NCBI GI	g4586241
BLAST score	37
E value	1.0e-11
Match length	145
% identity	83
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone T20K18 (ESSA project)

Seq. No.	160837
Seq. ID	LIB3177-010-P1-K2-A8
Method	BLASTX
NCBI GI	g2497733
BLAST score	607
E value	3.0e-63
Match length	118
% identity	99
NCBI Description	NONSPECIFIC LIPID-TRANSFER PROTEIN 1 PRECURSOR (LTP 1) >gi_1177796 (M80567) non-specific lipid transfer protein [Arabidopsis thaliana] >gi_3786018 (AC005499) unknown protein [Arabidopsis thaliana]

Seq. No.	160838
Seq. ID	LIB3177-010-P1-K2-A9
Method	BLASTX
NCBI GI	g2497733
BLAST score	418
E value	3.0e-41
Match length	89
% identity	92
NCBI Description	NONSPECIFIC LIPID-TRANSFER PROTEIN 1 PRECURSOR (LTP 1) >gi_1177796 (M80567) non-specific lipid transfer protein [Arabidopsis thaliana] >gi_3786018 (AC005499) unknown protein [Arabidopsis thaliana]

Seq. No.	160839
Seq. ID	LIB3177-010-P1-K2-B1
Method	BLASTN
NCBI GI	g1946354
BLAST score	99
E value	2.0e-48
Match length	123
% identity	95
NCBI Description	Arabidopsis thaliana chromosome II BAC T06B20 genomic sequence, complete sequence

Seq. No.	160840
Seq. ID	LIB3177-010-P1-K2-B10
Method	BLASTN
NCBI GI	g4454447
BLAST score	170
E value	6.0e-91
Match length	234
% identity	93
NCBI Description	Arabidopsis thaliana chromosome II BAC F5H14 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	160841
Seq. ID	LIB3177-010-P1-K2-B11
Method	BLASTN
NCBI GI	g4454447
BLAST score	56
E value	5.0e-23
Match length	88
% identity	91
NCBI Description	Arabidopsis thaliana chromosome II BAC F5H14 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	160842
Seq. ID	LIB3177-010-P1-K2-B3
Method	BLASTX
NCBI GI	g2190547
BLAST score	402
E value	3.0e-39
Match length	131
% identity	52
NCBI Description	(AC001229) ESTs gb_T43256,gb_46316,gb_N64930,gb_AA395255,gb_AA404382 come

from this gene. [Arabidopsis thaliana]

Seq. No.	160843
Seq. ID	LIB3177-010-P1-K2-B4
Method	BLASTN
NCBI GI	g2160155
BLAST score	32
E value	5.0e-09
Match length	40
% identity	95
NCBI Description	Sequence of BAC F21M12 from Arabidopsis thaliana chromosome 1, complete sequence [Arabidopsis thaliana]

Seq. No.	160844
Seq. ID	LIB3177-010-P1-K2-B8
Method	BLASTN
NCBI GI	g4454447
BLAST score	320
E value	1.0e-180
Match length	335
% identity	99
NCBI Description	Arabidopsis thaliana chromosome II BAC F5H14 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	160845
Seq. ID	LIB3177-010-P1-K2-B9
Method	BLASTN
NCBI GI	g4454447
BLAST score	239
E value	1.0e-132
Match length	258
% identity	98
NCBI Description	Arabidopsis thaliana chromosome II BAC F5H14 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	160846
Seq. ID	LIB3177-010-P1-K2-C1
Method	BLASTX
NCBI GI	g115783
BLAST score	630
E value	6.0e-66
Match length	119
% identity	99
NCBI Description	CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR (CAB-140) (LHCP) >gi_16376_emb_CAA27543_ (X03909) chlorophyll a/b binding protein (LHCP AB 140) [Arabidopsis thaliana]

Seq. No.	160847
Seq. ID	LIB3177-010-P1-K2-C11
Method	BLASTN
NCBI GI	g2264320
BLAST score	162
E value	5.0e-86
Match length	283
% identity	44
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:

MXI10, complete sequence [Arabidopsis thaliana]

Seq. No.	160848
Seq. ID	LIB3177-010-P1-K2-C12
Method	BLASTX
NCBI GI	g114335
BLAST score	596
E value	6.0e-62
Match length	116
% identity	100
NCBI Description	PLASMA MEMBRANE ATPASE 2 (PROTON PUMP) >gi_67973_pir__PXMUP2 H+-transporting ATPase (EC 3.6.1.35) type 2, plasma membrane - Arabidopsis thaliana >gi_166629 (J05570) H+-ATPase [Arabidopsis thaliana]

Seq. No.	160849
Seq. ID	LIB3177-010-P1-K2-C2
Method	BLASTN
NCBI GI	g4756963
BLAST score	294
E value	1.0e-164
Match length	378
% identity	100
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F10M23 (ESSA project)

Seq. No.	160850
Seq. ID	LIB3177-010-P1-K2-C3
Method	BLASTX
NCBI GI	g2244892
BLAST score	357
E value	4.0e-34
Match length	94
% identity	68
NCBI Description	(Z97338) similarity to cycloartenol synthase [Arabidopsis thaliana]

Seq. No.	160851
Seq. ID	LIB3177-010-P1-K2-C7
Method	BLASTN
NCBI GI	g2583106
BLAST score	51
E value	2.0e-20
Match length	59
% identity	97
NCBI Description	Arabidopsis thaliana chromosome II BAC F4L23 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	160852
Seq. ID	LIB3177-010-P1-K2-C8
Method	BLASTN
NCBI GI	g2224924
BLAST score	188
E value	1.0e-101
Match length	220
% identity	96
NCBI Description	Arabidopsis thaliana kinesin-like protein (ZWICHEL) gene,

complete cds

Seq. No.	160853
Seq. ID	LIB3177-010-P1-K2-D1
Method	BLASTX
NCBI GI	g99752
BLAST score	367
E value	3.0e-35
Match length	98
% identity	82
NCBI Description	protochlorophyllide reductase (EC 1.3.1.33) precursor - Arabidopsis thaliana

Seq. No.	160854
Seq. ID	LIB3177-010-P1-K2-D10
Method	BLASTX
NCBI GI	g3319350
BLAST score	241
E value	9.0e-23
Match length	67
% identity	91
NCBI Description	(AF077407) No definition line found [Arabidopsis thaliana]

Seq. No.	160855
Seq. ID	LIB3177-010-P1-K2-D12
Method	BLASTN
NCBI GI	g4757403
BLAST score	176
E value	2.0e-94
Match length	224
% identity	99
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MJL12, complete sequence

Seq. No.	160856
Seq. ID	LIB3177-010-P1-K2-D5
Method	BLASTN
NCBI GI	g1946354
BLAST score	132
E value	3.0e-68
Match length	240
% identity	91
NCBI Description	Arabidopsis thaliana chromosome II BAC T06B20 genomic sequence, complete sequence

Seq. No.	160857
Seq. ID	LIB3177-010-P1-K2-D7
Method	BLASTX
NCBI GI	g1702987
BLAST score	315
E value	3.0e-29
Match length	66
% identity	98
NCBI Description	14-3-3-LIKE PROTEIN GF14 PHI >gi_1493805 (L09111) GF14 protein phi chain [Arabidopsis thaliana] >gi_2232146 (AF001414) 14-3-3-like protein GF14 phi [Arabidopsis thaliana]

Seq. No.	160858
Seq. ID	LIB3177-010-P1-K2-E2
Method	BLASTN
NCBI GI	g4589440
BLAST score	54
E value	4.0e-22
Match length	58
% identity	98
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MSD21, complete sequence

Seq. No.	160859
Seq. ID	LIB3177-010-P1-K2-E4
Method	BLASTX
NCBI GI	g4322421
BLAST score	705
E value	1.0e-74
Match length	140
% identity	98
NCBI Description	(AF085230) cadmium resistance factor 1 [Arabidopsis thaliana]

Seq. No.	160860
Seq. ID	LIB3177-010-P1-K2-E5
Method	BLASTX
NCBI GI	g4768281
BLAST score	374
E value	7.0e-58
Match length	136
% identity	83
NCBI Description	(AF085231) cadmium resistance factor 1 [Arabidopsis thaliana]

Seq. No.	160861
Seq. ID	LIB3177-010-P1-K2-E7
Method	BLASTN
NCBI GI	g2760164
BLAST score	275
E value	1.0e-153
Match length	311
% identity	97
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K18P6, complete sequence [Arabidopsis thaliana]

Seq. No.	160862
Seq. ID	LIB3177-010-P1-K2-E9
Method	BLASTN
NCBI GI	g2760164
BLAST score	101
E value	1.0e-49
Match length	194
% identity	87
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K18P6, complete sequence [Arabidopsis thaliana]

Seq. No.	160863

Seq. ID	LIB3177-010-P1-K2-F11
Method	BLASTX
NCBI GI	g3273743
BLAST score	620
E value	1.0e-64
Match length	118
% identity	100
NCBI Description	(AF057357) lipid transfer protein 2 precursor [Arabidopsis thaliana] >gi_3786019 (AC005499) unknown protein [Arabidopsis thaliana]

Seq. No.	160864
Seq. ID	LIB3177-010-P1-K2-F12
Method	BLASTX
NCBI GI	g3273743
BLAST score	461
E value	3.0e-46
Match length	96
% identity	94
NCBI Description	(AF057357) lipid transfer protein 2 precursor [Arabidopsis thaliana] >gi_3786019 (AC005499) unknown protein [Arabidopsis thaliana]

Seq. No.	160865
Seq. ID	LIB3177-010-P1-K2-F2
Method	BLASTX
NCBI GI	g115783
BLAST score	662
E value	1.0e-69
Match length	125
% identity	99
NCBI Description	CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR (CAB-140) (LHCP) >gi_16376_emb_CAA27543_ (X03909) chlorophyll a/b binding protein (LHCP AB 140) [Arabidopsis thaliana]

Seq. No.	160866
Seq. ID	LIB3177-010-P1-K2-F4
Method	BLASTX
NCBI GI	g132074
BLAST score	624
E value	2.0e-65
Match length	122
% identity	93
NCBI Description	RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN 1A PRECURSOR (RUBISCO SMALL SUBUNIT 1A) >gi_68063_pir__RKMUA1 ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain A1 precursor - Arabidopsis thaliana

Seq. No.	160867
Seq. ID	LIB3177-010-P1-K2-F5
Method	BLASTX
NCBI GI	g3273743
BLAST score	194
E value	3.0e-15
Match length	66
% identity	58

NCBI Description	(AF057357) lipid transfer protein 2 precursor [Arabidopsis thaliana] >gi_3786019 (AC005499) unknown protein [Arabidopsis thaliana]

Seq. No.	160868
Seq. ID	LIB3177-010-P1-K2-F6
Method	BLASTN
NCBI GI	g4519191
BLAST score	46
E value	5.0e-17
Match length	118
% identity	86
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K9P8, complete sequence

Seq. No.	160869
Seq. ID	LIB3177-010-P1-K2-F7
Method	BLASTN
NCBI GI	g3168839
BLAST score	214
E value	1.0e-117
Match length	258
% identity	96
NCBI Description	Arabidopsis thaliana copper homeostasis factor (CCH) mRNA, complete cds

Seq. No.	160870
Seq. ID	LIB3177-010-P1-K2-F9
Method	BLASTX
NCBI GI	g3024697
BLAST score	323
E value	7.0e-31
Match length	84
% identity	85
NCBI Description	T-COMPLEX PROTEIN 1, EPSILON SUBUNIT (TCP-1-EPSILON) (CCT-EPSILON) >gi_2213618 (AC000103) F21J9.12 [Arabidopsis thaliana]

Seq. No.	160871
Seq. ID	LIB3177-010-P1-K2-G10
Method	BLASTN
NCBI GI	g2739359
BLAST score	195
E value	1.0e-106
Match length	227
% identity	96
NCBI Description	Arabidopsis thaliana chromosome II BAC T9J22 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	160872
Seq. ID	LIB3177-010-P1-K2-G11
Method	BLASTX
NCBI GI	g1170505
BLAST score	312
E value	8.0e-29
Match length	76
% identity	83

NCBI Description	EUKARYOTIC INITIATION FACTOR 4A-2 (EIF-4A-2) >gi_322504_pir__JC1453 translation initiation factor eIF-4A2 - Arabidopsis thaliana >gi_16556_emb_CAA46189_ (X65053) eukaryotic translation initiation factor 4A-2 [Arabidopsis thaliana] >gi_4585969_gb_AAD25605.1_AC005287_7 (AC005287) Eukaryotic Initiation Factor 4A-2 [Arabidopsis thaliana]
Seq. No.	160873
Seq. ID	LIB3177-010-P1-K2-G12
Method	BLASTX
NCBI GI	g2119846
BLAST score	576
E value	1.0e-59
Match length	116
% identity	97
NCBI Description	chlorophyll a/b-binding protein type I precursor Lhb1B2 - Arabidopsis thaliana >gi_16364_emb_CAA45790_ (X64460) photosystem II type I chlorophyll a /b binding protein [Arabidopsis thaliana] >gi_3128230 (AC004077) photosystem II type I chlorophyll a/b binding protein [Arabidopsis thaliana] >gi_3337371 (AC004481) photosystem II type I chlorophyll a/b binding protein [Arabidopsis thaliana]
Seq. No.	160874
Seq. ID	LIB3177-010-P1-K2-G3
Method	BLASTX
NCBI GI	g4544456
BLAST score	304
E value	6.0e-28
Match length	101
% identity	65
NCBI Description	(AC006592) putative cytochrome P450 [Arabidopsis thaliana]
Seq. No.	160875
Seq. ID	LIB3177-010-P1-K2-G4
Method	BLASTX
NCBI GI	g1170505
BLAST score	309
E value	2.0e-28
Match length	83
% identity	62
NCBI Description	EUKARYOTIC INITIATION FACTOR 4A-2 (EIF-4A-2) >gi_322504_pir__JC1453 translation initiation factor eIF-4A2 - Arabidopsis thaliana >gi_16556_emb_CAA46189_ (X65053) eukaryotic translation initiation factor 4A-2 [Arabidopsis thaliana] >gi_4585969_gb_AAD25605.1_AC005287_7 (AC005287) Eukaryotic Initiation Factor 4A-2 [Arabidopsis thaliana]
Seq. No.	160876
Seq. ID	LIB3177-010-P1-K2-G6
Method	BLASTX
NCBI GI	g3953473
BLAST score	533
E value	1.0e-54
Match length	117

% identity	93
NCBI Description	(AC002328) F22O2.18 [Arabidopsis thaliana]
Seq. No.	160877
Seq. ID	LIB3177-010-P1-K2-H1
Method	BLASTN
NCBI GI	g4205078
BLAST score	89
E value	2.0e-42
Match length	133
% identity	65
NCBI Description	Arabidopsis thaliana ankyrin repeat-containing protein 2 (AKR2) mRNA, complete cds
Seq. No.	160878
Seq. ID	LIB3177-010-P1-K2-H12
Method	BLASTX
NCBI GI	g120662
BLAST score	306
E value	2.0e-28
Match length	63
% identity	95
NCBI Description	GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE B PRECURSOR, CHLOROPLAST >gi_81621_pir__JQ1286 glyceraldehyde-3-phosphate dehydrogenase (NADP+) (phosphorylating) (EC 1.2.1.13) B precursor, chloroplast - Arabidopsis thaliana >gi_336390 (M64115) glyceraldehyde 3-phosphate dehydrogenase B subunit [Arabidopsis thaliana]
Seq. No.	160879
Seq. ID	LIB3177-010-P1-K2-H2
Method	BLASTX
NCBI GI	g120667
BLAST score	256
E value	2.0e-22
Match length	76
% identity	68
NCBI Description	GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE, CYTOSOLIC >gi_81622_pir__JQ1287 glyceraldehyde-3-phosphate dehydrogenase (EC 1.2.1.12), cytosolic - Arabidopsis thaliana >gi_166706 (M64116) cystolic glyceraldehyde-3-phosphate dehydrogenase [Arabidopsis thaliana] >gi_166710 (M64119) glyceraldehyde-3-phosphate dehydrogenase [Arabidopsis thaliana]
Seq. No.	160880
Seq. ID	LIB3177-010-P1-K2-H7
Method	BLASTX
NCBI GI	g4193388
BLAST score	476
E value	8.0e-48
Match length	127
% identity	74
NCBI Description	(AF091455) translationally controlled tumor protein [Hevea brasiliensis]
Seq. No.	160881

Seq. ID	LIB3177-010-P1-K2-H8
Method	BLASTX
NCBI GI	g495731
BLAST score	206
E value	2.0e-16
Match length	41
% identity	98
NCBI Description	(L16790) small ras-related protein [Arabidopsis thaliana]

Seq. No.	160882
Seq. ID	LIB3177-010-P1-K2-H9
Method	BLASTX
NCBI GI	g495731
BLAST score	170
E value	3.0e-12
Match length	40
% identity	85
NCBI Description	(L16790) small ras-related protein [Arabidopsis thaliana]

Seq. No.	160883
Seq. ID	LIB3177-012-P1-K1-A2
Method	BLASTX
NCBI GI	g4454037
BLAST score	199
E value	2.0e-15
Match length	120
% identity	39
NCBI Description	(AL035394) putative major latex protein [Arabidopsis thaliana]

Seq. No.	160884
Seq. ID	LIB3177-012-P1-K1-A3
Method	BLASTX
NCBI GI	g2146742
BLAST score	241
E value	2.0e-20
Match length	119
% identity	50
NCBI Description	pattern-formation protein GNOM - Arabidopsis thaliana >gi_1209631 (U36432) GNOM gene product [Arabidopsis thaliana]

Seq. No.	160885
Seq. ID	LIB3177-012-P1-K1-A4
Method	BLASTX
NCBI GI	g3241945
BLAST score	251
E value	1.0e-21
Match length	96
% identity	59
NCBI Description	(AC004625) unknown protein [Arabidopsis thaliana]

Seq. No.	160886
Seq. ID	LIB3177-012-P1-K1-A8
Method	BLASTX
NCBI GI	g4454037
BLAST score	152

E value	4.0e-10
Match length	59
% identity	49
NCBI Description	(AL035394) putative major latex protein [Arabidopsis thaliana]

Seq. No.	160887
Seq. ID	LIB3177-012-P1-K1-B2
Method	BLASTX
NCBI GI	g2119846
BLAST score	415
E value	8.0e-41
Match length	112
% identity	72
NCBI Description	chlorophyll a/b-binding protein type I precursor Lhb1B2 - Arabidopsis thaliana >gi_16364_emb_CAA45790_ (X64460) photosystem II type I chlorophyll a /b binding protein [Arabidopsis thaliana] >gi_3128230 (AC004077) photosystem II type I chlorophyll a/b binding protein [Arabidopsis thaliana] >gi_3337371 (AC004481) photosystem II type I chlorophyll a/b binding protein [Arabidopsis thaliana]

Seq. No.	160888
Seq. ID	LIB3177-012-P1-K1-B4
Method	BLASTX
NCBI GI	g99735
BLAST score	384
E value	4.0e-37
Match length	123
% identity	65
NCBI Description	L-ascorbate peroxidase (EC 1.11.1.11) precursor - Arabidopsis thaliana (fragment)

Seq. No.	160889
Seq. ID	LIB3177-012-P1-K1-B7
Method	BLASTN
NCBI GI	g3128134
BLAST score	57
E value	1.0e-23
Match length	133
% identity	86
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K18G13, complete sequence [Arabidopsis thaliana]

Seq. No.	160890
Seq. ID	LIB3177-012-P1-K1-B9
Method	BLASTN
NCBI GI	g2642427
BLAST score	53
E value	7.0e-21
Match length	269
% identity	80
NCBI Description	Arabidopsis thaliana chromosome II BAC T20D16 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	160891
Seq. ID	LIB3177-012-P1-K1-C1

Method	BLASTN
NCBI GI	g2351068
BLAST score	111
E value	2.0e-55
Match length	387
% identity	82
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MRH10, complete sequence [Arabidopsis thaliana]

Seq. No.	160892
Seq. ID	LIB3177-012-P1-K1-C12
Method	BLASTX
NCBI GI	g4755193
BLAST score	203
E value	4.0e-16
Match length	93
% identity	49
NCBI Description	(AC007018) putative ribosomal protein S17 [Arabidopsis thaliana]

Seq. No.	160893
Seq. ID	LIB3177-012-P1-K1-C2
Method	BLASTN
NCBI GI	g4741928
BLAST score	73
E value	9.0e-33
Match length	380
% identity	79
NCBI Description	Arabidopsis thaliana membrane related protein CP5 mRNA, complete cds

Seq. No.	160894
Seq. ID	LIB3177-012-P1-K1-C4
Method	BLASTX
NCBI GI	g2262167
BLAST score	241
E value	2.0e-20
Match length	93
% identity	58
NCBI Description	(AC002329) cytosolic ribosomal protein S4 [Arabidopsis thaliana]

Seq. No.	160895
Seq. ID	LIB3177-012-P1-K1-D1
Method	BLASTN
NCBI GI	g2264303
BLAST score	53
E value	7.0e-21
Match length	140
% identity	86
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MBB18, complete sequence [Arabidopsis thaliana]

Seq. No.	160896
Seq. ID	LIB3177-012-P1-K1-D2
Method	BLASTX
NCBI GI	g4585882

BLAST score	233
E value	2.0e-19
Match length	110
% identity	52
NCBI Description	(AC005850) PSI type III chlorophyll a/b-binding protein [Arabidopsis thaliana]

Seq. No.	160897
Seq. ID	LIB3177-012-P1-K1-D4
Method	BLASTX
NCBI GI	g4263525
BLAST score	391
E value	6.0e-38
Match length	117
% identity	69
NCBI Description	(AC004044) putative photosystem I reaction center subunit II precursor [Arabidopsis thaliana]

Seq. No.	160898
Seq. ID	LIB3177-012-P1-K1-D6
Method	BLASTN
NCBI GI	g2358139
BLAST score	50
E value	3.0e-19
Match length	182
% identity	82
NCBI Description	Arabidopsis thaliana chromosome 1 YAC yUP8H12 complete sequence [Arabidopsis thaliana]

Seq. No.	160899
Seq. ID	LIB3177-012-P1-K1-D9
Method	BLASTX
NCBI GI	g2062161
BLAST score	210
E value	6.0e-17
Match length	91
% identity	52
NCBI Description	(AC001645) jasmonate inducible protein isolog [Arabidopsis thaliana]

Seq. No.	160900
Seq. ID	LIB3177-012-P1-K1-E10
Method	BLASTX
NCBI GI	g4262156
BLAST score	147
E value	1.0e-09
Match length	84
% identity	43
NCBI Description	(AC005275) putative component of cytochrome B6-F complex [Arabidopsis thaliana]

Seq. No.	160901
Seq. ID	LIB3177-012-P1-K1-E2
Method	BLASTX
NCBI GI	g1707008
BLAST score	293
E value	2.0e-26

Match length	116
% identity	57
NCBI Description	(U78721) 30S ribosomal protein S5 isolog [Arabidopsis thaliana]

Seq. No.	160902
Seq. ID	LIB3177-012-P1-K1-E3
Method	BLASTN
NCBI GI	g2264316
BLAST score	42
E value	2.0e-14
Match length	86
% identity	87
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MRO11, complete sequence [Arabidopsis thaliana]

Seq. No.	160903
Seq. ID	LIB3177-012-P1-K1-E4
Method	BLASTX
NCBI GI	g4220512
BLAST score	171
E value	2.0e-12
Match length	100
% identity	40
NCBI Description	(AL035356) putative pectate lyase [Arabidopsis thaliana]

Seq. No.	160904
Seq. ID	LIB3177-012-P1-K1-E5
Method	BLASTX
NCBI GI	g132074
BLAST score	312
E value	1.0e-28
Match length	113
% identity	60
NCBI Description	RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN 1A PRECURSOR (RUBISCO SMALL SUBUNIT 1A) >gi_68063_pir__RKMUA1 ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain A1 precursor - Arabidopsis thaliana

Seq. No.	160905
Seq. ID	LIB3177-012-P1-K1-E8
Method	BLASTX
NCBI GI	g2781394
BLAST score	237
E value	7.0e-20
Match length	118
% identity	47
NCBI Description	(U70424) O-methyltransferase 1 [Arabidopsis thaliana]

Seq. No.	160906
Seq. ID	LIB3177-012-P1-K1-E9
Method	BLASTX
NCBI GI	g4582468
BLAST score	160
E value	2.0e-11
Match length	45
% identity	71

09604504.050800

NCBI Description	(AC007071) putative 40S ribosomal protein; contains C-terminal domain [Arabidopsis thaliana]
Seq. No.	160907
Seq. ID	LIB3177-012-P1-K1-F1
Method	BLASTN
NCBI GI	g3241923
BLAST score	57
E value	2.0e-23
Match length	213
% identity	82
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MMN10, complete sequence [Arabidopsis thaliana]
Seq. No.	160908
Seq. ID	LIB3177-012-P1-K1-F10
Method	BLASTX
NCBI GI	g1175012
BLAST score	367
E value	3.0e-35
Match length	103
% identity	75
NCBI Description	PLASMA MEMBRANE INTRINSIC PROTEIN 1C (TRANSMEMBRANE PROTEIN B) (TMP-B) >gi_396218_emb_CAA49155_ (X69294) transmembrane protein TMP-B [Arabidopsis thaliana]
Seq. No.	160909
Seq. ID	LIB3177-012-P1-K1-F3
Method	BLASTX
NCBI GI	g399298
BLAST score	162
E value	5.0e-11
Match length	63
% identity	57
NCBI Description	STRESS-INDUCED KIN2 PROTEIN (COLD-INDUCED COR6.6 PROTEIN) >gi_1084343_pir__S22529 cold-regulated protein kin2 - Arabidopsis thaliana >gi_16230_emb_CAA38894_ (X55053) cold regulated [Arabidopsis thaliana]
Seq. No.	160910
Seq. ID	LIB3177-012-P1-K1-F4
Method	BLASTX
NCBI GI	g3319348
BLAST score	174
E value	8.0e-13
Match length	70
% identity	50
NCBI Description	(AF077407) No definition line found [Arabidopsis thaliana]
Seq. No.	160911
Seq. ID	LIB3177-012-P1-K1-F5
Method	BLASTX
NCBI GI	g2062164
BLAST score	224
E value	3.0e-18
Match length	96
% identity	47

NCBI Description	(AC001645) jasmonate inducible protein isolog [Arabidopsis thaliana]
Seq. No.	160912
Seq. ID	LIB3177-012-P1-K1-F6
Method	BLASTX
NCBI GI	g3790567
BLAST score	226
E value	8.0e-19
Match length	90
% identity	57
NCBI Description	(AF078821) RING-H2 finger protein RHA1b [Arabidopsis thaliana]
Seq. No.	160913
Seq. ID	LIB3177-012-P1-K1-F8
Method	BLASTX
NCBI GI	g1076678
BLAST score	226
E value	1.0e-18
Match length	79
% identity	63
NCBI Description	ubiquitin / ribosomal protein S27a - potato (fragment)
Seq. No.	160914
Seq. ID	LIB3177-012-P1-K1-G10
Method	BLASTN
NCBI GI	g4584351
BLAST score	56
E value	9.0e-23
Match length	228
% identity	81
NCBI Description	Arabidopsis thaliana chromosome II BAC T12H3 genomic sequence, complete sequence
Seq. No.	160915
Seq. ID	LIB3177-012-P1-K1-G12
Method	BLASTX
NCBI GI	g3249081
BLAST score	309
E value	2.0e-28
Match length	113
% identity	58
NCBI Description	(AC004473) Strong similarity to AROGP2 gene gb_1762634 from Lycopersicon esculentum. [Arabidopsis thaliana]
Seq. No.	160916
Seq. ID	LIB3177-012-P1-K1-G3
Method	BLASTX
NCBI GI	g4741960
BLAST score	380
E value	1.0e-36
Match length	106
% identity	70
NCBI Description	(AF134130) Lhcb6 protein [Arabidopsis thaliana]
Seq. No.	160917

Seq. ID	LIB3177-012-P1-K1-G4
Method	BLASTX
NCBI GI	g132677
BLAST score	296
E value	6.0e-27
Match length	92
% identity	72
NCBI Description	50S RIBOSOMAL PROTEIN L15, CHLOROPLAST PRECURSOR (CL15) >gi_71241_pir__R5MUL5 ribosomal protein L15 precursor, chloroplast - Arabidopsis thaliana >gi_16497_emb_CAA77593_ (Z11508) Plastid ribosomal protein CL15 [Arabidopsis thaliana]

Seq. No.	160918
Seq. ID	LIB3177-012-P1-K1-G7
Method	BLASTX
NCBI GI	g4835233
BLAST score	267
E value	1.0e-23
Match length	96
% identity	58
NCBI Description	(AL049862) putative protein 1 photosystem II oxygen-evolving complex [Arabidopsis thaliana]

Seq. No.	160919
Seq. ID	LIB3177-012-P1-K1-G8
Method	BLASTX
NCBI GI	g3894193
BLAST score	169
E value	5.0e-12
Match length	106
% identity	35
NCBI Description	(AC005662) putative strictosidine synthase [Arabidopsis thaliana]

Seq. No.	160920
Seq. ID	LIB3177-012-P1-K1-G9
Method	BLASTX
NCBI GI	g541858
BLAST score	368
E value	2.0e-35
Match length	117
% identity	67
NCBI Description	endoxyloglucan transferase - Arabidopsis thaliana >gi_469484_dbj_BAA03921_ (D16454) endo-xyloglucan transferase [Arabidopsis thaliana] >gi_4063757 (AC005561) endo-xyloglucan transferase [Arabidopsis thaliana]

Seq. No.	160921
Seq. ID	LIB3177-012-P1-K1-H10
Method	BLASTX
NCBI GI	g132110
BLAST score	252
E value	9.0e-22
Match length	92
% identity	58
NCBI Description	RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN 3B PRECURSOR

(RUBISCO SMALL SUBUNIT 3B) >gi_68060_pir__RKMUB3 ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain B3 precursor - Arabidopsis thaliana >gi_16195_emb_CAA32702_ (X14564) ribulose bisphosphate carboxylase [Arabidopsis thaliana]

Seq. No.	160922
Seq. ID	LIB3177-012-P1-K1-H11
Method	BLASTX
NCBI GI	g729470
BLAST score	333
E value	3.0e-31
Match length	116
% identity	62
NCBI Description	MITOCHONDRIAL FORMATE DEHYDROGENASE PRECURSOR (NAD-DEPENDENT FORMATE DEHYDROGENASE) (FDH) >gi_542089_pir__JQ2272 formate dehydrogenase (EC 1.2.1.2) precursor, mitochondrial - potato >gi_297798_emb_CAA79702_ (Z21493) mitochondrial formate dehydrogenase precursor [Solanum tuberosum]

Seq. No.	160923
Seq. ID	LIB3177-012-P1-K1-H12
Method	BLASTN
NCBI GI	g3859840
BLAST score	42
E value	2.0e-14
Match length	158
% identity	85
NCBI Description	Plastid transformation vector pGS31A 16S ribosomal RNA gene, partial sequence; aminoglycoside 3'-adenyltransferase (aadA) gene, complete cds

Seq. No.	160924
Seq. ID	LIB3177-012-P1-K1-H2
Method	BLASTX
NCBI GI	g3157944
BLAST score	447
E value	2.0e-44
Match length	133
% identity	70
NCBI Description	(AC002131) Very strong similarity to aminomethyltransferase precursor gb_U79769 from Mesembryanthemum crystallinum. ESTs gb_T43167, gb_T21076, gb_H36999, gb_T22773, gb_N38038, gb_T13742, gb_Z26545, gb_T20753 and gb_W43123 come from this ge

Seq. No.	160925
Seq. ID	LIB3177-012-P1-K1-H3
Method	BLASTX
NCBI GI	g2499811
BLAST score	330
E value	7.0e-31
Match length	97
% identity	65
NCBI Description	PROFILIN 2 >gi_1353766 (U43323) profilin 2 [Arabidopsis thaliana] >gi_1353772 (U43326) profilin 2 [Arabidopsis

thaliana]

Seq. No.	160926
Seq. ID	LIB3177-012-P1-K1-H5
Method	BLASTX
NCBI GI	g1086833
BLAST score	188
E value	4.0e-14
Match length	123
% identity	31
NCBI Description	(U41264) coded for by C. elegans cDNA CEESN26F; coded for by C. elegans cDNA CEESI89F; similar to 60S acidic ribosomal protein Po (L10) [Caenorhabditis elegans]

Seq. No.	160927
Seq. ID	LIB3177-012-P1-K1-H8
Method	BLASTX
NCBI GI	g2244740
BLAST score	248
E value	4.0e-21
Match length	146
% identity	42
NCBI Description	(D88417) endo-1,4-beta-glucanase [Gossypium hirsutum]

Seq. No.	160928
Seq. ID	LIB3177-012-P1-K1-H9
Method	BLASTX
NCBI GI	g131381
BLAST score	230
E value	3.0e-19
Match length	104
% identity	53
NCBI Description	OXYGEN-EVOLVING ENHANCER PROTEIN 1 PRECURSOR (OEE1) (33 KD SUBUNIT OF OXYGEN EVOLVING SYSTEM OF PHOTOSYSTEM II) (33 KD THYLAKOID MEMBRANE PROTEIN) >gi_99745_pir__S11852 photosystem II oxygen-evolving complex protein 1 precursor - Arabidopsis thaliana >gi_22571_emb_CAA36675_ (X52428) 33 kDa oxygen-evolving protein [Arabidopsis thaliana]

Seq. No.	160929
Seq. ID	LIB3177-012-P1-K2-A2
Method	BLASTX
NCBI GI	g4454037
BLAST score	597
E value	4.0e-62
Match length	111
% identity	99
NCBI Description	(AL035394) putative major latex protein [Arabidopsis thaliana]

Seq. No.	160930
Seq. ID	LIB3177-012-P1-K2-A3
Method	BLASTX
NCBI GI	g2498329
BLAST score	608
E value	2.0e-63
Match length	123

% identity	97
NCBI Description	PATTERN FORMATION PROTEIN EMB30 >gi_2129665_pir__S65571 pattern-formation protein GNOM - Arabidopsis thaliana >gi_1209633 (U36433) GNOM gene product [Arabidopsis thaliana] >gi_1335997 (U56140) similar to the Saccharomyces cerevisiae Sec7 protein, GenBank Accession Number J03918 [Arabidopsis thaliana] >gi_1335999 (U56141) similar to the Saccharomyces cerevisiae Sec7 protein, GenBank Accession Number J03918 [Arabidopsis thaliana]
Seq. No.	160931
Seq. ID	LIB3177-012-P1-K2-A4
Method	BLASTN
NCBI GI	g3241939
BLAST score	77
E value	3.0e-35
Match length	285
% identity	94
NCBI Description	Arabidopsis thaliana chromosome II BAC T26J13 genomic sequence, complete sequence [Arabidopsis thaliana]
Seq. No.	160932
Seq. ID	LIB3177-012-P1-K2-A5
Method	BLASTX
NCBI GI	g133872
BLAST score	236
E value	8.0e-20
Match length	63
% identity	67
NCBI Description	30S RIBOSOMAL PROTEIN S1, CHLOROPLAST PRECURSOR (CS1) >gi_282838_pir__S26494 ribosomal protein S1, chloroplast - spinach >gi_322404_pir__A44121 small subunit ribosomal protein CS1, CS-S2 - spinach >gi_18060_emb_CAA46927_ (X66135) ribosomal protein S1 [Spinacia oleracea] >gi_170143 (M82923) chloroplast ribosomal protein S1 [Spinacia oleracea]
Seq. No.	160933
Seq. ID	LIB3177-012-P1-K2-A7
Method	BLASTX
NCBI GI	g3953467
BLAST score	478
E value	4.0e-48
Match length	117
% identity	44
NCBI Description	(AC002328) F20N2.12 [Arabidopsis thaliana]
Seq. No.	160934
Seq. ID	LIB3177-012-P1-K2-A9
Method	BLASTX
NCBI GI	g2160158
BLAST score	363
E value	1.0e-34
Match length	87
% identity	82
NCBI Description	(AC000132) Similar to elongation factor 1-gamma (gb_EF1G_XENLA). ESTs gb_T20564,gb_T45940,gb_T04527 come

from this gene. [Arabidopsis thaliana]

Seq. No.	160935
Seq. ID	LIB3177-012-P1-K2-B2
Method	BLASTX
NCBI GI	g2119846
BLAST score	562
E value	4.0e-58
Match length	108
% identity	98
NCBI Description	chlorophyll a/b-binding protein type I precursor Lhb1B2 - Arabidopsis thaliana >gi_16364_emb_CAA45790_ (X64460) photosystem II type I chlorophyll a /b binding protein [Arabidopsis thaliana] >gi_3128230 (AC004077) photosystem II type I chlorophyll a/b binding protein [Arabidopsis thaliana] >gi_3337371 (AC004481) photosystem II type I chlorophyll a/b binding protein [Arabidopsis thaliana]

Seq. No.	160936
Seq. ID	LIB3177-012-P1-K2-B4
Method	BLASTX
NCBI GI	g99735
BLAST score	641
E value	6.0e-67
Match length	133
% identity	96
NCBI Description	L-ascorbate peroxidase (EC 1.11.1.11) precursor - Arabidopsis thaliana (fragment)

Seq. No.	160937
Seq. ID	LIB3177-012-P1-K2-B5
Method	BLASTX
NCBI GI	g4704730
BLAST score	377
E value	2.0e-36
Match length	80
% identity	93
NCBI Description	(AF121355) peroxiredoxin TPx1 [Arabidopsis thaliana]

Seq. No.	160938
Seq. ID	LIB3177-012-P1-K2-B7
Method	BLASTX
NCBI GI	g2781394
BLAST score	328
E value	8.0e-31
Match length	87
% identity	83
NCBI Description	(U70424) O-methyltransferase 1 [Arabidopsis thaliana]

Seq. No.	160939
Seq. ID	LIB3177-012-P1-K2-B9
Method	BLASTX
NCBI GI	g2642443
BLAST score	280
E value	5.0e-25
Match length	65
% identity	88

NCBI Description	(AC002391) putative cytochrome P450 [Arabidopsis thaliana]
Seq. No.	160940
Seq. ID	LIB3177-012-P1-K2-C1
Method	BLASTN
NCBI GI	g2351068
BLAST score	98
E value	9.0e-48
Match length	256
% identity	86
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MRH10, complete sequence [Arabidopsis thaliana]
Seq. No.	160941
Seq. ID	LIB3177-012-P1-K2-C12
Method	BLASTX
NCBI GI	g4755193
BLAST score	44
E value	5.0e-19
Match length	95
% identity	68
NCBI Description	(AC007018) putative ribosomal protein S17 [Arabidopsis thaliana]
Seq. No.	160942
Seq. ID	LIB3177-012-P1-K2-C2
Method	BLASTX
NCBI GI	g4741929
BLAST score	588
E value	3.0e-61
Match length	112
% identity	96
NCBI Description	(AF130253) membrane related protein CP5 [Arabidopsis thaliana]
Seq. No.	160943
Seq. ID	LIB3177-012-P1-K2-C4
Method	BLASTX
NCBI GI	g3915865
BLAST score	461
E value	1.0e-52
Match length	109
% identity	97
NCBI Description	40S RIBOSOMAL PROTEIN S4
Seq. No.	160944
Seq. ID	LIB3177-012-P1-K2-D1
Method	BLASTN
NCBI GI	g2264303
BLAST score	156
E value	2.0e-82
Match length	397
% identity	97
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MBB18, complete sequence [Arabidopsis thaliana]
Seq. No.	160945

Seq. ID	LIB3177-012-P1-K2-D2
Method	BLASTX
NCBI GI	g4585882
BLAST score	284
E value	1.0e-25
Match length	56
% identity	100
NCBI Description	(AC005850) PSI type III chlorophyll a/b-binding protein [Arabidopsis thaliana]

Seq. No.	160946
Seq. ID	LIB3177-012-P1-K2-D4
Method	BLASTX
NCBI GI	g4263525
BLAST score	507
E value	1.0e-51
Match length	122
% identity	82
NCBI Description	(AC004044) putative photosystem I reaction center subunit II precursor [Arabidopsis thaliana]

Seq. No.	160947
Seq. ID	LIB3177-012-P1-K2-D6
Method	BLASTN
NCBI GI	g2358139
BLAST score	233
E value	1.0e-128
Match length	319
% identity	97
NCBI Description	Arabidopsis thaliana chromosome 1 YAC yUP8H12 complete sequence [Arabidopsis thaliana]

Seq. No.	160948
Seq. ID	LIB3177-012-P1-K2-D7
Method	BLASTX
NCBI GI	g1922244
BLAST score	256
E value	2.0e-22
Match length	66
% identity	76
NCBI Description	(Y10085) putative desication related protein LEA14 [Arabidopsis thaliana] >gi_2505882_emb_CAA73311_ (Y12776) LEA protein [Arabidopsis thaliana]

Seq. No.	160949
Seq. ID	LIB3177-012-P1-K2-D9
Method	BLASTX
NCBI GI	g2062161
BLAST score	94
E value	5.0e-19
Match length	93
% identity	62
NCBI Description	(AC001645) jasmonate inducible protein isolog [Arabidopsis thaliana]

Seq. No.	160950
Seq. ID	LIB3177-012-P1-K2-E10

Method	BLASTN
NCBI GI	g3299824
BLAST score	49
E value	1.0e-18
Match length	88
% identity	95
NCBI Description	Arabidopsis thaliana BAC F4C21 from chromosome IV, top arm, near 17 cM, complete sequence [Arabidopsis thaliana]

Seq. No.	160951
Seq. ID	LIB3177-012-P1-K2-E3
Method	BLASTN
NCBI GI	g2264316
BLAST score	61
E value	1.0e-25
Match length	440
% identity	45
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MRO11, complete sequence [Arabidopsis thaliana]

Seq. No.	160952
Seq. ID	LIB3177-012-P1-K2-E4
Method	BLASTX
NCBI GI	g4220512
BLAST score	448
E value	1.0e-45
Match length	113
% identity	83
NCBI Description	(AL035356) putative pectate lyase [Arabidopsis thaliana]

Seq. No.	160953
Seq. ID	LIB3177-012-P1-K2-E5
Method	BLASTX
NCBI GI	g132074
BLAST score	334
E value	2.0e-31
Match length	63
% identity	98
NCBI Description	RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN 1A PRECURSOR (RUBISCO SMALL SUBUNIT 1A) >gi_68063_pir__RKMUA1 ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain A1 precursor - Arabidopsis thaliana

Seq. No.	160954
Seq. ID	LIB3177-012-P1-K2-E7
Method	BLASTX
NCBI GI	g266731
BLAST score	155
E value	2.0e-10
Match length	48
% identity	60
NCBI Description	PHENYLALANINE AMMONIA-LYASE 1 >gi_282927_pir__S25303 phenylalanine ammonia-lyase (EC 4.3.1.5) - garden pea >gi_217980_dbj_BAA00885_ (D10001) phenylalanine ammonia-lyase [Pisum sativum] >gi_217982_dbj_BAA00886_ (D10002) phenylalanine ammonia-lyase [Pisum sativum]

Seq. No.	160955
Seq. ID	LIB3177-012-P1-K2-E8
Method	BLASTX
NCBI GI	g2781394
BLAST score	582
E value	2.0e-60
Match length	118
% identity	99
NCBI Description	(U70424) O-methyltransferase 1 [Arabidopsis thaliana]

Seq. No.	160956
Seq. ID	LIB3177-012-P1-K2-F1
Method	BLASTX
NCBI GI	g4185509
BLAST score	103
E value	4.0e-44
Match length	110
% identity	77
NCBI Description	(AF102821) actin depolymerizing factor 3 [Arabidopsis thaliana]

Seq. No.	160957
Seq. ID	LIB3177-012-P1-K2-F10
Method	BLASTX
NCBI GI	g1175012
BLAST score	244
E value	7.0e-21
Match length	77
% identity	69
NCBI Description	PLASMA MEMBRANE INTRINSIC PROTEIN 1C (TRANSMEMBRANE PROTEIN B) (TMP-B) >gi_396218_emb_CAA49155_ (X69294) transmembrane protein TMP-B [Arabidopsis thaliana]

Seq. No.	160958
Seq. ID	LIB3177-012-P1-K2-F4
Method	BLASTX
NCBI GI	g3319348
BLAST score	463
E value	2.0e-57
Match length	136
% identity	83
NCBI Description	(AF077407) No definition line found [Arabidopsis thaliana]

Seq. No.	160959
Seq. ID	LIB3177-012-P1-K2-F5
Method	BLASTX
NCBI GI	g2062165
BLAST score	174
E value	7.0e-13
Match length	63
% identity	54
NCBI Description	(AC001645) jasmonate inducible protein isolog [Arabidopsis thaliana]

Seq. No.	160960
Seq. ID	LIB3177-012-P1-K2-F6
Method	BLASTX

NCBI GI	g3790567
BLAST score	405
E value	8.0e-40
Match length	87
% identity	92
NCBI Description	(AF078821) RING-H2 finger protein RHA1b [Arabidopsis thaliana]

Seq. No.	160961
Seq. ID	LIB3177-012-P1-K2-F8
Method	BLASTX
NCBI GI	g280386
BLAST score	434
E value	4.0e-43
Match length	97
% identity	89
NCBI Description	ubiquitin / ribosomal protein CEP52 - Arabidopsis thaliana >gi_166930 (J05507) ubiquitin extension protein (UBQ1) [Arabidopsis thaliana] >gi_166932 (J05508) ubiquitin extension protein (UBQ2) [Arabidopsis thaliana] >gi_4678227_gb_AAD26972.1_AC007135_8 (AC007135) ubiquitin/ribosomal protein CEP52 [Arabidopsis thaliana]

Seq. No.	160962
Seq. ID	LIB3177-012-P1-K2-G10
Method	BLASTN
NCBI GI	g4584351
BLAST score	60
E value	3.0e-25
Match length	132
% identity	86
NCBI Description	Arabidopsis thaliana chromosome II BAC T12H3 genomic sequence, complete sequence

Seq. No.	160963
Seq. ID	LIB3177-012-P1-K2-G12
Method	BLASTX
NCBI GI	g3249081
BLAST score	43
E value	5.0e-69
Match length	139
% identity	96
NCBI Description	(AC004473) Strong similarity to AROGP2 gene gb_1762634 from Lycopersicon esculentum. [Arabidopsis thaliana]

Seq. No.	160964
Seq. ID	LIB3177-012-P1-K2-G2
Method	BLASTN
NCBI GI	g3510339
BLAST score	171
E value	2.0e-91
Match length	354
% identity	92
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K3K7, complete sequence [Arabidopsis thaliana]

Seq. No.	160965

Seq. ID	LIB3177-012-P1-K2-G3
Method	BLASTX
NCBI GI	g4741960
BLAST score	455
E value	2.0e-45
Match length	102
% identity	86
NCBI Description	(AF134130) Lhcb6 protein [Arabidopsis thaliana]

Seq. No.	160966
Seq. ID	LIB3177-012-P1-K2-G4
Method	BLASTX
NCBI GI	g132677
BLAST score	174
E value	1.0e-12
Match length	67
% identity	58
NCBI Description	50S RIBOSOMAL PROTEIN L15, CHLOROPLAST PRECURSOR (CL15) >gi_71241_pir__R5MUL5 ribosomal protein L15 precursor, chloroplast - Arabidopsis thaliana >gi_16497_emb_CAA77593_ (Z11508) Plastid ribosomal protein CL15 [Arabidopsis thaliana]

Seq. No.	160967
Seq. ID	LIB3177-012-P1-K2-G7
Method	BLASTX
NCBI GI	g4835233
BLAST score	268
E value	2.0e-23
Match length	133
% identity	69
NCBI Description	(AL049862) putative protein 1 photosystem II oxygen-evolving complex [Arabidopsis thaliana]

Seq. No.	160968
Seq. ID	LIB3177-012-P1-K2-G8
Method	BLASTX
NCBI GI	g3894193
BLAST score	328
E value	1.0e-30
Match length	113
% identity	55
NCBI Description	(AC005662) putative strictosidine synthase [Arabidopsis thaliana]

Seq. No.	160969
Seq. ID	LIB3177-012-P1-K2-G9
Method	BLASTX
NCBI GI	g541858
BLAST score	743
E value	3.0e-79
Match length	139
% identity	94
NCBI Description	endoxyloglucan transferase - Arabidopsis thaliana >gi_469484_dbj_BAA03921_ (D16454) endo-xyloglucan transferase [Arabidopsis thaliana] >gi_4063757 (AC005561) endo-xyloglucan transferase [Arabidopsis thaliana]

Seq. No.	160970
Seq. ID	LIB3177-012-P1-K2-H10
Method	BLASTX
NCBI GI	g132110
BLAST score	330
E value	4.0e-31
Match length	77
% identity	87
NCBI Description	RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN 3B PRECURSOR (RUBISCO SMALL SUBUNIT 3B) >gi_68060_pir__RKMUB3 ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain B3 precursor - Arabidopsis thaliana >gi_16195_emb_CAA32702_ (X14564) ribulose bisphosphate carboxylase [Arabidopsis thaliana]

Seq. No.	160971
Seq. ID	LIB3177-012-P1-K2-H11
Method	BLASTX
NCBI GI	g4760553
BLAST score	460
E value	3.0e-46
Match length	107
% identity	86
NCBI Description	(AB019533) Nad-dependent formate dehydrogenase [Oryza sativa]

Seq. No.	160972
Seq. ID	LIB3177-012-P1-K2-H2
Method	BLASTX
NCBI GI	g3157944
BLAST score	515
E value	1.0e-52
Match length	114
% identity	89
NCBI Description	(AC002131) Very strong similarity to aminomethyltransferase precursor gb_U79769 from Mesembryanthemum crystallinum. ESTs gb_T43167, gb_T21076, gb_H36999, gb_T22773, gb_N38038, gb_T13742, gb_Z26545, gb_T20753 and gb_W43123 come from this ge

Seq. No.	160973
Seq. ID	LIB3177-012-P1-K2-H3
Method	BLASTX
NCBI GI	g2499811
BLAST score	438
E value	1.0e-43
Match length	91
% identity	91
NCBI Description	PROFILIN 2 >gi_1353766 (U43323) profilin 2 [Arabidopsis thaliana] >gi_1353772 (U43326) profilin 2 [Arabidopsis thaliana]

Seq. No.	160974
Seq. ID	LIB3177-012-P1-K2-H5
Method	BLASTX
NCBI GI	g1086833

BLAST score	227
E value	7.0e-19
Match length	106
% identity	37
NCBI Description	(U41264) coded for by C. elegans cDNA CEESN26F; coded for by C. elegans cDNA CEESI89F; similar to 60S acidic ribosomal protein Po (L10) [Caenorhabditis elegans]

Seq. No.	160975
Seq. ID	LIB3177-012-P1-K2-H7
Method	BLASTX
NCBI GI	g3721926
BLAST score	492
E value	5.0e-50
Match length	99
% identity	97
NCBI Description	(AB017480) chloroplast FtsH protease [Nicotiana tabacum]

Seq. No.	160976
Seq. ID	LIB3177-012-P1-K2-H8
Method	BLASTX
NCBI GI	g4165132
BLAST score	333
E value	2.0e-31
Match length	72
% identity	83
NCBI Description	(AF098292) endo-beta-1,4-D-glucanase [Lycopersicon esculentum]

Seq. No.	160977
Seq. ID	LIB3177-012-P1-K2-H9
Method	BLASTX
NCBI GI	g131381
BLAST score	44
E value	3.0e-12
Match length	63
% identity	76
NCBI Description	OXYGEN-EVOLVING ENHANCER PROTEIN 1 PRECURSOR (OEE1) (33 KD SUBUNIT OF OXYGEN EVOLVING SYSTEM OF PHOTOSYSTEM II) (33 KD THYLAKOID MEMBRANE PROTEIN) >gi_99745_pir__S11852 photosystem II oxygen-evolving complex protein 1 precursor - Arabidopsis thaliana >gi_22571_emb_CAA36675_ (X52428) 33 kDa oxygen-evolving protein [Arabidopsis thaliana]

Seq. No.	160978
Seq. ID	LIB3177-013-P1-K1-A1
Method	BLASTX
NCBI GI	g3335340
BLAST score	292
E value	2.0e-26
Match length	107
% identity	58
NCBI Description	(AC004512) Strong similarity to xylglucan endo-transglycolsylase (TCH4) gene gb_U27609, first exon contains strong similarity to meri 5 gene gb_Z17989 from A. thaliana. EST gb_N37583 comes from this gene. [Arabidopsis thaliana]

Seq. No.	160979
Seq. ID	LIB3177-013-P1-K1-A11
Method	BLASTN
NCBI GI	g4512656
BLAST score	72
E value	3.0e-32
Match length	241
% identity	86
NCBI Description	Arabidopsis thaliana chromosome II BAC F7D19 genomic sequence, complete sequence

Seq. No.	160980
Seq. ID	LIB3177-013-P1-K1-A3
Method	BLASTX
NCBI GI	g1769905
BLAST score	208
E value	1.0e-16
Match length	98
% identity	47
NCBI Description	(X98108) 23 kDa polypeptide of oxygen-evolving comlex (OEC) [Arabidopsis thaliana]

Seq. No.	160981
Seq. ID	LIB3177-013-P1-K1-B2
Method	BLASTX
NCBI GI	g2996158
BLAST score	150
E value	1.0e-09
Match length	39
% identity	69
NCBI Description	(AF051753) GASA5-like protein [Picea mariana] >gi_2996160 (AF051754) GASA5-like protein [Picea mariana]

Seq. No.	160982
Seq. ID	LIB3177-013-P1-K1-B4
Method	BLASTX
NCBI GI	g541546
BLAST score	322
E value	8.0e-30
Match length	117
% identity	13
NCBI Description	ubiquitin precursor - Volvox carteri >gi_395295_emb_CAA52290_ (X74214) polyubiquitin [Volvox carteri]

Seq. No.	160983
Seq. ID	LIB3177-013-P1-K1-B5
Method	BLASTN
NCBI GI	g2924654
BLAST score	47
E value	2.0e-17
Match length	149
% identity	86
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MHK7, complete sequence [Arabidopsis thaliana]

Seq. No.	160984
Seq. ID	LIB3177-013-P1-K1-C1
Method	BLASTN
NCBI GI	g2980757
BLAST score	116
E value	2.0e-58
Match length	304
% identity	85
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F6I18 (ESSAII project)

Seq. No.	160985
Seq. ID	LIB3177-013-P1-K1-C3
Method	BLASTX
NCBI GI	g421826
BLAST score	237
E value	6.0e-20
Match length	96
% identity	51
NCBI Description	chlorophyll a/b-binding protein CP29 - Arabidopsis thaliana >gi_298036_emb_CAA50712_ (X71878) CP29 [Arabidopsis thaliana]

Seq. No.	160986
Seq. ID	LIB3177-013-P1-K1-D11
Method	BLASTX
NCBI GI	g477819
BLAST score	173
E value	2.0e-12
Match length	103
% identity	36
NCBI Description	mitochondrial processing peptidase (EC 3.4.99.41) beta chain precursor - potato >gi_410634_bbs_136741 cytochrome c reductase-processing peptidase subunit II, MPP subunit II, P53 [potatoes, var. Marfona, tuber, Peptide Mitochondrial, 530 aa]

Seq. No.	160987
Seq. ID	LIB3177-013-P1-K1-D2
Method	BLASTN
NCBI GI	g2618677
BLAST score	67
E value	3.0e-29
Match length	192
% identity	88
NCBI Description	Arabidopsis thaliana BAC F21B7 chromosome 1, complete sequence [Arabidopsis thaliana]

Seq. No.	160988
Seq. ID	LIB3177-013-P1-K1-D3
Method	BLASTN
NCBI GI	g4159703
BLAST score	57
E value	2.0e-23
Match length	289
% identity	80
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:

K5F14, complete sequence

Seq. No.	160989
Seq. ID	LIB3177-013-P1-K1-E4
Method	BLASTX
NCBI GI	g2781394
BLAST score	307
E value	3.0e-28
Match length	102
% identity	56
NCBI Description	(U70424) O-methyltransferase 1 [Arabidopsis thaliana]

Seq. No.	160990
Seq. ID	LIB3177-013-P1-K1-E5
Method	BLASTX
NCBI GI	g2895510
BLAST score	147
E value	2.0e-09
Match length	128
% identity	34
NCBI Description	(AF033204) putative pectin methylesterase [Arabidopsis thaliana]

Seq. No.	160991
Seq. ID	LIB3177-013-P1-K1-E6
Method	BLASTX
NCBI GI	g3421090
BLAST score	169
E value	4.0e-12
Match length	93
% identity	42
NCBI Description	(AF043525) 20S proteasome subunit PAE2 [Arabidopsis thaliana]

Seq. No.	160992
Seq. ID	LIB3177-013-P1-K1-F1
Method	BLASTX
NCBI GI	g3885511
BLAST score	151
E value	8.0e-10
Match length	106
% identity	39
NCBI Description	(AF084200) similar to PSI-K subunit of photosystem I from barley [Medicago sativa]

Seq. No.	160993
Seq. ID	LIB3177-013-P1-K1-F2
Method	BLASTX
NCBI GI	g1769905
BLAST score	198
E value	2.0e-15
Match length	75
% identity	53
NCBI Description	(X98108) 23 kDa polypeptide of oxygen-evolving comlex (OEC) [Arabidopsis thaliana]

Seq. No. 160994

Seq. ID	LIB3177-013-P1-K1-F5
Method	BLASTX
NCBI GI	g132074
BLAST score	148
E value	1.0e-09
Match length	75
% identity	45
NCBI Description	RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN 1A PRECURSOR (RUBISCO SMALL SUBUNIT 1A) >gi_68063_pir__RKMUA1 ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain A1 precursor - Arabidopsis thaliana

Seq. No.	160995
Seq. ID	LIB3177-013-P1-K1-F6
Method	BLASTN
NCBI GI	g2266989
BLAST score	43
E value	6.0e-15
Match length	226
% identity	81
NCBI Description	Arabidopsis thaliana vacuolar type ATPase subunit A mRNA, complete cds

Seq. No.	160996
Seq. ID	LIB3177-013-P1-K1-G1
Method	BLASTX
NCBI GI	g1363489
BLAST score	222
E value	4.0e-18
Match length	118
% identity	42
NCBI Description	thioglucosidase (EC 3.2.3.1) 3D precursor - Arabidopsis thaliana >gi_984052_emb_CAA61592_ (X89413) thioglucoside glucohydrolase [Arabidopsis thaliana]

Seq. No.	160997
Seq. ID	LIB3177-013-P1-K1-G3
Method	BLASTN
NCBI GI	g4678371
BLAST score	48
E value	7.0e-18
Match length	152
% identity	83
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone T6G15 (ESSA project)

Seq. No.	160998
Seq. ID	LIB3177-013-P1-K1-G6
Method	BLASTN
NCBI GI	g2760164
BLAST score	41
E value	1.0e-13
Match length	169
% identity	81
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K18P6, complete sequence [Arabidopsis thaliana]

Seq. No.	160999
Seq. ID	LIB3177-013-P1-K1-H4
Method	BLASTX
NCBI GI	g2062158
BLAST score	286
E value	1.0e-25
Match length	129
% identity	24
NCBI Description	(AC001645) jasmonate inducible protein isolog [Arabidopsis thaliana]

Seq. No.	161000
Seq. ID	LIB3177-013-P1-K2-A1
Method	BLASTX
NCBI GI	g3335340
BLAST score	524
E value	1.0e-53
Match length	126
% identity	79
NCBI Description	(AC004512) Strong similarity to xylglucan endo-transglycolsylase (TCH4) gene gb_U27609, first exon contains strong similarity to meri 5 gene gb_Z17989 from A. thaliana. EST gb_N37583 comes from this gene. [Arabidopsis thaliana]

Seq. No.	161001
Seq. ID	LIB3177-013-P1-K2-A11
Method	BLASTN
NCBI GI	g4512656
BLAST score	285
E value	1.0e-159
Match length	437
% identity	93
NCBI Description	Arabidopsis thaliana chromosome II BAC F7D19 genomic sequence, complete sequence

Seq. No.	161002
Seq. ID	LIB3177-013-P1-K2-A3
Method	BLASTX
NCBI GI	g1769905
BLAST score	558
E value	2.0e-57
Match length	113
% identity	96
NCBI Description	(X98108) 23 kDa polypeptide of oxygen-evolving comlex (OEC) [Arabidopsis thaliana]

Seq. No.	161003
Seq. ID	LIB3177-013-P1-K2-A4
Method	BLASTX
NCBI GI	g416681
BLAST score	264
E value	6.0e-23
Match length	145
% identity	42
NCBI Description	ATP SYNTHASE DELTA CHAIN, CHLOROPLAST PRECURSOR >gi_280404_pir__S26198 H+-transporting ATP synthase (EC

3.6.1.34) delta chain precursor, chloroplast - common tobacco >gi_19787_emb_CAA45153_ (X63607) chloroplast ATP synthase (delta subunit) [Nicotiana tabacum]

Seq. No.	161004
Seq. ID	LIB3177-013-P1-K2-A5
Method	BLASTX
NCBI GI	g1706130
BLAST score	243
E value	9.0e-21
Match length	73
% identity	67
NCBI Description	CDPK-RELATED PROTEIN KINASE (PK421) >gi_2129917_pir__S60052 calcium-dependent protein kinase homolog - carrot >gi_1103386_emb_CAA58750_ (X83869) CDPK-related protein kinase [Daucus carota]

Seq. No.	161005
Seq. ID	LIB3177-013-P1-K2-A7
Method	BLASTX
NCBI GI	g3249039
BLAST score	185
E value	1.0e-13
Match length	86
% identity	45
NCBI Description	(AF071221) N-carbamyl-L-amino acid amidohydrolase [Arthrobacter aurescens]

Seq. No.	161006
Seq. ID	LIB3177-013-P1-K2-B1
Method	BLASTN
NCBI GI	g4539331
BLAST score	445
E value	0.0e+00
Match length	453
% identity	100
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F22I13 (ESSA project)

Seq. No.	161007
Seq. ID	LIB3177-013-P1-K2-B2
Method	BLASTX
NCBI GI	g2996158
BLAST score	333
E value	4.0e-31
Match length	61
% identity	85
NCBI Description	(AF051753) GASA5-like protein [Picea mariana] >gi_2996160 (AF051754) GASA5-like protein [Picea mariana]

Seq. No.	161008
Seq. ID	LIB3177-013-P1-K2-B3
Method	BLASTX
NCBI GI	g3482915
BLAST score	295
E value	1.0e-26
Match length	74

% identity	76
NCBI Description	(AC003970) Similar to 12-oxophytodienoate reductase, gi_2765083 and old-yellow-enzyme homolog, gi_2232254 [Arabidopsis thaliana]
Seq. No.	161009
Seq. ID	LIB3177-013-P1-K2-B4
Method	BLASTX
NCBI GI	g1076708
BLAST score	602
E value	1.0e-62
Match length	121
% identity	28
NCBI Description	seed tetraubiquitin - common sunflower >gi_303901_dbj_BAA03764_ (D16248) ubiquitin [Glycine max] >gi_456714_dbj_BAA05670_ (D28123) Ubiquitin [Glycine max] >gi_556688_emb_CAA84440_ (Z34988) seed tetraubiquitin [Helianthus annuus] >gi_994785_dbj_BAA05085_ (D26092) Ubiquitin [Glycine max] >gi_4263514_gb_AAD15340_ (AC004044) putative polyubiquitin [Arabidopsis thaliana] >gi_1096513_prf__2111434A tetraubiquitin [Helianthus annuus]
Seq. No.	161010
Seq. ID	LIB3177-013-P1-K2-B5
Method	BLASTX
NCBI GI	g82263
BLAST score	314
E value	5.0e-40
Match length	98
% identity	86
NCBI Description	ubiquinol--cytochrome-c reductase (EC 1.10.2.2) cytochrome c1 precursor (clone pC(1)3II) - potato
Seq. No.	161011
Seq. ID	LIB3177-013-P1-K2-B7
Method	BLASTX
NCBI GI	g99735
BLAST score	63
E value	6.0e-14
Match length	81
% identity	58
NCBI Description	L-ascorbate peroxidase (EC 1.11.1.11) precursor - Arabidopsis thaliana (fragment)
Seq. No.	161012
Seq. ID	LIB3177-013-P1-K2-B8
Method	BLASTX
NCBI GI	g2827704
BLAST score	490
E value	1.0e-49
Match length	108
% identity	90
NCBI Description	(AL021684) LRR-like protein [Arabidopsis thaliana]
Seq. No.	161013
Seq. ID	LIB3177-013-P1-K2-C1

Method	BLASTX
NCBI GI	g2980768
BLAST score	500
E value	1.0e-50
Match length	101
% identity	97
NCBI Description	(AL022198) putative protein [Arabidopsis thaliana]

Seq. No.	161014
Seq. ID	LIB3177-013-P1-K2-C10
Method	BLASTN
NCBI GI	g3650026
BLAST score	92
E value	2.0e-44
Match length	180
% identity	88
NCBI Description	Arabidopsis thaliana chromosome II BAC T26I20 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	161015
Seq. ID	LIB3177-013-P1-K2-C2
Method	BLASTN
NCBI GI	g4584841
BLAST score	167
E value	7.0e-89
Match length	455
% identity	99
NCBI Description	Genomic sequence for Arabidopsis thaliana BAC T23E23, complete sequence

Seq. No.	161016
Seq. ID	LIB3177-013-P1-K2-C3
Method	BLASTX
NCBI GI	g421826
BLAST score	633
E value	3.0e-66
Match length	143
% identity	83
NCBI Description	chlorophyll a/b-binding protein CP29 - Arabidopsis thaliana >gi_298036_emb_CAA50712_ (X71878) CP29 [Arabidopsis thaliana]

Seq. No.	161017
Seq. ID	LIB3177-013-P1-K2-C7
Method	BLASTX
NCBI GI	g119905
BLAST score	407
E value	9.0e-40
Match length	88
% identity	84
NCBI Description	FERREDOXIN--NADP REDUCTASE, LEAF ISOZYME PRECURSOR (FNR) >gi_81898_pir__S04030 ferredoxin--NADP+ reductase (EC 1.18.1.2) precursor - garden pea >gi_20722_emb_CAA30978_ (X12446) ferredoxin-NADH+ reductase preprotein (AA -52 to 308) [Pisum sativum] >gi_226545_prf__1601517A ferredoxin NADP reductase [Arachis hypogaea]

Seq. No.	161018
Seq. ID	LIB3177-013-P1-K2-C9
Method	BLASTN
NCBI GI	g2244901
BLAST score	50
E value	4.0e-19
Match length	213
% identity	85
NCBI Description	Arabidopsis thaliana DNA chromosome 4, ESSA I contig fragment No

Seq. No.	161019
Seq. ID	LIB3177-013-P1-K2-D11
Method	BLASTX
NCBI GI	g477819
BLAST score	480
E value	2.0e-48
Match length	118
% identity	78
NCBI Description	mitochondrial processing peptidase (EC 3.4.99.41) beta chain precursor - potato >gi_410634_bbs_136741 cytochrome c reductase-processing peptidase subunit II, MPP subunit II, P53 [potatoes, var. Marfona, tuber, Peptide Mitochondrial, 530 aa]

Seq. No.	161020
Seq. ID	LIB3177-013-P1-K2-D2
Method	BLASTX
NCBI GI	g2809242
BLAST score	709
E value	4.0e-75
Match length	143
% identity	100
NCBI Description	(AC002560) F21B7.11 [Arabidopsis thaliana]

Seq. No.	161021
Seq. ID	LIB3177-013-P1-K2-D3
Method	BLASTX
NCBI GI	g4454467
BLAST score	213
E value	5.0e-17
Match length	140
% identity	34
NCBI Description	(AC006234) unknown protein [Arabidopsis thaliana]

Seq. No.	161022
Seq. ID	LIB3177-013-P1-K2-D4
Method	BLASTN
NCBI GI	g2961335
BLAST score	244
E value	1.0e-135
Match length	252
% identity	99
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F1N20 (ESSAII project)

Seq. No.	161023

Seq. ID	LIB3177-013-P1-K2-D5
Method	BLASTN
NCBI GI	g2264315
BLAST score	141
E value	2.0e-73
Match length	195
% identity	93
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MRN17, complete sequence [Arabidopsis thaliana]

Seq. No.	161024
Seq. ID	LIB3177-013-P1-K2-E10
Method	BLASTX
NCBI GI	g132675
BLAST score	253
E value	5.0e-26
Match length	78
% identity	85
NCBI Description	CHLOROPLAST 50S RIBOSOMAL PROTEIN L14 >gi_71222_pir__R5NT14 ribosomal protein L14 - common tobacco chloroplast >gi_11864_emb_CAA77379_ (Z00044) ribosomal protein L14 [Nicotiana tabacum] >gi_225233_prf__1211235BQ ribosomal protein L14 [Nicotiana tabacum]

Seq. No.	161025
Seq. ID	LIB3177-013-P1-K2-E2
Method	BLASTX
NCBI GI	g4586256
BLAST score	593
E value	1.0e-61
Match length	130
% identity	91
NCBI Description	(AL049640) probable photosystem I chain XI precursor [Arabidopsis thaliana]

Seq. No.	161026
Seq. ID	LIB3177-013-P1-K2-E4
Method	BLASTX
NCBI GI	g2781394
BLAST score	631
E value	1.0e-67
Match length	137
% identity	94
NCBI Description	(U70424) O-methyltransferase 1 [Arabidopsis thaliana]

Seq. No.	161027
Seq. ID	LIB3177-013-P1-K2-E5
Method	BLASTX
NCBI GI	g2895510
BLAST score	57
E value	2.0e-49
Match length	126
% identity	87
NCBI Description	(AF033204) putative pectin methylesterase [Arabidopsis thaliana]

Seq. No.	161028

Seq. ID	LIB3177-013-P1-K2-E6
Method	BLASTX
NCBI GI	g3421087
BLAST score	478
E value	5.0e-48
Match length	100
% identity	96
NCBI Description	(AF043524) 20S proteasome subunit PAE1 [Arabidopsis thaliana]

Seq. No.	161029
Seq. ID	LIB3177-013-P1-K2-E7
Method	BLASTX
NCBI GI	g1652892
BLAST score	286
E value	1.0e-25
Match length	89
% identity	39
NCBI Description	(D90909) ABC transporter [Synechocystis sp.]

Seq. No.	161030
Seq. ID	LIB3177-013-P1-K2-E8
Method	BLASTX
NCBI GI	g166708
BLAST score	327
E value	9.0e-31
Match length	87
% identity	80
NCBI Description	(M64118) glyceraldehyde-3-phosphate dehydrogenase [Arabidopsis thaliana]

Seq. No.	161031
Seq. ID	LIB3177-013-P1-K2-E9
Method	BLASTX
NCBI GI	g3688799
BLAST score	445
E value	3.0e-44
Match length	131
% identity	82
NCBI Description	(AF057137) gamma tonoplast intrinsic protein 2 [Arabidopsis thaliana]

Seq. No.	161032
Seq. ID	LIB3177-013-P1-K2-F1
Method	BLASTX
NCBI GI	g3885511
BLAST score	416
E value	8.0e-41
Match length	102
% identity	81
NCBI Description	(AF084200) similar to PSI-K subunit of photosystem I from barley [Medicago sativa]

Seq. No.	161033
Seq. ID	LIB3177-013-P1-K2-F10
Method	BLASTX
NCBI GI	g3059095

BLAST score	233
E value	9.0e-20
Match length	69
% identity	68
NCBI Description	(AJ001091) magnesium chelatase subunit [Glycine max]

Seq. No.	161034
Seq. ID	LIB3177-013-P1-K2-F2
Method	BLASTX
NCBI GI	g1769905
BLAST score	469
E value	5.0e-47
Match length	135
% identity	68
NCBI Description	(X98108) 23 kDa polypeptide of oxygen-evolving comlex (OEC) [Arabidopsis thaliana]

Seq. No.	161035
Seq. ID	LIB3177-013-P1-K2-F4
Method	BLASTX
NCBI GI	g2660664
BLAST score	46
E value	7.0e-43
Match length	121
% identity	82
NCBI Description	(AC002342) unknown protein [Arabidopsis thaliana]

Seq. No.	161036
Seq. ID	LIB3177-013-P1-K2-F7
Method	BLASTX
NCBI GI	g3885511
BLAST score	408
E value	7.0e-40
Match length	103
% identity	80
NCBI Description	(AF084200) similar to PSI-K subunit of photosystem I from barley [Medicago sativa]

Seq. No.	161037
Seq. ID	LIB3177-013-P1-K2-F8
Method	BLASTX
NCBI GI	g224293
BLAST score	383
E value	5.0e-37
Match length	78
% identity	99
NCBI Description	histone H4 [Triticum aestivum]

Seq. No.	161038
Seq. ID	LIB3177-013-P1-K2-F9
Method	BLASTN
NCBI GI	g3449316
BLAST score	48
E value	6.0e-18
Match length	202
% identity	84
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:

K9D7, complete sequence [Arabidopsis thaliana]

Seq. No.	161039
Seq. ID	LIB3177-013-P1-K2-G1
Method	BLASTX
NCBI GI	g1363489
BLAST score	499
E value	2.0e-65
Match length	123
% identity	99
NCBI Description	thioglucosidase (EC 3.2.3.1) 3D precursor - Arabidopsis thaliana >gi_984052_emb_CAA61592_ (X89413) thioglucoside glucohydrolase [Arabidopsis thaliana]

Seq. No.	161040
Seq. ID	LIB3177-013-P1-K2-G10
Method	BLASTN
NCBI GI	g4662640
BLAST score	364
E value	0.0e+00
Match length	445
% identity	46
NCBI Description	Arabidopsis thaliana chromosome II BAC F15K19 genomic sequence, complete sequence

Seq. No.	161041
Seq. ID	LIB3177-013-P1-K2-G11
Method	BLASTX
NCBI GI	g1491710
BLAST score	167
E value	1.0e-11
Match length	56
% identity	54
NCBI Description	(X96506) alpha subunit; forms heterodimer with NC2 alpha/Dr1 [Homo sapiens]

Seq. No.	161042
Seq. ID	LIB3177-013-P1-K2-G12
Method	BLASTX
NCBI GI	g730645
BLAST score	134
E value	1.0e-22
Match length	78
% identity	78
NCBI Description	40S RIBOSOMAL PROTEIN S15 >gi_629556_pir__S43412 ribosomal protein S15 - Arabidopsis thaliana >gi_313152_emb_CAA80679_ (Z23161) ribosomal protein S15 [Arabidopsis thaliana] >gi_313188_emb_CAA80681_ (Z23162) ribosomal protein S15 [Arabidopsis thaliana] >gi_1903366_gb_AAB70449_ (AC000104) Strong similarity to Oryza 40S ribosomal protein S15. ESTs gb_R29788,gb_ATTS0365 come from this gene. [Arabidopsis thaliana]

Seq. No.	161043
Seq. ID	LIB3177-013-P1-K2-G2
Method	BLASTX
NCBI GI	g2924772

BLAST score	670
E value	1.0e-70
Match length	130
% identity	97
NCBI Description	(AC002334) unknown protein [Arabidopsis thaliana]

Seq. No.	161044
Seq. ID	LIB3177-013-P1-K2-G3
Method	BLASTN
NCBI GI	g3309276
BLAST score	190
E value	1.0e-102
Match length	435
% identity	52
NCBI Description	Arabidopsis thaliana BAC T26N6 from chromosome IV at 19.3 cM, complete sequence

Seq. No.	161045
Seq. ID	LIB3177-013-P1-K2-G4
Method	BLASTX
NCBI GI	g2529229
BLAST score	574
E value	2.0e-59
Match length	131
% identity	87
NCBI Description	(AB007907) 6-phosphogluconate dehydrogenase [Glycine max]

Seq. No.	161046
Seq. ID	LIB3177-013-P1-K2-G5
Method	BLASTN
NCBI GI	g3047088
BLAST score	36
E value	8.0e-11
Match length	172
% identity	80
NCBI Description	Arabidopsis thaliana BAC T26D22

Seq. No.	161047
Seq. ID	LIB3177-013-P1-K2-G6
Method	BLASTX
NCBI GI	g170131
BLAST score	316
E value	5.0e-29
Match length	76
% identity	76
NCBI Description	(M55322) ribosomal protein 30S subunit [Spinacia oleracea]

Seq. No.	161048
Seq. ID	LIB3177-013-P1-K2-G7
Method	BLASTX
NCBI GI	g115767
BLAST score	618
E value	2.0e-64
Match length	122
% identity	95
NCBI Description	CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR (CAB-165/180) (LHCP) >gi_81603_pir__A29280 chlorophyll

a/b-binding protein ab165 - Arabidopsis thaliana
>gi_16368_emb_CAA27540_ (X03907) chlorophyll a/b binding protein (LHCP AB 65) [Arabidopsis thaliana]
>gi_16372_emb_CAA27541_ (X03908) chlorophyll a/b binding protein (LHCP AB 180) [Arabidopsis thaliana]

Seq. No.	161049
Seq. ID	LIB3177-013-P1-K2-G8
Method	BLASTX
NCBI GI	g4455170
BLAST score	609
E value	8.0e-68
Match length	150
% identity	86
NCBI Description	(AL035521) fatty acid elongase-like protein [Arabidopsis thaliana]

Seq. No.	161050
Seq. ID	LIB3177-013-P1-K2-G9
Method	BLASTX
NCBI GI	g4454037
BLAST score	447
E value	5.0e-46
Match length	112
% identity	86
NCBI Description	(AL035394) putative major latex protein [Arabidopsis thaliana]

Seq. No.	161051
Seq. ID	LIB3177-013-P1-K2-H1
Method	BLASTX
NCBI GI	g3264757
BLAST score	448
E value	2.0e-48
Match length	143
% identity	70
NCBI Description	(AF071888) zeaxanthin epoxidase [Prunus armeniaca]

Seq. No.	161052
Seq. ID	LIB3177-013-P1-K2-H4
Method	BLASTX
NCBI GI	g2062158
BLAST score	422
E value	1.0e-41
Match length	90
% identity	48
NCBI Description	(AC001645) jasmonate inducible protein isolog [Arabidopsis thaliana]

Seq. No.	161053
Seq. ID	LIB3177-014-P1-K1-A2
Method	BLASTN
NCBI GI	g2564047
BLAST score	41
E value	7.0e-14
Match length	183
% identity	87

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NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MJB21, complete sequence [Arabidopsis thaliana]
Seq. No.	161054
Seq. ID	LIB3177-014-P1-K1-A7
Method	BLASTX
NCBI GI	g3860259
BLAST score	165
E value	5.0e-12
Match length	62
% identity	58
NCBI Description	(AC005824) unknown protein [Arabidopsis thaliana]
Seq. No.	161055
Seq. ID	LIB3177-014-P1-K1-E10
Method	BLASTN
NCBI GI	g4678219
BLAST score	82
E value	3.0e-38
Match length	243
% identity	82
NCBI Description	Arabidopsis thaliana chromosome II BAC F9C22 genomic sequence, complete sequence
Seq. No.	161056
Seq. ID	LIB3177-014-P1-K1-E4
Method	BLASTX
NCBI GI	g3236248
BLAST score	168
E value	4.0e-12
Match length	69
% identity	46
NCBI Description	(AC004684) unknown protein [Arabidopsis thaliana]
Seq. No.	161057
Seq. ID	LIB3177-014-P1-K1-F3
Method	BLASTX
NCBI GI	g1483218
BLAST score	154
E value	2.0e-10
Match length	71
% identity	51
NCBI Description	(X99793) induced upon wounding stress [Arabidopsis thaliana]
Seq. No.	161058
Seq. ID	LIB3177-014-P1-K1-H9
Method	BLASTX
NCBI GI	g119975
BLAST score	264
E value	3.0e-23
Match length	92
% identity	61
NCBI Description	FERREDOXIN PRECURSOR >gi_99692_pir__S09979 ferredoxin [2Fe-2S] precursor - Arabidopsis thaliana >gi_16437_emb_CAA35754_ (X51370) ferredoxin precursor [Arabidopsis thaliana] >gi_166698 (M35868) ferrodoxin A

[Arabidopsis thaliana]

Seq. No.	161059
Seq. ID	LIB3177-014-P1-K2-A1
Method	BLASTN
NCBI GI	g2564047
BLAST score	81
E value	1.0e-37
Match length	348
% identity	98
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MJB21, complete sequence [Arabidopsis thaliana]

Seq. No.	161060
Seq. ID	LIB3177-014-P1-K2-A10
Method	BLASTN
NCBI GI	g4454447
BLAST score	281
E value	1.0e-157
Match length	285
% identity	100
NCBI Description	Arabidopsis thaliana chromosome II BAC F5H14 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	161061
Seq. ID	LIB3177-014-P1-K2-A3
Method	BLASTX
NCBI GI	g132102
BLAST score	616
E value	2.0e-64
Match length	115
% identity	97
NCBI Description	RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN 2B PRECURSOR (RUBISCO SMALL SUBUNIT 2B) >gi_68061_pir__RKMUB2 ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain B2 precursor - Arabidopsis thaliana >gi_16194_emb_CAA32701_ (X14564) ribulose bisphosphate carboxylase [Arabidopsis thaliana]

Seq. No.	161062
Seq. ID	LIB3177-014-P1-K2-A6
Method	BLASTX
NCBI GI	g4107103
BLAST score	59
E value	4.0e-22
Match length	79
% identity	72
NCBI Description	(AB015143) AHP3 [Arabidopsis thaliana]

Seq. No.	161063
Seq. ID	LIB3177-014-P1-K2-A9
Method	BLASTX
NCBI GI	g4559354
BLAST score	143
E value	5.0e-09
Match length	65
% identity	4

NCBI Description	(AC006585) unknown protein [Arabidopsis thaliana]

Seq. No.	161064
Seq. ID	LIB3177-014-P1-K2-B1
Method	BLASTN
NCBI GI	g3298610
BLAST score	153
E value	5.0e-81
Match length	157
% identity	99
NCBI Description	Arabidopsis thaliana BAC T2H3

Seq. No.	161065
Seq. ID	LIB3177-014-P1-K2-B11
Method	BLASTN
NCBI GI	g2739359
BLAST score	34
E value	2.0e-09
Match length	150
% identity	83
NCBI Description	Arabidopsis thaliana chromosome II BAC T9J22 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	161066
Seq. ID	LIB3177-014-P1-K2-B2
Method	BLASTN
NCBI GI	g2618605
BLAST score	84
E value	2.0e-39
Match length	301
% identity	97
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MUK11, complete sequence [Arabidopsis thaliana]

Seq. No.	161067
Seq. ID	LIB3177-014-P1-K2-B4
Method	BLASTX
NCBI GI	g3142294
BLAST score	284
E value	2.0e-25
Match length	111
% identity	61
NCBI Description	(AC002411) Strong similarity to initiation factor eIF-2, gb_U37354 from S. pombe. ESTs gb_T41979, gb_N37284 and gb_N37529 come from this gene. [Arabidopsis thaliana]

Seq. No.	161068
Seq. ID	LIB3177-014-P1-K2-B5
Method	BLASTX
NCBI GI	g2739382
BLAST score	532
E value	2.0e-54
Match length	151
% identity	75
NCBI Description	(AC002505) myosin heavy chain-like protein [Arabidopsis thaliana]

Seq. No.	161069
Seq. ID	LIB3177-014-P1-K2-B6
Method	BLASTX
NCBI GI	g4678332
BLAST score	460
E value	6.0e-46
Match length	130
% identity	65
NCBI Description	(AL049658) putative peptide transporter [Arabidopsis thaliana]

Seq. No.	161070
Seq. ID	LIB3177-014-P1-K2-C3
Method	BLASTN
NCBI GI	g4263694
BLAST score	74
E value	9.0e-34
Match length	102
% identity	93
NCBI Description	Arabidopsis thaliana chromosome II BAC F22D22 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	161071
Seq. ID	LIB3177-014-P1-K2-C6
Method	BLASTX
NCBI GI	g132074
BLAST score	170
E value	1.0e-15
Match length	108
% identity	54
NCBI Description	RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN 1A PRECURSOR (RUBISCO SMALL SUBUNIT 1A) >gi_68063_pir__RKMUA1 ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain A1 precursor - Arabidopsis thaliana

Seq. No.	161072
Seq. ID	LIB3177-014-P1-K2-C8
Method	BLASTN
NCBI GI	g4589428
BLAST score	154
E value	3.0e-81
Match length	276
% identity	95
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MFH8, complete sequence

Seq. No.	161073
Seq. ID	LIB3177-014-P1-K2-C9
Method	BLASTX
NCBI GI	g1402918
BLAST score	412
E value	1.0e-40
Match length	78
% identity	99
NCBI Description	(X98320) peroxidase [Arabidopsis thaliana] >gi_1429215_emb_CAA67310_ (X98774) peroxidase ATP6a [Arabidopsis thaliana]

Seq. No.	161074
Seq. ID	LIB3177-014-P1-K2-D1
Method	BLASTX
NCBI GI	g1076531
BLAST score	91
E value	3.0e-51
Match length	125
% identity	77
NCBI Description	hypothetical protein, pollen allergen homolog - garden pea >gi_2129891_pir__S65056 pollen allergen homolog precursor (clone PPA1) - garden pea >gi_732905_emb_CAA59470_ (X85187) homology with pollen allergens [Pisum sativum]

Seq. No.	161075
Seq. ID	LIB3177-014-P1-K2-D12
Method	BLASTX
NCBI GI	g3236248
BLAST score	369
E value	2.0e-35
Match length	119
% identity	67
NCBI Description	(AC004684) unknown protein [Arabidopsis thaliana]

Seq. No.	161076
Seq. ID	LIB3177-014-P1-K2-D2
Method	BLASTX
NCBI GI	g3639089
BLAST score	793
E value	5.0e-85
Match length	148
% identity	97
NCBI Description	(AF090445) phospholipase D1 [Brassica oleracea] >gi_4324969_gb_AAD17208_ (AF113918) phospholipase D1 [Brassica oleracea var. capitata]

Seq. No.	161077
Seq. ID	LIB3177-014-P1-K2-D6
Method	BLASTN
NCBI GI	g4220637
BLAST score	194
E value	1.0e-105
Match length	442
% identity	97
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MIE1, complete sequence [Arabidopsis thaliana]

Seq. No.	161078
Seq. ID	LIB3177-014-P1-K2-D9
Method	BLASTX
NCBI GI	g132090
BLAST score	665
E value	5.0e-70
Match length	136
% identity	90
NCBI Description	RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN 1B PRECURSOR (RUBISCO SMALL SUBUNIT 1B) >gi_68062_pir__RKMUB1

	ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain B1 precursor - Arabidopsis thaliana >gi_16193_emb_CAA32700_ (X14564) ribulose bisphosphate carboxylase [Arabidopsis thaliana]
Seq. No.	161079
Seq. ID	LIB3177-014-P1-K2-E1
Method	BLASTN
NCBI GI	g2828187
BLAST score	138
E value	2.0e-71
Match length	449
% identity	98
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K21C13, complete sequence [Arabidopsis thaliana]
Seq. No.	161080
Seq. ID	LIB3177-014-P1-K2-E12
Method	BLASTN
NCBI GI	g2351069
BLAST score	83
E value	7.0e-39
Match length	131
% identity	91
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MSH12, complete sequence [Arabidopsis thaliana]
Seq. No.	161081
Seq. ID	LIB3177-014-P1-K2-E3
Method	BLASTX
NCBI GI	g133872
BLAST score	372
E value	1.0e-35
Match length	99
% identity	71
NCBI Description	30S RIBOSOMAL PROTEIN S1, CHLOROPLAST PRECURSOR (CS1) >gi_282838_pir__S26494 ribosomal protein S1, chloroplast - spinach >gi_322404_pir__A44121 small subunit ribosomal protein CS1, CS-S2 - spinach >gi_18060_emb_CAA46927_ (X66135) ribosomal protein S1 [Spinacia oleracea] >gi_170143 (M82923) chloroplast ribosomal protein S1 [Spinacia oleracea]
Seq. No.	161082
Seq. ID	LIB3177-014-P1-K2-E4
Method	BLASTN
NCBI GI	g4678219
BLAST score	314
E value	1.0e-176
Match length	449
% identity	96
NCBI Description	Arabidopsis thaliana chromosome II BAC F9C22 genomic sequence, complete sequence
Seq. No.	161083
Seq. ID	LIB3177-014-P1-K2-E5
Method	BLASTX

NCBI GI	g2827039
BLAST score	504
E value	2.0e-51
Match length	109
% identity	90
NCBI Description	(AF008444) chloroplast processing enzyme [Arabidopsis thaliana]

Seq. No.	161084
Seq. ID	LIB3177-014-P1-K2-E6
Method	BLASTX
NCBI GI	g729479
BLAST score	227
E value	6.0e-19
Match length	68
% identity	65
NCBI Description	FERREDOXIN--NADP REDUCTASE PRECURSOR (FNR) >gi_551131 (U14956) ferredoxin NADP+ reductase precursor [Vicia faba]

Seq. No.	161085
Seq. ID	LIB3177-014-P1-K2-E7
Method	BLASTX
NCBI GI	g3176668
BLAST score	628
E value	1.0e-65
Match length	134
% identity	91
NCBI Description	(AC004393) Similar to ribosomal protein L17 gb_X62724 from Hordeum vulgare. ESTs gb_Z34728, gb_F19974, gb_T75677 and gb_Z33937 come from this gene. [Arabidopsis thaliana]

Seq. No.	161086
Seq. ID	LIB3177-014-P1-K2-E8
Method	BLASTX
NCBI GI	g2244850
BLAST score	156
E value	2.0e-10
Match length	76
% identity	43
NCBI Description	(Z97337) hypothetical protein [Arabidopsis thaliana]

Seq. No.	161087
Seq. ID	LIB3177-014-P1-K2-E9
Method	BLASTX
NCBI GI	g4589980
BLAST score	478
E value	4.0e-48
Match length	115
% identity	82
NCBI Description	(AC007195) cyclophilin, 3' partial [Arabidopsis thaliana]

Seq. No.	161088
Seq. ID	LIB3177-014-P1-K2-F1
Method	BLASTN
NCBI GI	g1707006
BLAST score	316
E value	1.0e-178

Match length	377
% identity	100
NCBI Description	Arabidopsis thaliana chromosome II BAC T1B8 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	161089
Seq. ID	LIB3177-014-P1-K2-F2
Method	BLASTN
NCBI GI	g1483217
BLAST score	329
E value	0.0e+00
Match length	437
% identity	97
NCBI Description	A.thaliana gene induced upon wounding stress

Seq. No.	161090
Seq. ID	LIB3177-014-P1-K2-F3
Method	BLASTX
NCBI GI	g3738336
BLAST score	345
E value	1.0e-32
Match length	94
% identity	78
NCBI Description	(AC005170) unknown protein [Arabidopsis thaliana]

Seq. No.	161091
Seq. ID	LIB3177-014-P1-K2-G1
Method	BLASTX
NCBI GI	g1703108
BLAST score	51
E value	3.0e-52
Match length	122
% identity	89
NCBI Description	ACTIN 2/7 >gi_2129525_pir__S71210 actin 2 - Arabidopsis thaliana >gi_2129528_pir__S68107 actin 7 - Arabidopsis thaliana >gi_1049307 (U37281) actin-2 [Arabidopsis thaliana] >gi_1943863 (U27811) actin7 [Arabidopsis thaliana]

Seq. No.	161092
Seq. ID	LIB3177-014-P1-K2-G11
Method	BLASTX
NCBI GI	g2117612
BLAST score	486
E value	4.0e-49
Match length	103
% identity	92
NCBI Description	catalase (EC 1.11.1.6) 3 - Arabidopsis thaliana

Seq. No.	161093
Seq. ID	LIB3177-014-P1-K2-G2
Method	BLASTN
NCBI GI	g3046851
BLAST score	219
E value	1.0e-120
Match length	382
% identity	69

NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MIJ24, complete sequence [Arabidopsis thaliana]
Seq. No.	161094
Seq. ID	LIB3177-014-P1-K2-G3
Method	BLASTX
NCBI GI	g1871577
BLAST score	253
E value	8.0e-22
Match length	90
% identity	53
NCBI Description	(Y11553) putative 21kD protein precursor [Medicago sativa]
Seq. No.	161095
Seq. ID	LIB3177-014-P1-K2-G7
Method	BLASTX
NCBI GI	g4063552
BLAST score	87
E value	3.0e-46
Match length	117
% identity	89
NCBI Description	(AF035908) ATP synthase beta subunit [Muntingia calabura]
Seq. No.	161096
Seq. ID	LIB3177-014-P1-K2-H1
Method	BLASTX
NCBI GI	g3639089
BLAST score	718
E value	3.0e-76
Match length	145
% identity	95
NCBI Description	(AF090445) phospholipase D1 [Brassica oleracea] >gi_4324969_gb_AAD17208_ (AF113918) phospholipase D1 [Brassica oleracea var. capitata]
Seq. No.	161097
Seq. ID	LIB3177-014-P1-K2-H3
Method	BLASTX
NCBI GI	g119975
BLAST score	61
E value	6.0e-56
Match length	145
% identity	83
NCBI Description	FERREDOXIN PRECURSOR >gi_99692_pir__S09979 ferredoxin [2Fe-2S] precursor - Arabidopsis thaliana >gi_16437_emb_CAA35754_ (X51370) ferredoxin precursor [Arabidopsis thaliana] >gi_166698 (M35868) ferrodoxin A [Arabidopsis thaliana]
Seq. No.	161098
Seq. ID	LIB3177-014-P1-K2-H5
Method	BLASTN
NCBI GI	g4455262
BLAST score	96
E value	1.0e-46
Match length	280
% identity	95

NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F17L22 (ESSAII project)

Seq. No.	161099
Seq. ID	LIB3177-014-P1-K2-H8
Method	BLASTX
NCBI GI	g1172873
BLAST score	154
E value	3.0e-10
Match length	97
% identity	45
NCBI Description	CYSTEINE PROTEINASE RD21A PRECURSOR >gi_541857_pir__JN0719 drought-inducible cysteine proteinase (EC 3.4.22.-) RD21A precursor - Arabidopsis thaliana >gi_435619_dbj_BAA02374_ (D13043) thiol protease [Arabidopsis thaliana]

Seq. No.	161100
Seq. ID	LIB3177-015-P1-K1-A2
Method	BLASTX
NCBI GI	g4630748
BLAST score	309
E value	2.0e-28
Match length	91
% identity	68
NCBI Description	(AC007236) putative anion exchange protein 3 [Arabidopsis thaliana]

Seq. No.	161101
Seq. ID	LIB3177-015-P1-K1-A3
Method	BLASTX
NCBI GI	g2982262
BLAST score	206
E value	3.0e-16
Match length	108
% identity	43
NCBI Description	(AF051214) probable glutathione S-transferase [Picea mariana]

Seq. No.	161102
Seq. ID	LIB3177-015-P1-K1-A8
Method	BLASTN
NCBI GI	g1769906
BLAST score	93
E value	8.0e-45
Match length	260
% identity	87
NCBI Description	A.thaliana mRNA for xyloglucan endo-transglycosylase

Seq. No.	161103
Seq. ID	LIB3177-015-P1-K1-B1
Method	BLASTN
NCBI GI	g414339
BLAST score	70
E value	5.0e-31
Match length	272
% identity	83
NCBI Description	A.thaliana rd19A gene for thiol protease, exon 1, exon 2

and exon

Seq. No.	161104
Seq. ID	LIB3177-015-P1-K1-B4
Method	BLASTX
NCBI GI	g1710424
BLAST score	256
E value	3.0e-22
Match length	95
% identity	59
NCBI Description	50S RIBOSOMAL PROTEIN L21, CHLOROPLAST PRECURSOR (CL21) >gi_2129718_pir__S71282 ribosomal protein L21 - Arabidopsis thaliana >gi_1149573_emb_CAA89887_ (Z49787) chloroplast ribosomal large subunit protein L21 [Arabidopsis thaliana]

Seq. No.	161105
Seq. ID	LIB3177-015-P1-K1-B5
Method	BLASTX
NCBI GI	g1168748
BLAST score	323
E value	6.0e-30
Match length	122
% identity	57
NCBI Description	CALMODULIN-4 >gi_479693_pir__S35185 calmodulin 4 - Arabidopsis thaliana >gi_16223_emb_CAA78057_ (Z12022) calmodulin [Arabidopsis thaliana]

Seq. No.	161106
Seq. ID	LIB3177-015-P1-K1-B6
Method	BLASTX
NCBI GI	g132110
BLAST score	167
E value	5.0e-12
Match length	72
% identity	50
NCBI Description	RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN 3B PRECURSOR (RUBISCO SMALL SUBUNIT 3B) >gi_68060_pir__RKMUB3 ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain B3 precursor - Arabidopsis thaliana >gi_16195_emb_CAA32702_ (X14564) ribulose bisphosphate carboxylase [Arabidopsis thaliana]

Seq. No.	161107
Seq. ID	LIB3177-015-P1-K1-B7
Method	BLASTX
NCBI GI	g1172873
BLAST score	186
E value	7.0e-14
Match length	75
% identity	47
NCBI Description	CYSTEINE PROTEINASE RD21A PRECURSOR >gi_541857_pir__JN0719 drought-inducible cysteine proteinase (EC 3.4.22.-) RD21A precursor - Arabidopsis thaliana >gi_435619_dbj_BAA02374_ (D13043) thiol protease [Arabidopsis thaliana]

Seq. No.	161108
Seq. ID	LIB3177-015-P1-K1-B8

Method	BLASTX
NCBI GI	g1173045
BLAST score	184
E value	1.0e-13
Match length	89
% identity	51
NCBI Description	60S RIBOSOMAL PROTEIN L37A >gi_421866_pir__S34661 ribosomal protein L37a - turnip >gi_347062 (L21897) ribosomal protein [Brassica rapa] >gi_395077_emb_CAA80864_ (Z24739) ribosomal protein L37a [Brassica rapa]

Seq. No.	161109
Seq. ID	LIB3177-015-P1-K1-C3
Method	BLASTX
NCBI GI	g4630748
BLAST score	407
E value	8.0e-40
Match length	135
% identity	62
NCBI Description	(AC007236) putative anion exchange protein 3 [Arabidopsis thaliana]

Seq. No.	161110
Seq. ID	LIB3177-015-P1-K1-C4
Method	BLASTN
NCBI GI	g4741184
BLAST score	63
E value	8.0e-27
Match length	257
% identity	88
NCBI Description	Arabidopsis thaliana DNA chromosome 3, BAC clone T23J7 (ESSA project)

Seq. No.	161111
Seq. ID	LIB3177-015-P1-K1-C7
Method	BLASTX
NCBI GI	g3738296
BLAST score	231
E value	3.0e-19
Match length	106
% identity	49
NCBI Description	(AC005309) hypothetical protein [Arabidopsis thaliana]

Seq. No.	161112
Seq. ID	LIB3177-015-P1-K1-D11
Method	BLASTN
NCBI GI	g58207
BLAST score	35
E value	4.0e-10
Match length	95
% identity	84
NCBI Description	Cloning vector pGEM-4Z

Seq. No.	161113
Seq. ID	LIB3177-015-P1-K1-D2
Method	BLASTX
NCBI GI	g1170089

BLAST score	46
E value	3.0e-34
Match length	132
% identity	61
NCBI Description	GLUTATHIONE S-TRANSFERASE ERD13 (CLASS PHI) >gi_481822_pir__S39542 probable glutathione transferase (EC 2.5.1.18) (clone ERD13) - Arabidopsis thaliana >gi_497789_dbj_BAA04554_ (D17673) glutathione S-transferase [Arabidopsis thaliana] >gi_3201614 (AC004669) glutathione S-transferase [Arabidopsis thaliana]

Seq. No.	161114
Seq. ID	LIB3177-015-P1-K1-D3
Method	BLASTX
NCBI GI	g2262151
BLAST score	375
E value	5.0e-36
Match length	139
% identity	58
NCBI Description	(AC002330) predicted protein of unknown function [Arabidopsis thaliana]

Seq. No.	161115
Seq. ID	LIB3177-015-P1-K1-D4
Method	BLASTN
NCBI GI	g3985934
BLAST score	68
E value	8.0e-30
Match length	216
% identity	82
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MJE7, complete sequence [Arabidopsis thaliana]

Seq. No.	161116
Seq. ID	LIB3177-015-P1-K1-E1
Method	BLASTX
NCBI GI	g3036813
BLAST score	174
E value	2.0e-12
Match length	98
% identity	42
NCBI Description	(AL022373) hypothetical protein [Arabidopsis thaliana]

Seq. No.	161117
Seq. ID	LIB3177-015-P1-K1-E2
Method	BLASTN
NCBI GI	g2160716
BLAST score	87
E value	3.0e-41
Match length	250
% identity	84
NCBI Description	Arabidopsis thaliana GUT15 mRNA, complete cds

Seq. No.	161118
Seq. ID	LIB3177-015-P1-K1-E3
Method	BLASTX
NCBI GI	g4585935

BLAST score	433
E value	7.0e-43
Match length	125
% identity	66
NCBI Description	(AC007211) putative chlorophyll A/B binding protein [Arabidopsis thaliana] >gi_4741946_gb_AAD28770.1_AF134123_1 (AF134123) Lhcb2 protein [Arabidopsis thaliana]

Seq. No.	161119
Seq. ID	LIB3177-015-P1-K1-E9
Method	BLASTX
NCBI GI	g131381
BLAST score	249
E value	2.0e-21
Match length	96
% identity	57
NCBI Description	OXYGEN-EVOLVING ENHANCER PROTEIN 1 PRECURSOR (OEE1) (33 KD SUBUNIT OF OXYGEN EVOLVING SYSTEM OF PHOTOSYSTEM II) (33 KD THYLAKOID MEMBRANE PROTEIN) >gi_99745_pir__S11852 photosystem II oxygen-evolving complex protein 1 precursor - Arabidopsis thaliana >gi_22571_emb_CAA36675_ (X52428) 33 kDa oxygen-evolving protein [Arabidopsis thaliana]

Seq. No.	161120
Seq. ID	LIB3177-015-P1-K1-F1
Method	BLASTX
NCBI GI	g4454036
BLAST score	434
E value	6.0e-43
Match length	127
% identity	64
NCBI Description	(AL035394) putative major latex protein [Arabidopsis thaliana]

Seq. No.	161121
Seq. ID	LIB3177-015-P1-K1-F3
Method	BLASTX
NCBI GI	g16374
BLAST score	309
E value	3.0e-28
Match length	103
% identity	60
NCBI Description	(X03908) chlorophyll a/b binding protein (LHCP AB 180) [Arabidopsis thaliana]

Seq. No.	161122
Seq. ID	LIB3177-015-P1-K1-F4
Method	BLASTX
NCBI GI	g2347098
BLAST score	198
E value	3.0e-17
Match length	113
% identity	34
NCBI Description	(U76845) ubiquitin-specific protease [Arabidopsis thaliana] >gi_4490742_emb_CAB38904.1_ (AL035708) ubiquitin-specific protease (AtUBP3) [Arabidopsis thaliana]

Seq. No.	161123
Seq. ID	LIB3177-015-P1-K1-F5
Method	BLASTX
NCBI GI	g2828267
BLAST score	221
E value	5.0e-18
Match length	89
% identity	52
NCBI Description	(Y14044) geranylgeranyl reductase [Arabidopsis thaliana]

Seq. No.	161124
Seq. ID	LIB3177-015-P1-K1-G1
Method	BLASTX
NCBI GI	g4741960
BLAST score	283
E value	3.0e-25
Match length	117
% identity	51
NCBI Description	(AF134130) Lhcb6 protein [Arabidopsis thaliana]

Seq. No.	161125
Seq. ID	LIB3177-015-P1-K1-G2
Method	BLASTX
NCBI GI	g2832241
BLAST score	398
E value	9.0e-39
Match length	132
% identity	39
NCBI Description	(AF030864) nonphototropic hypocotyl 1 [Arabidopsis thaliana]

Seq. No.	161126
Seq. ID	LIB3177-015-P1-K1-G3
Method	BLASTX
NCBI GI	g1352683
BLAST score	233
E value	2.0e-19
Match length	118
% identity	46
NCBI Description	PROTEIN PHOSPHATASE 2C PPH1 (PP2C) >gi_995839 (U34803) protein phosphatase homolog [Arabidopsis thaliana]

Seq. No.	161127
Seq. ID	LIB3177-015-P1-K1-G6
Method	BLASTX
NCBI GI	g115783
BLAST score	126
E value	3.0e-19
Match length	73
% identity	58
NCBI Description	CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR (CAB-140) (LHCP) >gi_16376_emb_CAA27543_ (X03909) chlorophyll a/b binding protein (LHCP AB 140) [Arabidopsis thaliana]

Seq. No.	161128
Seq. ID	LIB3177-015-P1-K1-H1

Method	BLASTX
NCBI GI	g3702336
BLAST score	351
E value	3.0e-33
Match length	120
% identity	56
NCBI Description	(AC005397) putative 3-methyl-2-oxobutanoate hydroxy-methyl-transferase [Arabidopsis thaliana]

Seq. No.	161129
Seq. ID	LIB3177-015-P1-K1-H4
Method	BLASTX
NCBI GI	g115767
BLAST score	325
E value	4.0e-30
Match length	124
% identity	54
NCBI Description	CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR (CAB-165/180) (LHCP) >gi_81603_pir__A29280 chlorophyll a/b-binding protein ab165 - Arabidopsis thaliana >gi_16368_emb_CAA27540_ (X03907) chlorophyll a/b binding protein (LHCP AB 65) [Arabidopsis thaliana] >gi_16372_emb_CAA27541_ (X03908) chlorophyll a/b binding protein (LHCP AB 180) [Arabidopsis thaliana]

Seq. No.	161130
Seq. ID	LIB3177-015-P1-K2-A1
Method	BLASTN
NCBI GI	g259446
BLAST score	154
E value	3.0e-81
Match length	198
% identity	99
NCBI Description	glycine-rich protein {clone atGRP-3} [Arabidopsis thaliana, C24, mRNA, 680 nt]

Seq. No.	161131
Seq. ID	LIB3177-015-P1-K2-A11
Method	BLASTN
NCBI GI	g3702734
BLAST score	73
E value	4.0e-33
Match length	128
% identity	89
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MNB8, complete sequence [Arabidopsis thaliana]

Seq. No.	161132
Seq. ID	LIB3177-015-P1-K2-A2
Method	BLASTX
NCBI GI	g4630748
BLAST score	629
E value	7.0e-66
Match length	124
% identity	98
NCBI Description	(AC007236) putative anion exchange protein 3 [Arabidopsis thaliana]

Seq. No.	161133
Seq. ID	LIB3177-015-P1-K2-A3
Method	BLASTX
NCBI GI	g2190992
BLAST score	306
E value	5.0e-28
Match length	95
% identity	62
NCBI Description	(AF004358) glutathione S-transferase TSI-1 [Aegilops tauschii]

Seq. No.	161134
Seq. ID	LIB3177-015-P1-K2-A4
Method	BLASTX
NCBI GI	g4115936
BLAST score	211
E value	9.0e-17
Match length	107
% identity	37
NCBI Description	(AF118223) No definition line found [Arabidopsis thaliana]

Seq. No.	161135
Seq. ID	LIB3177-015-P1-K2-A6
Method	BLASTN
NCBI GI	g3449327
BLAST score	73
E value	7.0e-33
Match length	292
% identity	92
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MCA23, complete sequence [Arabidopsis thaliana]

Seq. No.	161136
Seq. ID	LIB3177-015-P1-K2-A7
Method	BLASTX
NCBI GI	g4204793
BLAST score	397
E value	1.0e-38
Match length	119
% identity	33
NCBI Description	(U52079) P-glycoprotein [Solanum tuberosum]

Seq. No.	161137
Seq. ID	LIB3177-015-P1-K2-A8
Method	BLASTX
NCBI GI	g1769907
BLAST score	263
E value	5.0e-23
Match length	64
% identity	75
NCBI Description	(X92975) xyloglucan endo-transglycosylase [Arabidopsis thaliana]

Seq. No.	161138
Seq. ID	LIB3177-015-P1-K2-B1
Method	BLASTX

NCBI GI	g4539329
BLAST score	373
E value	7.0e-36
Match length	67
% identity	97
NCBI Description	(AL035679) ES43 like protein [Arabidopsis thaliana]

Seq. No.	161139
Seq. ID	LIB3177-015-P1-K2-B2
Method	BLASTN
NCBI GI	g2618602
BLAST score	164
E value	4.0e-87
Match length	432
% identity	97
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MSJ1, complete sequence [Arabidopsis thaliana]

Seq. No.	161140
Seq. ID	LIB3177-015-P1-K2-B3
Method	BLASTN
NCBI GI	g58298
BLAST score	52
E value	2.0e-20
Match length	106
% identity	89
NCBI Description	Synthetic DNA for A.thaliana ats1A leader spliced to B.thuringiensis CryIA(c)

Seq. No.	161141
Seq. ID	LIB3177-015-P1-K2-B4
Method	BLASTX
NCBI GI	g1710424
BLAST score	557
E value	2.0e-57
Match length	145
% identity	80
NCBI Description	50S RIBOSOMAL PROTEIN L21, CHLOROPLAST PRECURSOR (CL21) >gi_2129718_pir__S71282 ribosomal protein L21 - Arabidopsis thaliana >gi_1149573_emb_CAA89887_ (Z49787) chloroplast ribosomal large subunit protein L21 [Arabidopsis thaliana]

Seq. No.	161142
Seq. ID	LIB3177-015-P1-K2-B5
Method	BLASTX
NCBI GI	g115511
BLAST score	633
E value	3.0e-66
Match length	131
% identity	63
NCBI Description	CALMODULIN >gi_231682_sp_P29612_CALM_ORYSA CALMODULIN >gi_71682_pir__MCBH calmodulin - barley >gi_100666_pir__S24952 calmodulin 1 (clone lambda DASH) - rice >gi_20188_emb_CAA78287_ (Z12827) calmodulin [Oryza sativa] >gi_167008 (M27303) calmodulin [Hordeum vulgare] >gi_170072 (L01431) calmodulin [Glycine max] >gi_310315 (L18913) calmodulin [Oryza sativa] >gi_506850 (L20691)

calmodulin [Vigna radiata] >gi_1478370_bbs_176852 (S81594) auxin-regulated calmodulin, arCaM [Vigna radiata=mung bean, Wilczek, seedling, Peptide, 149 aa] [Vigna radiata] >gi_1742989_emb_CAA70982_ (Y09853) CaM protein [Cicer arietinum] >gi_1754991 (U48242) calmodulin TaCaM1-1 [Triticum aestivum] >gi_1754993 (U48688) calmodulin TaCaM1-2 [Triticum aestivum] >gi_1754995 (U48689) calmodulin TaCaM1-3 [Triticum aestivum] >gi_1755003 (U48693) calmodulin TaCaM3-1 [Triticum aestivum] >gi_1755005 (U49103) calmodulin TaCaM3-2 [Triticum aestivum] >gi_1755007 (U49104) calmodulin TaCaM3-3 [Triticum aestivum] >gi_1755009 (U49105) calmodulin TaCaM4-1 [Triticum aestivum] >gi_3617842 (AF042840) calmodulin [Oryza sativa] >gi_226769_prf__1604476A calmodulin [Hordeum vulgare var. distichum] >gi_1583768_prf__2121384B calmodulin [Glycine max]

Seq. No.	161143
Seq. ID	LIB3177-015-P1-K2-B7
Method	BLASTX
NCBI GI	g1172873
BLAST score	670
E value	1.0e-70
Match length	139
% identity	96
NCBI Description	CYSTEINE PROTEINASE RD21A PRECURSOR >gi_541857_pir__JN0719 drought-inducible cysteine proteinase (EC 3.4.22.-) RD21A precursor - Arabidopsis thaliana >gi_435619_dbj_BAA02374_ (D13043) thiol protease [Arabidopsis thaliana]

Seq. No.	161144
Seq. ID	LIB3177-015-P1-K2-B8
Method	BLASTX
NCBI GI	g1173045
BLAST score	457
E value	1.0e-45
Match length	92
% identity	97
NCBI Description	60S RIBOSOMAL PROTEIN L37A >gi_421866_pir__S34661 ribosomal protein L37a - turnip >gi_347062 (L21897) ribosomal protein [Brassica rapa] >gi_395077_emb_CAA80864_ (Z24739) ribosomal protein L37a [Brassica rapa]

Seq. No.	161145
Seq. ID	LIB3177-015-P1-K2-C1
Method	BLASTX
NCBI GI	g131286
BLAST score	222
E value	3.0e-18
Match length	63
% identity	68
NCBI Description	PHOTOSYSTEM II 44 KD REACTION CENTRE PROTEIN PRECURSOR (P6 PROTEIN) (CP43) >gi_2144937_pir__F2SP44 photosystem II chlorophyll a-binding protein psbC - spinach chloroplast >gi_12281_emb_CAA25864_ (X01724) 44 kd reaction-centre protein [Spinacia oleracea] >gi_343362 (M36833) 44 kD chlorophyll a apoprotein [Spinacia oleracea]

Seq. No.	161146
Seq. ID	LIB3177-015-P1-K2-C3
Method	BLASTX
NCBI GI	g4630748
BLAST score	597
E value	3.0e-62
Match length	114
% identity	99
NCBI Description	(AC007236) putative anion exchange protein 3 [Arabidopsis thaliana]

Seq. No.	161147
Seq. ID	LIB3177-015-P1-K2-C4
Method	BLASTX
NCBI GI	g4741198
BLAST score	563
E value	5.0e-58
Match length	107
% identity	98
NCBI Description	(AL049746) putative protein [Arabidopsis thaliana]

Seq. No.	161148
Seq. ID	LIB3177-015-P1-K2-C7
Method	BLASTX
NCBI GI	g3738296
BLAST score	587
E value	6.0e-61
Match length	123
% identity	93
NCBI Description	(AC005309) hypothetical protein [Arabidopsis thaliana]

Seq. No.	161149
Seq. ID	LIB3177-015-P1-K2-D2
Method	BLASTX
NCBI GI	g1170089
BLAST score	633
E value	2.0e-66
Match length	129
% identity	97
NCBI Description	GLUTATHIONE S-TRANSFERASE ERD13 (CLASS PHI) >gi_481822_pir__S39542 probable glutathione transferase (EC 2.5.1.18) (clone ERD13) - Arabidopsis thaliana >gi_497789_dbj_BAA04554_ (D17673) glutathione S-transferase [Arabidopsis thaliana] >gi_3201614 (AC004669) glutathione S-transferase [Arabidopsis thaliana]

Seq. No.	161150
Seq. ID	LIB3177-015-P1-K2-D3
Method	BLASTN
NCBI GI	g2262135
BLAST score	315
E value	1.0e-177
Match length	401
% identity	98
NCBI Description	Arabidopsis thaliana BAC T10P11 from chromosome IV, near 15 cM, complete sequence

Seq. No.	161151
Seq. ID	LIB3177-015-P1-K2-D4
Method	BLASTN
NCBI GI	g3985934
BLAST score	338
E value	0.0e+00
Match length	410
% identity	99
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MJE7, complete sequence [Arabidopsis thaliana]

Seq. No.	161152
Seq. ID	LIB3177-015-P1-K2-D5
Method	BLASTX
NCBI GI	g3668097
BLAST score	646
E value	8.0e-68
Match length	132
% identity	95
NCBI Description	(AC004667) putative glycine cleavage system protein H precursor [Arabidopsis thaliana]

Seq. No.	161153
Seq. ID	LIB3177-015-P1-K2-D7
Method	BLASTX
NCBI GI	g4759280
BLAST score	186
E value	5.0e-14
Match length	101
% identity	44
NCBI Description	U5 snRNP-specific protein, 116 kD >gi_434759_dbj_BAA04699_ (D21163) similar to human elongation factor 2 mRNA (HSEF2). [Homo sapiens]

Seq. No.	161154
Seq. ID	LIB3177-015-P1-K2-E1
Method	BLASTX
NCBI GI	g3036813
BLAST score	423
E value	1.0e-41
Match length	102
% identity	81
NCBI Description	(AL022373) hypothetical protein [Arabidopsis thaliana]

Seq. No.	161155
Seq. ID	LIB3177-015-P1-K2-E10
Method	BLASTX
NCBI GI	g730645
BLAST score	555
E value	4.0e-57
Match length	124
% identity	90
NCBI Description	40S RIBOSOMAL PROTEIN S15 >gi_629556_pir__S43412 ribosomal protein S15 - Arabidopsis thaliana >gi_313152_emb_CAA80679_ (Z23161) ribosomal protein S15 [Arabidopsis thaliana] >gi_313188_emb_CAA80681_ (Z23162) ribosomal protein S15

	[Arabidopsis thaliana] >gi_1903366_gb_AAB70449_ (AC000104) Strong similarity to Oryza 40S ribosomal protein S15. ESTs gb_R29788,gb_ATTS0365 come from this gene. [Arabidopsis thaliana]
Seq. No.	161156
Seq. ID	LIB3177-015-P1-K2-E2
Method	BLASTN
NCBI GI	g2160716
BLAST score	328
E value	0.0e+00
Match length	363
% identity	98
NCBI Description	Arabidopsis thaliana GUT15 mRNA, complete cds
Seq. No.	161157
Seq. ID	LIB3177-015-P1-K2-E3
Method	BLASTX
NCBI GI	g4585935
BLAST score	608
E value	2.0e-63
Match length	121
% identity	95
NCBI Description	(AC007211) putative chlorophyll A/B binding protein [Arabidopsis thaliana] >gi_4741946_gb_AAD28770.1_AF134123_1 (AF134123) Lhcb2 protein [Arabidopsis thaliana]
Seq. No.	161158
Seq. ID	LIB3177-015-P1-K2-E6
Method	BLASTX
NCBI GI	g1708461
BLAST score	642
E value	3.0e-67
Match length	148
% identity	86
NCBI Description	IAA-AMINO ACID HYDROLASE HOMOLOG 1 PRECURSOR >gi_902789 (U23795) ILL1 [Arabidopsis thaliana] >gi_2921829_gb_AAC04865.1_ (AF047031) IAA-amino acid hydrolase [Arabidopsis thaliana]
Seq. No.	161159
Seq. ID	LIB3177-015-P1-K2-E8
Method	BLASTX
NCBI GI	g2062164
BLAST score	527
E value	6.0e-54
Match length	104
% identity	98
NCBI Description	(AC001645) jasmonate inducible protein isolog [Arabidopsis thaliana]
Seq. No.	161160
Seq. ID	LIB3177-015-P1-K2-E9
Method	BLASTX
NCBI GI	g3286693
BLAST score	64
E value	6.0e-54

Match length	116
% identity	99
NCBI Description	(Y15433) 33 kDa polypeptide of oxygen-evolving complex (OEC) in photosystem II [Arabidopsis thaliana]

Seq. No.	161161
Seq. ID	LIB3177-015-P1-K2-F1
Method	BLASTX
NCBI GI	g4454036
BLAST score	726
E value	4.0e-77
Match length	135
% identity	99
NCBI Description	(AL035394) putative major latex protein [Arabidopsis thaliana]

Seq. No.	161162
Seq. ID	LIB3177-015-P1-K2-F3
Method	BLASTX
NCBI GI	g115783
BLAST score	530
E value	3.0e-54
Match length	107
% identity	95
NCBI Description	CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR (CAB-140) (LHCP) >gi_16376_emb_CAA27543_ (X03909) chlorophyll a/b binding protein (LHCP AB 140) [Arabidopsis thaliana]

Seq. No.	161163
Seq. ID	LIB3177-015-P1-K2-F4
Method	BLASTX
NCBI GI	g2347098
BLAST score	380
E value	4.0e-51
Match length	102
% identity	86
NCBI Description	(U76845) ubiquitin-specific protease [Arabidopsis thaliana] >gi_4490742_emb_CAB38904.1_ (AL035708) ubiquitin-specific protease (AtUBP3) [Arabidopsis thaliana]

Seq. No.	161164
Seq. ID	LIB3177-015-P1-K2-F5
Method	BLASTX
NCBI GI	g2828267
BLAST score	461
E value	4.0e-46
Match length	119
% identity	80
NCBI Description	(Y14044) geranylgeranyl reductase [Arabidopsis thaliana]

Seq. No.	161165
Seq. ID	LIB3177-015-P1-K2-F9
Method	BLASTN
NCBI GI	g4056429
BLAST score	221
E value	1.0e-121

Match length	443
% identity	95
NCBI Description	Arabidopsis thaliana chromosome 1 BAC F5O8 sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	161166
Seq. ID	LIB3177-015-P1-K2-G1
Method	BLASTX
NCBI GI	g4741960
BLAST score	571
E value	5.0e-59
Match length	128
% identity	85
NCBI Description	(AF134130) Lhcb6 protein [Arabidopsis thaliana]

Seq. No.	161167
Seq. ID	LIB3177-015-P1-K2-G2
Method	BLASTX
NCBI GI	g2832241
BLAST score	705
E value	1.0e-74
Match length	149
% identity	58
NCBI Description	(AF030864) nonphototropic hypocotyl 1 [Arabidopsis thaliana]

Seq. No.	161168
Seq. ID	LIB3177-015-P1-K2-G3
Method	BLASTN
NCBI GI	g995838
BLAST score	214
E value	1.0e-117
Match length	264
% identity	95
NCBI Description	Arabidopsis thaliana protein phosphatase homolog (PPH1) mRNA, partial cds

Seq. No.	161169
Seq. ID	LIB3177-015-P1-K2-G6
Method	BLASTX
NCBI GI	g115783
BLAST score	315
E value	3.0e-29
Match length	87
% identity	72
NCBI Description	CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR (CAB-140) (LHCP) >gi_16376_emb_CAA27543_ (X03909) chlorophyll a/b binding protein (LHCP AB 140) [Arabidopsis thaliana]

Seq. No.	161170
Seq. ID	LIB3177-015-P1-K2-G9
Method	BLASTN
NCBI GI	g2618601
BLAST score	39
E value	4.0e-13
Match length	70

% identity	89
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MHJ24, complete sequence [Arabidopsis thaliana]

Seq. No:	161171
Seq. ID	LIB3177-015-P1-K2-H1
Method	BLASTX
NCBI GI	g3702336
BLAST score	618
E value	2.0e-64
Match length	133
% identity	88
NCBI Description	(AC005397) putative 3-methyl-2-oxobutanoate hydroxy-methyl-transferase [Arabidopsis thaliana]

Seq. No.	161172
Seq. ID	LIB3177-015-P1-K2-H3
Method	BLASTX
NCBI GI	g2117612
BLAST score	71
E value	1.0e-54
Match length	117
% identity	92
NCBI Description	catalase (EC 1.11.1.6) 3 - Arabidopsis thaliana

Seq. No.	161173
Seq. ID	LIB3177-015-P1-K2-H4
Method	BLASTX
NCBI GI	g115783
BLAST score	650
E value	3.0e-68
Match length	131
% identity	95
NCBI Description	CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR (CAB-140) (LHCP) >gi_16376_emb_CAA27543_ (X03909) chlorophyll a/b binding protein (LHCP AB 140) [Arabidopsis thaliana]

Seq. No.	161174
Seq. ID	LIB3177-015-P1-K2-H5
Method	BLASTX
NCBI GI	g2924520
BLAST score	594
E value	1.0e-61
Match length	123
% identity	92
NCBI Description	(AL022023) plasma membrane intrinsic protein (SIMIP) [Arabidopsis thaliana]

Seq. No.	161175
Seq. ID	LIB3177-015-P1-K2-H6
Method	BLASTX
NCBI GI	g4741952
BLAST score	523
E value	2.0e-53
Match length	103
% identity	70

NCBI Description	(AF134126) Lhcb3 protein [Arabidopsis thaliana]

Seq. No.	161176
Seq. ID	LIB3177-016-P1-K1-A10
Method	BLASTN
NCBI GI	g3985952
BLAST score	95
E value	5.0e-46
Match length	331
% identity	82
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MRC8, complete sequence [Arabidopsis thaliana]

Seq. No.	161177
Seq. ID	LIB3177-016-P1-K1-A11
Method	BLASTX
NCBI GI	g4538961
BLAST score	207
E value	1.0e-16
Match length	92
% identity	53
NCBI Description	(AL049488) isoleucine-tRNA ligase-like protein [Arabidopsis thaliana]

Seq. No.	161178
Seq. ID	LIB3177-016-P1-K1-A2
Method	BLASTX
NCBI GI	g3885511
BLAST score	219
E value	8.0e-18
Match length	96
% identity	52
NCBI Description	(AF084200) similar to PSI-K subunit of photosystem I from barley [Medicago sativa]

Seq. No.	161179
Seq. ID	LIB3177-016-P1-K1-A3
Method	BLASTN
NCBI GI	g4581084
BLAST score	44
E value	2.0e-15
Match length	175
% identity	86
NCBI Description	Arabidopsis thaliana chromosome I BAC T30F21 genomic sequence, complete sequence

Seq. No.	161180
Seq. ID	LIB3177-016-P1-K1-A4
Method	BLASTX
NCBI GI	g99696
BLAST score	358
E value	4.0e-34
Match length	114
% identity	64
NCBI Description	glutamate--ammonia ligase (EC 6.3.1.2) precursor, chloroplast (clone lambdaAtgsl1) - Arabidopsis thaliana >gi_240070_bbs_69728 (S69727) light-regulated glutamine

	synthetase isoenzyme [Arabidopsis thaliana, Peptide, 430 aa] [Arabidopsis thaliana] >gi_228453_prf__1804333A Gln synthetase [Arabidopsis thaliana]
Seq. No.	161181
Seq. ID	LIB3177-016-P1-K1-A5
Method	BLASTX
NCBI GI	g224159
BLAST score	367
E value	4.0e-35
Match length	124
% identity	64
NCBI Description	cytochrome b559 [Spinacia oleracea]
Seq. No.	161182
Seq. ID	LIB3177-016-P1-K1-A7
Method	BLASTX
NCBI GI	g99771
BLAST score	202
E value	3.0e-16
Match length	80
% identity	56
NCBI Description	ubiquitin 81-aa extension protein 1 - Arabidopsis thaliana >gi_166934 (J05539) ubiquitin extension protein (UBQ5) [Arabidopsis thaliana]
Seq. No.	161183
Seq. ID	LIB3177-016-P1-K1-A9
Method	BLASTN
NCBI GI	g4584351
BLAST score	83
E value	6.0e-39
Match length	279
% identity	82
NCBI Description	Arabidopsis thaliana chromosome II BAC T12H3 genomic sequence, complete sequence
Seq. No.	161184
Seq. ID	LIB3177-016-P1-K1-B1
Method	BLASTX
NCBI GI	g4741954
BLAST score	300
E value	2.0e-27
Match length	80
% identity	74
NCBI Description	(AF134127) Lhcb4.2 protein [Arabidopsis thaliana]
Seq. No.	161185
Seq. ID	LIB3177-016-P1-K1-B2
Method	BLASTN
NCBI GI	g3659491
BLAST score	126
E value	2.0e-64
Match length	217
% identity	90
NCBI Description	Sequence of BAC T22H22 from Arabidopsis thaliana chromosome 1, complete sequence [Arabidopsis thaliana]

Seq. No.	161186
Seq. ID	LIB3177-016-P1-K1-B5
Method	BLASTX
NCBI GI	g1922964
BLAST score	182
E value	2.0e-13
Match length	72
% identity	54
NCBI Description	(AC000106) Similar to Schizosaccharomyces CCAAT-binding factor (gb_U88525). EST gb_T04310 comes from this gene. [Arabidopsis thaliana]

Seq. No.	161187
Seq. ID	LIB3177-016-P1-K1-B6
Method	BLASTX
NCBI GI	g4538963
BLAST score	443
E value	5.0e-44
Match length	124
% identity	72
NCBI Description	(AL049488) chlorophyll a/b-binding protein-like [Arabidopsis thaliana] >gi_4741958_gb_AAD28776.1_AF134129_1 (AF134129) Lhcb5 protein [Arabidopsis thaliana]

Seq. No.	161188
Seq. ID	LIB3177-016-P1-K1-C10
Method	BLASTX
NCBI GI	g135406
BLAST score	317
E value	2.0e-29
Match length	95
% identity	66
NCBI Description	TUBULIN ALPHA-3/ALPHA-5 CHAIN >gi_99768_pir__A32712 tubulin alpha-5 chain - Arabidopsis thaliana >gi_166912 (M17189) alpha-tubulin [Arabidopsis thaliana] >gi_166918 (M84698) alpha-5 tubulin [Arabidopsis thaliana]

Seq. No.	161189
Seq. ID	LIB3177-016-P1-K1-C3
Method	BLASTX
NCBI GI	g2914707
BLAST score	182
E value	2.0e-13
Match length	110
% identity	39
NCBI Description	(AC003974) putative disease resistance protein (Cf-2.2) [Arabidopsis thaliana] >gi_3298554 (AC004681) putative disease resistance protein [Arabidopsis thaliana]

Seq. No.	161190
Seq. ID	LIB3177-016-P1-K1-C4
Method	BLASTX
NCBI GI	g1350768
BLAST score	336
E value	1.0e-31
Match length	101

% identity	68
NCBI Description	60S RIBOSOMAL PROTEIN L7A

Seq. No.	161191
Seq. ID	LIB3177-016-P1-K1-C5
Method	BLASTX
NCBI GI	g3953601
BLAST score	417
E value	6.0e-41
Match length	136
% identity	68
NCBI Description	(AB008489) response regulator 6 [Arabidopsis thaliana]

Seq. No.	161192
Seq. ID	LIB3177-016-P1-K1-C6
Method	BLASTX
NCBI GI	g4538963
BLAST score	391
E value	5.0e-38
Match length	117
% identity	68
NCBI Description	(AL049488) chlorophyll a/b-binding protein-like [Arabidopsis thaliana] >gi_4741958_gb_AAD28776.1_AF134129_1 (AF134129) Lhcb5 protein [Arabidopsis thaliana]

Seq. No.	161193
Seq. ID	LIB3177-016-P1-K1-C9
Method	BLASTX
NCBI GI	g2160142
BLAST score	196
E value	4.0e-15
Match length	67
% identity	67
NCBI Description	(AC000375) Strong similarity to Arabidopsis APR2 (gb_U56921). [Arabidopsis thaliana] >gi_2738758 (AF016283) 5'-adenylylsulfate reductase [Arabidopsis thaliana]

Seq. No.	161194
Seq. ID	LIB3177-016-P1-K1-D1
Method	BLASTX
NCBI GI	g115385
BLAST score	323
E value	5.0e-30
Match length	92
% identity	75
NCBI Description	CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR (CAB-4) (LHCP) >gi_166646 (M63931) light-harvesting chlorophyll a/b binding protein [Arabidopsis thaliana]

Seq. No.	161195
Seq. ID	LIB3177-016-P1-K1-D12
Method	BLASTX
NCBI GI	g117238
BLAST score	319
E value	1.0e-29
Match length	104
% identity	66

NCBI Description	MAGNESIUM-CHELATASE SUBUNIT CHLI PRECURSOR (PROTEIN CS/CH-42) (MG-PROTOPORPHYRIN IX CHELATASE) >gi_81656_pir__S12785 protein ch-42 precursor, chloroplast - Arabidopsis thaliana >gi_1020100_emb_CAA62754_ (X91411) protoporphyrin-IX Mg-chetalase [Arabidopsis thaliana] >gi_2832653_emb_CAA16728_ (AL021710) protein ch-42 precursor, chloroplast [Arabidopsis thaliana] >gi_4490290_emb_CAB38561.1_ (X51799) chloroplast protein [Arabidopsis thaliana] >gi_228771_prf__1811226A ccsA gene [Euglena gracilis]

Seq. No.	161196
Seq. ID	LIB3177-016-P1-K1-D2
Method	BLASTX
NCBI GI	g4588906
BLAST score	165
E value	2.0e-11
Match length	73
% identity	49
NCBI Description	(AF118149) ribosomal protein S7 [Secale cereale]

Seq. No.	161197
Seq. ID	LIB3177-016-P1-K1-D3
Method	BLASTX
NCBI GI	g1652653
BLAST score	172
E value	2.0e-12
Match length	94
% identity	43
NCBI Description	(D90907) ABC transporter [Synechocystis sp.]

Seq. No.	161198
Seq. ID	LIB3177-016-P1-K1-D4
Method	BLASTX
NCBI GI	g3821254
BLAST score	173
E value	2.0e-12
Match length	63
% identity	57
NCBI Description	(AJ007789) geranylgeranyl reductase [Nicotiana tabacum]

Seq. No.	161199
Seq. ID	LIB3177-016-P1-K1-D7
Method	BLASTX
NCBI GI	g3323208
BLAST score	116
E value	2.0e-10
Match length	121
% identity	38
NCBI Description	(AE001258) translation initiation factor 2 (infB) [Treponema pallidum]

Seq. No.	161200
Seq. ID	LIB3177-016-P1-K1-E1
Method	BLASTN
NCBI GI	g2351064
BLAST score	49

E value	1.0e-18
Match length	296
% identity	85
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MDJ22, complete sequence [Arabidopsis thaliana]

Seq. No.	161201
Seq. ID	LIB3177-016-P1-K1-E2
Method	BLASTX
NCBI GI	g4204285
BLAST score	277
E value	1.0e-24
Match length	129
% identity	47
NCBI Description	(AC003027) lcl_prt_seq No definition line found [Arabidopsis thaliana]

Seq. No.	161202
Seq. ID	LIB3177-016-P1-K1-E3
Method	BLASTX
NCBI GI	g115783
BLAST score	374
E value	5.0e-36
Match length	116
% identity	67
NCBI Description	CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR (CAB-140) (LHCP) >gi_16376_emb_CAA27543_ (X03909) chlorophyll a/b binding protein (LHCP AB 140) [Arabidopsis thaliana]

Seq. No.	161203
Seq. ID	LIB3177-016-P1-K1-E4
Method	BLASTX
NCBI GI	g231683
BLAST score	467
E value	6.0e-47
Match length	125
% identity	74
NCBI Description	CALNEXIN HOMOLOG PRECURSOR >gi_421825_pir__JN0597 calnexin-like protein - Arabidopsis thaliana >gi_16211_emb_CAA79144_ (Z18242) calnexin homolog [Arabidopsis thaliana]

Seq. No.	161204
Seq. ID	LIB3177-016-P1-K1-E5
Method	BLASTX
NCBI GI	g1546690
BLAST score	217
E value	1.0e-17
Match length	109
% identity	50
NCBI Description	(X98803) peroxidase ATP14a [Arabidopsis thaliana]

Seq. No.	161205
Seq. ID	LIB3177-016-P1-K1-E6
Method	BLASTX
NCBI GI	g1168728

BLAST score	374
E value	6.0e-36
Match length	120
% identity	64
NCBI Description	CINNAMYL-ALCOHOL DEHYDROGENASE 1 (CAD) >gi_598071 (L37883) cinnamyl-alcohol dehydrogenase [Arabidopsis thaliana]

Seq. No.	161206
Seq. ID	LIB3177-016-P1-K1-E7
Method	BLASTX
NCBI GI	g4454037
BLAST score	186
E value	2.0e-14
Match length	67
% identity	58
NCBI Description	(AL035394) putative major latex protein [Arabidopsis thaliana]

Seq. No.	161207
Seq. ID	LIB3177-016-P1-K1-E8
Method	BLASTX
NCBI GI	g1168728
BLAST score	179
E value	2.0e-13
Match length	71
% identity	54
NCBI Description	CINNAMYL-ALCOHOL DEHYDROGENASE 1 (CAD) >gi_598071 (L37883) cinnamyl-alcohol dehydrogenase [Arabidopsis thaliana]

Seq. No.	161208
Seq. ID	LIB3177-016-P1-K1-E9
Method	BLASTX
NCBI GI	g132074
BLAST score	236
E value	9.0e-20
Match length	112
% identity	52
NCBI Description	RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN 1A PRECURSOR (RUBISCO SMALL SUBUNIT 1A) >gi_68063_pir__RKMUA1 ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain A1 precursor - Arabidopsis thaliana

Seq. No.	161209
Seq. ID	LIB3177-016-P1-K1-F2
Method	BLASTX
NCBI GI	g4741950
BLAST score	411
E value	2.0e-40
Match length	108
% identity	73
NCBI Description	(AF134125) Lhcb2 protein [Arabidopsis thaliana]

Seq. No.	161210
Seq. ID	LIB3177-016-P1-K1-F6
Method	BLASTX
NCBI GI	g3341685
BLAST score	274

E value	3.0e-24
Match length	93
% identity	65
NCBI Description	(AC003672) unknown protein [Arabidopsis thaliana]

Seq. No.	161211
Seq. ID	LIB3177-016-P1-K1-F7
Method	BLASTX
NCBI GI	g1170028
BLAST score	231
E value	2.0e-19
Match length	93
% identity	59
NCBI Description	GLUTAMATE-1-SEMIALDEHYDE 2,1-AMINOMUTASE 1 PRECURSOR (GSA 1) (GLUTAMATE-1-SEMIALDEHYDE AMINOTRANSFERASE 1) (GSA-AT 1) >gi_454357 (U03773) glutamate-1-semialdehyde-2,1-aminomutase [Arabidopsis thaliana]

Seq. No.	161212
Seq. ID	LIB3177-016-P1-K1-F8
Method	BLASTX
NCBI GI	g4741952
BLAST score	323
E value	5.0e-30
Match length	88
% identity	68
NCBI Description	(AF134126) Lhcb3 protein [Arabidopsis thaliana]

Seq. No.	161213
Seq. ID	LIB3177-016-P1-K1-G10
Method	BLASTX
NCBI GI	g2507281
BLAST score	348
E value	7.0e-33
Match length	100
% identity	69
NCBI Description	GTP-BINDING NUCLEAR PROTEIN RAN-2 >gi_1668706_emb_CAA66048_ (X97380) atran2 [Arabidopsis thaliana]

Seq. No.	161214
Seq. ID	LIB3177-016-P1-K1-G2
Method	BLASTX
NCBI GI	g4406777
BLAST score	233
E value	5.0e-20
Match length	70
% identity	64
NCBI Description	(AC006532) putative zinc-finger protein [Arabidopsis thaliana]

Seq. No.	161215
Seq. ID	LIB3177-016-P1-K1-G5
Method	BLASTN
NCBI GI	g4584351
BLAST score	32
E value	1.0e-08

Match length	56
% identity	89
NCBI Description	Arabidopsis thaliana chromosome II BAC T12H3 genomic sequence, complete sequence

Seq. No.	161216
Seq. ID	LIB3177-016-P1-K1-G6
Method	BLASTX
NCBI GI	g1174592
BLAST score	238
E value	5.0e-20
Match length	88
% identity	53
NCBI Description	TUBULIN ALPHA-1 CHAIN >gi_2119270_pir__S60233 alpha-tubulin - garden pea >gi_525332 (U12589) alpha-tubulin [Pisum sativum]

Seq. No.	161217
Seq. ID	LIB3177-016-P1-K1-G8
Method	BLASTX
NCBI GI	g2119846
BLAST score	142
E value	9.0e-09
Match length	94
% identity	35
NCBI Description	chlorophyll a/b-binding protein type I precursor Lhb1B2 - Arabidopsis thaliana >gi_16364_emb_CAA45790_ (X64460) photosystem II type I chlorophyll a /b binding protein [Arabidopsis thaliana] >gi_3128230 (AC004077) photosystem II type I chlorophyll a/b binding protein [Arabidopsis thaliana] >gi_3337371 (AC004481) photosystem II type I chlorophyll a/b binding protein [Arabidopsis thaliana]

Seq. No.	161218
Seq. ID	LIB3177-016-P1-K1-H2
Method	BLASTX
NCBI GI	g2760362
BLAST score	331
E value	7.0e-31
Match length	119
% identity	60
NCBI Description	(AF016511) 15.9 kDa subunit of RNA polymerase II [Arabidopsis thaliana]

Seq. No.	161219
Seq. ID	LIB3177-016-P1-K1-H3
Method	BLASTX
NCBI GI	g1173218
BLAST score	145
E value	1.0e-09
Match length	51
% identity	59
NCBI Description	40S RIBOSOMAL PROTEIN S15A >gi_440824 (L27461) ribosomal protein S15 [Arabidopsis thaliana] >gi_2150130 (AF001412) cytoplasmic ribosomal protein S15a [Arabidopsis thaliana]

Seq. No.	161220

Seq. ID	LIB3177-016-P1-K1-H7
Method	BLASTX
NCBI GI	g4741944
BLAST score	203
E value	4.0e-16
Match length	101
% identity	46
NCBI Description	(AF134122) Lhcb2 protein [Arabidopsis thaliana]

Seq. No.	161221
Seq. ID	LIB3177-016-P1-K2-A10
Method	BLASTN
NCBI GI	g3985952
BLAST score	431
E value	0.0e+00
Match length	443
% identity	99
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MRC8, complete sequence [Arabidopsis thaliana]

Seq. No.	161222
Seq. ID	LIB3177-016-P1-K2-A11
Method	BLASTN
NCBI GI	g4538949
BLAST score	52
E value	2.0e-20
Match length	116
% identity	91
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F24G24 (ESSA project)

Seq. No.	161223
Seq. ID	LIB3177-016-P1-K2-A12
Method	BLASTN
NCBI GI	g3242700
BLAST score	208
E value	1.0e-113
Match length	254
% identity	98
NCBI Description	Arabidopsis thaliana chromosome II BAC F26B6 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	161224
Seq. ID	LIB3177-016-P1-K2-A2
Method	BLASTX
NCBI GI	g3885511
BLAST score	435
E value	4.0e-43
Match length	114
% identity	77
NCBI Description	(AF084200) similar to PSI-K subunit of photosystem I from barley [Medicago sativa]

Seq. No.	161225
Seq. ID	LIB3177-016-P1-K2-A3
Method	BLASTN
NCBI GI	g4581084

BLAST score	249
E value	1.0e-138
Match length	393
% identity	99
NCBI Description	Arabidopsis thaliana chromosome I BAC T30F21 genomic sequence, complete sequence

Seq. No.	161226
Seq. ID	LIB3177-016-P1-K2-A4
Method	BLASTX
NCBI GI	g99696
BLAST score	728
E value	2.0e-77
Match length	142
% identity	94
NCBI Description	glutamate--ammonia ligase (EC 6.3.1.2) precursor, chloroplast (clone lambdaAtgsl1) - Arabidopsis thaliana >gi_240070_bbs_69728 (S69727) light-regulated glutamine synthetase isoenzyme [Arabidopsis thaliana, Peptide, 430 aa] [Arabidopsis thaliana] >gi_228453_prf__1804333A Gln synthetase [Arabidopsis thaliana]

Seq. No.	161227
Seq. ID	LIB3177-016-P1-K2-A5
Method	BLASTX
NCBI GI	g224159
BLAST score	556
E value	3.0e-57
Match length	124
% identity	90
NCBI Description	cytochrome b559 [Spinacia oleracea]

Seq. No.	161228
Seq. ID	LIB3177-016-P1-K2-A7
Method	BLASTX
NCBI GI	g99771
BLAST score	557
E value	2.0e-57
Match length	139
% identity	81
NCBI Description	ubiquitin 81-aa extension protein 1 - Arabidopsis thaliana >gi_166934 (J05539) ubiquitin extension protein (UBQ5) [Arabidopsis thaliana]

Seq. No.	161229
Seq. ID	LIB3177-016-P1-K2-A9
Method	BLASTN
NCBI GI	g4584351
BLAST score	345
E value	0.0e+00
Match length	365
% identity	99
NCBI Description	Arabidopsis thaliana chromosome II BAC T12H3 genomic sequence, complete sequence

Seq. No.	161230
Seq. ID	LIB3177-016-P1-K2-B1

Method	BLASTX
NCBI GI	g4741954
BLAST score	695
E value	2.0e-73
Match length	131
% identity	100
NCBI Description	(AF134127) Lhcb4.2 protein [Arabidopsis thaliana]

Seq. No.	161231
Seq. ID	LIB3177-016-P1-K2-B2
Method	BLASTN
NCBI GI	g3659491
BLAST score	326
E value	0.0e+00
Match length	344
% identity	99
NCBI Description	Sequence of BAC T22H22 from Arabidopsis thaliana chromosome 1, complete sequence [Arabidopsis thaliana]

Seq. No.	161232
Seq. ID	LIB3177-016-P1-K2-B3
Method	BLASTX
NCBI GI	g3402716
BLAST score	212
E value	7.0e-17
Match length	112
% identity	47
NCBI Description	(AC004261) unknown protein [Arabidopsis thaliana]

Seq. No.	161233
Seq. ID	LIB3177-016-P1-K2-B5
Method	BLASTX
NCBI GI	g1922964
BLAST score	427
E value	4.0e-42
Match length	97
% identity	84
NCBI Description	(AC000106) Similar to Schizosaccharomyces CCAAT-binding factor (gb_U88525). EST gb_T04310 comes from this gene. [Arabidopsis thaliana]

Seq. No.	161234
Seq. ID	LIB3177-016-P1-K2-B6
Method	BLASTX
NCBI GI	g4538963
BLAST score	683
E value	4.0e-72
Match length	129
% identity	76
NCBI Description	(AL049488) chlorophyll a/b-binding protein-like [Arabidopsis thaliana] >gi_4741958_gb_AAD28776.1_AF134129_1 (AF134129) Lhcb5 protein [Arabidopsis thaliana]

Seq. No.	161235
Seq. ID	LIB3177-016-P1-K2-B7
Method	BLASTX
NCBI GI	g3461821

BLAST score	178
E value	7.0e-13
Match length	90
% identity	42
NCBI Description	(AC004138) putative nucleoside triphosphatase [Arabidopsis thaliana]

Seq. No.	161236
Seq. ID	LIB3177-016-P1-K2-C1
Method	BLASTN
NCBI GI	g3337347
BLAST score	127
E value	2.0e-65
Match length	140
% identity	97
NCBI Description	Arabidopsis thaliana chromosome II BAC F13P17 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	161237
Seq. ID	LIB3177-016-P1-K2-C10
Method	BLASTX
NCBI GI	g135406
BLAST score	621
E value	7.0e-65
Match length	118
% identity	97
NCBI Description	TUBULIN ALPHA-3/ALPHA-5 CHAIN >gi_99768_pir__A32712 tubulin alpha-5 chain - Arabidopsis thaliana >gi_166912 (M17189) alpha-tubulin [Arabidopsis thaliana] >gi_166918 (M84698) alpha-5 tubulin [Arabidopsis thaliana]

Seq. No.	161238
Seq. ID	LIB3177-016-P1-K2-C12
Method	BLASTX
NCBI GI	g116923
BLAST score	164
E value	3.0e-11
Match length	115
% identity	40
NCBI Description	COATOMER BETA SUBUNIT (BETA-COAT PROTEIN) (BETA-COP) >gi_111414_pir__S13520 beta-COP protein - rat >gi_55819_emb_CAA40505_ (X57228) beta COP [Rattus norvegicus]

Seq. No.	161239
Seq. ID	LIB3177-016-P1-K2-C3
Method	BLASTX
NCBI GI	g2914707
BLAST score	300
E value	3.0e-27
Match length	125
% identity	10
NCBI Description	(AC003974) putative disease resistance protein (Cf-2.2) [Arabidopsis thaliana] >gi_3298554 (AC004681) putative disease resistance protein [Arabidopsis thaliana]

Seq. No. 161240

Seq. ID	LIB3177-016-P1-K2-C4
Method	BLASTX
NCBI GI	g2529665
BLAST score	622
E value	5.0e-65
Match length	143
% identity	85
NCBI Description	(AC002535) putative ribosomal protein L7A [Arabidopsis thaliana]

Seq. No.	161241
Seq. ID	LIB3177-016-P1-K2-C5
Method	BLASTX
NCBI GI	g3953601
BLAST score	535
E value	6.0e-55
Match length	112
% identity	96
NCBI Description	(AB008489) response regulator 6 [Arabidopsis thaliana]

Seq. No.	161242
Seq. ID	LIB3177-016-P1-K2-C6
Method	BLASTX
NCBI GI	g4538963
BLAST score	205
E value	1.0e-16
Match length	42
% identity	90
NCBI Description	(AL049488) chlorophyll a/b-binding protein-like [Arabidopsis thaliana] >gi_4741958_gb_AAD28776.1_AF134129_1 (AF134129) Lhcb5 protein [Arabidopsis thaliana]

Seq. No.	161243
Seq. ID	LIB3177-016-P1-K2-C8
Method	BLASTX
NCBI GI	g4741966
BLAST score	199
E value	2.0e-15
Match length	81
% identity	58
NCBI Description	(AF134133) Lil3 protein [Arabidopsis thaliana]

Seq. No.	161244
Seq. ID	LIB3177-016-P1-K2-C9
Method	BLASTX
NCBI GI	g2160142
BLAST score	444
E value	4.0e-44
Match length	89
% identity	100
NCBI Description	(AC000375) Strong similarity to Arabidopsis APR2 (gb_U56921). [Arabidopsis thaliana] >gi_2738758 (AF016283) 5'-adenylylsulfate reductase [Arabidopsis thaliana]

Seq. No.	161245
Seq. ID	LIB3177-016-P1-K2-D11
Method	BLASTX

NCBI GI	g3281855
BLAST score	302
E value	2.0e-27
Match length	118
% identity	56
NCBI Description	(AL031004) hypothetical protein [Arabidopsis thaliana]

Seq. No.	161246
Seq. ID	LIB3177-016-P1-K2-D12
Method	BLASTX
NCBI GI	g117238
BLAST score	86
E value	3.0e-54
Match length	136
% identity	88
NCBI Description	MAGNESIUM-CHELATASE SUBUNIT CHLI PRECURSOR (PROTEIN CS/CH-42) (MG-PROTOPORPHYRIN IX CHELATASE) >gi_81656_pir__S12785 protein ch-42 precursor, chloroplast - Arabidopsis thaliana >gi_1020100_emb_CAA62754_ (X91411) protoporphyrin-IX Mg-chetalase [Arabidopsis thaliana] >gi_2832653_emb_CAA16728_ (AL021710) protein ch-42 precursor, chloroplast [Arabidopsis thaliana] >gi_4490290_emb_CAB38561.1_ (X51799) chloroplast protein [Arabidopsis thaliana] >gi_228771_prf__1811226A ccsA gene [Euglena gracilis]

Seq. No.	161247
Seq. ID	LIB3177-016-P1-K2-D2
Method	BLASTX
NCBI GI	g3851636
BLAST score	474
E value	1.0e-47
Match length	120
% identity	72
NCBI Description	(AF098519) unknown [Avicennia marina] >gi_4128206 (AF056316) 40S ribosome protein S7 [Avicennia marina]

Seq. No.	161248
Seq. ID	LIB3177-016-P1-K2-D3
Method	BLASTX
NCBI GI	g2746911
BLAST score	188
E value	3.0e-14
Match length	100
% identity	38
NCBI Description	(AF040659) similar to the ATP-binding transport protein family [Caenorhabditis elegans]

Seq. No.	161249
Seq. ID	LIB3177-016-P1-K2-D4
Method	BLASTX
NCBI GI	g2828267
BLAST score	277
E value	1.0e-24
Match length	60
% identity	93
NCBI Description	(Y14044) geranylgeranyl reductase [Arabidopsis thaliana]

Seq. No.	161250
Seq. ID	LIB3177-016-P1-K2-D7
Method	BLASTX
NCBI GI	g2497281
BLAST score	87
E value	2.0e-29
Match length	123
% identity	59
NCBI Description	TRANSLATION INITIATION FACTOR IF-2 >gi_1651769_dbj_BAA16696_ (D90900) initiation factor IF-2 [Synechocystis sp.]

Seq. No.	161251
Seq. ID	LIB3177-016-P1-K2-D9
Method	BLASTX
NCBI GI	g2781354
BLAST score	559
E value	1.0e-57
Match length	109
% identity	97
NCBI Description	(AC003113) F24O1.10 [Arabidopsis thaliana]

Seq. No.	161252
Seq. ID	LIB3177-016-P1-K2-E11
Method	BLASTX
NCBI GI	g3281855
BLAST score	275
E value	2.0e-24
Match length	120
% identity	51
NCBI Description	(AL031004) hypothetical protein [Arabidopsis thaliana]

Seq. No.	161253
Seq. ID	LIB3177-016-P1-K2-E2
Method	BLASTX
NCBI GI	g4204285
BLAST score	762
E value	2.0e-81
Match length	147
% identity	97
NCBI Description	(AC003027) lcl_prt_seq No definition line found [Arabidopsis thaliana]

Seq. No.	161254
Seq. ID	LIB3177-016-P1-K2-E3
Method	BLASTX
NCBI GI	g115767
BLAST score	724
E value	6.0e-77
Match length	143
% identity	97
NCBI Description	CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR (CAB-165/180) (LHCP) >gi_81603_pir__A29280 chlorophyll a/b-binding protein ab165 - Arabidopsis thaliana >gi_16368_emb_CAA27540_ (X03907) chlorophyll a/b binding protein (LHCP AB 65) [Arabidopsis thaliana]

	>gi_16372_emb_CAA27541_ (X03908) chlorophyll a/b binding protein (LHCP AB 180) [Arabidopsis thaliana]
Seq. No.	161255
Seq. ID	LIB3177-016-P1-K2-E4
Method	BLASTX
NCBI GI	g231683
BLAST score	495
E value	4.0e-50
Match length	125
% identity	78
NCBI Description	CALNEXIN HOMOLOG PRECURSOR >gi_421825_pir__JN0597 calnexin-like protein - Arabidopsis thaliana >gi_16211_emb_CAA79144_ (Z18242) calnexin homolog [Arabidopsis thaliana]
Seq. No.	161256
Seq. ID	LIB3177-016-P1-K2-E5
Method	BLASTX
NCBI GI	g1546690
BLAST score	657
E value	4.0e-69
Match length	138
% identity	95
NCBI Description	(X98803) peroxidase ATP14a [Arabidopsis thaliana]
Seq. No.	161257
Seq. ID	LIB3177-016-P1-K2-E6
Method	BLASTX
NCBI GI	g1168728
BLAST score	618
E value	2.0e-64
Match length	134
% identity	87
NCBI Description	CINNAMYL-ALCOHOL DEHYDROGENASE 1 (CAD) >gi_598071 (L37883) cinnamyl-alcohol dehydrogenase [Arabidopsis thaliana]
Seq. No.	161258
Seq. ID	LIB3177-016-P1-K2-E8
Method	BLASTX
NCBI GI	g4417281
BLAST score	168
E value	4.0e-16
Match length	104
% identity	46
NCBI Description	(AC007019) putative cinnamyl-alcohol dehydrogenase [Arabidopsis thaliana]
Seq. No.	161259
Seq. ID	LIB3177-016-P1-K2-E9
Method	BLASTX
NCBI GI	g132074
BLAST score	658
E value	3.0e-69
Match length	126
% identity	97
NCBI Description	RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN 1A PRECURSOR

	(RUBISCO SMALL SUBUNIT 1A) >gi_68063_pir__RKMUA1 ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain A1 precursor - Arabidopsis thaliana
Seq. No.	161260
Seq. ID	LIB3177-016-P1-K2-F1
Method	BLASTX
NCBI GI	g4583542
BLAST score	316
E value	4.0e-29
Match length	127
% identity	57
NCBI Description	(Y16847) 16 kDa polypeptide of oxygen-evolving complex [Arabidopsis thaliana]
Seq. No.	161261
Seq. ID	LIB3177-016-P1-K2-F11
Method	BLASTX
NCBI GI	g132110
BLAST score	417
E value	4.0e-41
Match length	86
% identity	88
NCBI Description	RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN 3B PRECURSOR (RUBISCO SMALL SUBUNIT 3B) >gi_68060_pir__RKMUB3 ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain B3 precursor - Arabidopsis thaliana >gi_16195_emb_CAA32702_ (X14564) ribulose bisphosphate carboxylase [Arabidopsis thaliana]
Seq. No.	161262
Seq. ID	LIB3177-016-P1-K2-F12
Method	BLASTX
NCBI GI	g3128176
BLAST score	184
E value	3.0e-14
Match length	66
% identity	45
NCBI Description	(AC004521) unknown protein [Arabidopsis thaliana]
Seq. No.	161263
Seq. ID	LIB3177-016-P1-K2-F2
Method	BLASTX
NCBI GI	g4741950
BLAST score	653
E value	1.0e-68
Match length	134
% identity	91
NCBI Description	(AF134125) Lhcb2 protein [Arabidopsis thaliana]
Seq. No.	161264
Seq. ID	LIB3177-016-P1-K2-F6
Method	BLASTX
NCBI GI	g3341685
BLAST score	655
E value	8.0e-69
Match length	133

% identity	95
NCBI Description	(AC003672) unknown protein [Arabidopsis thaliana]

Seq. No.	161265
Seq. ID	LIB3177-016-P1-K2-F7
Method	BLASTX
NCBI GI	g1170028
BLAST score	143
E value	8.0e-55
Match length	124
% identity	93
NCBI Description	GLUTAMATE-1-SEMIALDEHYDE 2,1-AMINOMUTASE 1 PRECURSOR (GSA 1) (GLUTAMATE-1-SEMIALDEHYDE AMINOTRANSFERASE 1) (GSA-AT 1) >gi_454357 (U03773) glutamate-1-semialdehyde-2,1-aminomutase [Arabidopsis thaliana]

Seq. No.	161266
Seq. ID	LIB3177-016-P1-K2-F8
Method	BLASTX
NCBI GI	g4741952
BLAST score	611
E value	1.0e-63
Match length	131
% identity	69
NCBI Description	(AF134126) Lhcb3 protein [Arabidopsis thaliana]

Seq. No.	161267
Seq. ID	LIB3177-016-P1-K2-G10
Method	BLASTX
NCBI GI	g2507281
BLAST score	475
E value	8.0e-48
Match length	97
% identity	91
NCBI Description	GTP-BINDING NUCLEAR PROTEIN RAN-2 >gi_1668706_emb_CAA66048_ (X97380) atran2 [Arabidopsis thaliana]

Seq. No.	161268
Seq. ID	LIB3177-016-P1-K2-G2
Method	BLASTN
NCBI GI	g4406776
BLAST score	417
E value	0.0e+00
Match length	449
% identity	98
NCBI Description	Arabidopsis thaliana chromosome II BAC F14H20 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	161269
Seq. ID	LIB3177-016-P1-K2-G4
Method	BLASTN
NCBI GI	g555977
BLAST score	276
E value	1.0e-154
Match length	308
% identity	97

NCBI Description	Arabidopsis thaliana metallothionein-like protein (AtMT-q) mRNA, complete cds
Seq. No.	161270
Seq. ID	LIB3177-016-P1-K2-G5
Method	BLASTN
NCBI GI	g4584351
BLAST score	229
E value	1.0e-126
Match length	362
% identity	92
NCBI Description	Arabidopsis thaliana chromosome II BAC T12H3 genomic sequence, complete sequence
Seq. No.	161271
Seq. ID	LIB3177-016-P1-K2-G6
Method	BLASTX
NCBI GI	g4165488
BLAST score	468
E value	5.0e-47
Match length	91
% identity	96
NCBI Description	(AJ132399) alpha-tubulin 3 [Hordeum vulgare]
Seq. No.	161272
Seq. ID	LIB3177-016-P1-K2-H1
Method	BLASTX
NCBI GI	g1402914
BLAST score	257
E value	2.0e-22
Match length	90
% identity	66
NCBI Description	(X98318) peroxidase [Arabidopsis thaliana]
Seq. No.	161273
Seq. ID	LIB3177-016-P1-K2-H2
Method	BLASTX
NCBI GI	g2760362
BLAST score	537
E value	5.0e-55
Match length	115
% identity	92
NCBI Description	(AF016511) 15.9 kDa subunit of RNA polymerase II [Arabidopsis thaliana]
Seq. No.	161274
Seq. ID	LIB3177-017-P1-K1-A1
Method	BLASTX
NCBI GI	g132110
BLAST score	346
E value	1.0e-32
Match length	111
% identity	65
NCBI Description	RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN 3B PRECURSOR (RUBISCO SMALL SUBUNIT 3B) >gi_68060_pir__RKMUB3 ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain B3 precursor - Arabidopsis thaliana >gi_16195_emb_CAA32702_

	(X14564) ribulose bisphosphate carboxylase [Arabidopsis thaliana]
Seq. No.	161275
Seq. ID	LIB3177-017-P1-K1-A3
Method	BLASTX
NCBI GI	g2648032
BLAST score	279
E value	8.0e-25
Match length	120
% identity	47
NCBI Description	(AJ001374) alpha-glucosidase [Solanum tuberosum]
Seq. No.	161276
Seq. ID	LIB3177-017-P1-K1-A4
Method	BLASTX
NCBI GI	g4206206
BLAST score	253
E value	6.0e-22
Match length	109
% identity	50
NCBI Description	(AF071527) putative M-type thioredoxin [Arabidopsis thaliana] >gi_4263039_gb_AAD15308_ (AC005142) putative M-type thioredoxin [Arabidopsis thaliana]
Seq. No.	161277
Seq. ID	LIB3177-017-P1-K1-A8
Method	BLASTX
NCBI GI	g1352664
BLAST score	223
E value	3.0e-18
Match length	77
% identity	65
NCBI Description	SERINE/THREONINE PROTEIN PHOSPHATASE PP2A-4 CATALYTIC SUBUNIT >gi_2117984_pir__S52660 phosphoprotein phosphatase (EC 3.1.3.16) 2A isoform 4 - Arabidopsis thaliana >gi_473259 (U08047) Ser/Thr protein phosphatase [Arabidopsis thaliana] >gi_4204949 (U60136) serine/threonine protein phosphatase 2A-4 catalytic subunit [Arabidopsis thaliana]
Seq. No.	161278
Seq. ID	LIB3177-017-P1-K1-B10
Method	BLASTN
NCBI GI	g4581161
BLAST score	90
E value	4.0e-43
Match length	282
% identity	37
NCBI Description	Arabidopsis thaliana chromosome II BAC T20G20 genomic sequence, complete sequence
Seq. No.	161279
Seq. ID	LIB3177-017-P1-K1-B2
Method	BLASTX
NCBI GI	g4741929
BLAST score	168

E value	7.0e-12
Match length	89
% identity	44
NCBI Description	(AF130253) membrane related protein CP5 [Arabidopsis thaliana]

Seq. No.	161280
Seq. ID	LIB3177-017-P1-K1-B3
Method	BLASTX
NCBI GI	g2499810
BLAST score	285
E value	1.0e-25
Match length	100
% identity	61
NCBI Description	PROFILIN 1 >gi_2981657_pdb_1A0K_ Profilin I From Arabidopsis Thaliana >gi_1353763 (U43322) profilin 1 [Arabidopsis thaliana] >gi_1353770 (U43325) profilin 1 [Arabidopsis thaliana] >gi_1835878_bbs_179026 (S82691) profilin isoform 1 [Arabidopsis thaliana, Columbia, flowers, Peptide, 131 aa] [Arabidopsis thaliana] >gi_3687242 (AC005169) profilin 1 [Arabidopsis thaliana]

Seq. No.	161281
Seq. ID	LIB3177-017-P1-K1-B4
Method	BLASTX
NCBI GI	g544122
BLAST score	247
E value	3.0e-21
Match length	102
% identity	52
NCBI Description	APOCYTOCHROME F PRECURSOR >gi_629599_pir__S45661 plastoquinol--plastocyanin reductase (EC 1.10.99.1) cytochrome f precursor - turnip chloroplast >gi_441282_emb_CAA54307_ (X77011) cytochrome f [Brassica rapa]

Seq. No.	161282
Seq. ID	LIB3177-017-P1-K1-B6
Method	BLASTN
NCBI GI	g2351073
BLAST score	36
E value	1.0e-10
Match length	173
% identity	87
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MYJ24, complete sequence [Arabidopsis thaliana]

Seq. No.	161283
Seq. ID	LIB3177-017-P1-K1-B9
Method	BLASTX
NCBI GI	g1651828
BLAST score	197
E value	3.0e-15
Match length	100
% identity	48
NCBI Description	(D90900) dihydrolipoamide dehydrogenase [Synechocystis sp.]

Seq. No.	161284
Seq. ID	LIB3177-017-P1-K1-C10
Method	BLASTX
NCBI GI	g2281111
BLAST score	192
E value	8.0e-15
Match length	71
% identity	54
NCBI Description	(AC002333) endochitinase isolog [Arabidopsis thaliana] >gi_2288991 (AC002335) endochitinase isolog [Arabidopsis thaliana]

Seq. No.	161285
Seq. ID	LIB3177-017-P1-K1-C11
Method	BLASTX
NCBI GI	g4587600
BLAST score	215
E value	2.0e-17
Match length	75
% identity	61
NCBI Description	(AC006951) putative translation initiation factor EIF-1A [Arabidopsis thaliana]

Seq. No.	161286
Seq. ID	LIB3177-017-P1-K1-C4
Method	BLASTX
NCBI GI	g3319350
BLAST score	285
E value	1.0e-25
Match length	107
% identity	58
NCBI Description	(AF077407) No definition line found [Arabidopsis thaliana]

Seq. No.	161287
Seq. ID	LIB3177-017-P1-K1-D1
Method	BLASTX
NCBI GI	g730526
BLAST score	303
E value	1.0e-27
Match length	125
% identity	50
NCBI Description	60S RIBOSOMAL PROTEIN L13 (BBC1 PROTEIN HOMOLOG) >gi_480787_pir__S37271 ribosomal protein L13 - Arabidopsis thaliana >gi_404166_emb_CAA53005_ (X75162) BBC1 protein [Arabidopsis thaliana]

Seq. No.	161288
Seq. ID	LIB3177-017-P1-K1-D2
Method	BLASTX
NCBI GI	g1076385
BLAST score	278
E value	1.0e-24
Match length	111
% identity	55
NCBI Description	protein kinase (EC 2.7.1.37) tousled - Arabidopsis thaliana >gi_433052 (L23985) protein kinase [Arabidopsis thaliana]

Seq. No.	161289
Seq. ID	LIB3177-017-P1-K1-D3
Method	BLASTX
NCBI GI	g1865683
BLAST score	108
E value	2.0e-09
Match length	76
% identity	53
NCBI Description	(Z83321) plastocyanin [Arabidopsis thaliana]

Seq. No.	161290
Seq. ID	LIB3177-017-P1-K1-D4
Method	BLASTX
NCBI GI	g1946362
BLAST score	178
E value	4.0e-13
Match length	86
% identity	45
NCBI Description	(U93215) photosystem II reaction center 6.1KD protein [Arabidopsis thaliana]

Seq. No.	161291
Seq. ID	LIB3177-017-P1-K1-D9
Method	BLASTX
NCBI GI	g4588906
BLAST score	220
E value	6.0e-18
Match length	99
% identity	46
NCBI Description	(AF118149) ribosomal protein S7 [Secale cereale]

Seq. No.	161292
Seq. ID	LIB3177-017-P1-K1-E2
Method	BLASTX
NCBI GI	g3334412
BLAST score	296
E value	6.0e-27
Match length	120
% identity	57
NCBI Description	VACUOLAR ATP SYNTHASE 16 KD PROTEOLIPID SUBUNIT (V-TYPE H+-ATPASE 16 KD SUBUNIT) >gi_1622721 (U16244) V-type H+-ATPase 16 kDa subunit [Kalanchoe daigremontiana]

Seq. No.	161293
Seq. ID	LIB3177-017-P1-K1-E3
Method	BLASTX
NCBI GI	g1363489
BLAST score	354
E value	1.0e-33
Match length	119
% identity	61
NCBI Description	thioglucosidase (EC 3.2.3.1) 3D precursor - Arabidopsis thaliana >gi_984052_emb_CAA61592_ (X89413) thioglucoside glucohydrolase [Arabidopsis thaliana]

Seq. No.	161294
Seq. ID	LIB3177-017-P1-K1-E4

Method	BLASTX
NCBI GI	g16374
BLAST score	491
E value	1.0e-49
Match length	140
% identity	69
NCBI Description	(X03908) chlorophyll a/b binding protein (LHCP AB 180) [Arabidopsis thaliana]

Seq. No.	161295
Seq. ID	LIB3177-017-P1-K1-E5
Method	BLASTX
NCBI GI	g585536
BLAST score	424
E value	7.0e-42
Match length	121
% identity	72
NCBI Description	MYROSINASE PRECURSOR (SINIGRINASE) (THIOGLUCOSIDASE) >gi_1362006_pir__S56653 thioglucosidase (EC 3.2.3.1) - Arabidopsis thaliana >gi_304115 (L11454) thioglucosidase [Arabidopsis thaliana] >gi_871990_emb_CAA55786_ (X79194) thioglucosidase [Arabidopsis thaliana]

Seq. No.	161296
Seq. ID	LIB3177-017-P1-K1-E6
Method	BLASTX
NCBI GI	g1169201
BLAST score	292
E value	2.0e-26
Match length	123
% identity	54
NCBI Description	DNA-DAMAGE-REPAIR/TOLERATION PROTEIN DRT112 PRECURSOR >gi_421830_pir__S33707 DRT112 protein - Arabidopsis thaliana >gi_166696 (M98456) DRT112 [Arabidopsis thaliana]

Seq. No.	161297
Seq. ID	LIB3177-017-P1-K1-E8
Method	BLASTX
NCBI GI	g2369714
BLAST score	419
E value	3.0e-41
Match length	133
% identity	60
NCBI Description	(Z97178) elongation factor 2 [Beta vulgaris]

Seq. No.	161298
Seq. ID	LIB3177-017-P1-K1-F10
Method	BLASTX
NCBI GI	g4741962
BLAST score	295
E value	7.0e-27
Match length	101
% identity	35
NCBI Description	(AF134131) PsbS protein [Arabidopsis thaliana]

Seq. No.	161299
Seq. ID	LIB3177-017-P1-K1-F2

Method	BLASTX
NCBI GI	g1732570
BLAST score	387
E value	2.0e-37
Match length	124
% identity	62
NCBI Description	(U72153) beta-glucosidase [Arabidopsis thaliana]

Seq. No.	161300
Seq. ID	LIB3177-017-P1-K1-F3
Method	BLASTX
NCBI GI	g1773330
BLAST score	364
E value	8.0e-35
Match length	125
% identity	62
NCBI Description	(U80071) glycolate oxidase [Mesembryanthemum crystallinum]

Seq. No.	161301
Seq. ID	LIB3177-017-P1-K1-F4
Method	BLASTX
NCBI GI	g115767
BLAST score	306
E value	7.0e-28
Match length	134
% identity	53
NCBI Description	CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR (CAB-165/180) (LHCP) >gi_81603_pir__A29280 chlorophyll a/b-binding protein ab165 - Arabidopsis thaliana >gi_16368_emb_CAA27540_ (X03907) chlorophyll a/b binding protein (LHCP AB 65) [Arabidopsis thaliana] >gi_16372_emb_CAA27541_ (X03908) chlorophyll a/b binding protein (LHCP AB 180) [Arabidopsis thaliana]

Seq. No.	161302
Seq. ID	LIB3177-017-P1-K1-F6
Method	BLASTX
NCBI GI	g2129538
BLAST score	376
E value	4.0e-36
Match length	145
% identity	54
NCBI Description	AT103 protein - Arabidopsis thaliana >gi_1033195 (U38232) AT103 [Arabidopsis thaliana]

Seq. No.	161303
Seq. ID	LIB3177-017-P1-K1-F7
Method	BLASTX
NCBI GI	g464840
BLAST score	190
E value	8.0e-15
Match length	55
% identity	67
NCBI Description	TUBULIN ALPHA-1 CHAIN >gi_421781_pir__S32666 tubulin alpha-1 chain - fern (Anemia phyllitidis) >gi_296494_emb_CAA48927_ (X69183) alpha tubulin [Anemia phyllitidis]

Seq. No.	161304
Seq. ID	LIB3177-017-P1-K1-F8
Method	BLASTX
NCBI GI	g2342727
BLAST score	192
E value	1.0e-14
Match length	95
% identity	51
NCBI Description	(AC002341) hypothetical protein [Arabidopsis thaliana]

Seq. No.	161305
Seq. ID	LIB3177-017-P1-K1-G10
Method	BLASTN
NCBI GI	g4159709
BLAST score	44
E value	1.0e-15
Match length	175
% identity	80
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MLN21, complete sequence

Seq. No.	161306
Seq. ID	LIB3177-017-P1-K1-G2
Method	BLASTX
NCBI GI	g464849
BLAST score	283
E value	2.0e-25
Match length	70
% identity	76
NCBI Description	TUBULIN ALPHA CHAIN >gi_486847_pir__S36232 tubulin alpha chain - almond >gi_20413_emb_CAA47635_ (X67162) alpha-tubulin [Prunus dulcis]

Seq. No.	161307
Seq. ID	LIB3177-017-P1-K1-G3
Method	BLASTN
NCBI GI	g3599967
BLAST score	78
E value	8.0e-36
Match length	346
% identity	81
NCBI Description	Arabidopsis thaliana clp protease (CLP) mRNA, partial cds

Seq. No.	161308
Seq. ID	LIB3177-017-P1-K1-G8
Method	BLASTX
NCBI GI	g4583542
BLAST score	219
E value	7.0e-18
Match length	115
% identity	49
NCBI Description	(Y16847) 16 kDa polypeptide of oxygen-evolving complex [Arabidopsis thaliana]

Seq. No.	161309
Seq. ID	LIB3177-017-P1-K1-G9

Method	BLASTX
NCBI GI	g4056469
BLAST score	248
E value	3.0e-21
Match length	113
% identity	52
NCBI Description	(AC005990) Strong similarity to gb_M95166 ADP-ribosylation factor from Arabidopsis thaliana. ESTs gb_Z25826, gb_R90191, gb_N65697, gb_AA713150, gb_T46332, gb_AA040967, gb_AA712956, gb_T46403, gb_T46050, gb_AI100391 and gb_Z25043 come from t

Seq. No.	161310
Seq. ID	LIB3177-017-P1-K1-H1
Method	BLASTN
NCBI GI	g3046853
BLAST score	65
E value	5.0e-28
Match length	327
% identity	84
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MRA19, complete sequence [Arabidopsis thaliana]

Seq. No.	161311
Seq. ID	LIB3177-017-P1-K1-H10
Method	BLASTN
NCBI GI	g2760168
BLAST score	81
E value	1.0e-37
Match length	232
% identity	85
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MEE6, complete sequence [Arabidopsis thaliana]

Seq. No.	161312
Seq. ID	LIB3177-017-P1-K1-H12
Method	BLASTX
NCBI GI	g1170939
BLAST score	214
E value	2.0e-17
Match length	72
% identity	62
NCBI Description	S-ADENOSYLMETHIONINE SYNTHETASE 3 (METHIONINE ADENOSYLTRANSFERASE 3) (ADOMET SYNTHETASE 3) >gi_1084408_pir__S46540 methionine adenosyltransferase (EC 2.5.1.6) - tomato >gi_429108_emb_CAA80867_ (Z24743) S-adenosyl-L-methionine synthetase [Lycopersicon esculentum]

Seq. No.	161313
Seq. ID	LIB3177-017-P1-K1-H5
Method	BLASTX
NCBI GI	g3927825
BLAST score	282
E value	3.0e-25
Match length	97
% identity	58

NCBI Description	(AC005727) putative dTDP-glucose 4-6-dehydratase [Arabidopsis thaliana]

Seq. No.	161314
Seq. ID	LIB3177-017-P1-K2-A1
Method	BLASTX
NCBI GI	g132110
BLAST score	646
E value	8.0e-68
Match length	120
% identity	98
NCBI Description	RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN 3B PRECURSOR (RUBISCO SMALL SUBUNIT 3B) >gi_68060_pir__RKMUB3 ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain B3 precursor - Arabidopsis thaliana >gi_16195_emb_CAA32702_ (X14564) ribulose bisphosphate carboxylase [Arabidopsis thaliana]

Seq. No.	161315
Seq. ID	LIB3177-017-P1-K2-A2
Method	BLASTX
NCBI GI	g4689386
BLAST score	323
E value	6.0e-30
Match length	86
% identity	72
NCBI Description	(AF139468) photosystem I reaction center subunit III [Vigna radiata]

Seq. No.	161316
Seq. ID	LIB3177-017-P1-K2-A3
Method	BLASTX
NCBI GI	g2648032
BLAST score	531
E value	3.0e-54
Match length	139
% identity	72
NCBI Description	(AJ001374) alpha-glucosidase [Solanum tuberosum]

Seq. No.	161317
Seq. ID	LIB3177-017-P1-K2-A4
Method	BLASTX
NCBI GI	g4206206
BLAST score	720
E value	2.0e-76
Match length	150
% identity	92
NCBI Description	(AF071527) putative M-type thioredoxin [Arabidopsis thaliana] >gi_4263039_gb_AAD15308_ (AC005142) putative M-type thioredoxin [Arabidopsis thaliana]

Seq. No.	161318
Seq. ID	LIB3177-017-P1-K2-A5
Method	BLASTN
NCBI GI	g4757409
BLAST score	77
E value	2.0e-35

Match length	178
% identity	96
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MVC8, complete sequence

Seq. No.	161319
Seq. ID	LIB3177-017-P1-K2-A7
Method	BLASTN
NCBI GI	g2853071
BLAST score	55
E value	3.0e-22
Match length	113
% identity	94
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F24J7 (ESSA project)

Seq. No.	161320
Seq. ID	LIB3177-017-P1-K2-A8
Method	BLASTX
NCBI GI	g1352664
BLAST score	471
E value	3.0e-47
Match length	90
% identity	99
NCBI Description	SERINE/THREONINE PROTEIN PHOSPHATASE PP2A-4 CATALYTIC SUBUNIT >gi_2117984_pir__S52660 phosphoprotein phosphatase (EC 3.1.3.16) 2A isoform 4 - Arabidopsis thaliana >gi_473259 (U08047) Ser/Thr protein phosphatase [Arabidopsis thaliana] >gi_4204949 (U60136) serine/threonine protein phosphatase 2A-4 catalytic subunit [Arabidopsis thaliana]

Seq. No.	161321
Seq. ID	LIB3177-017-P1-K2-B1
Method	BLASTX
NCBI GI	g416681
BLAST score	241
E value	3.0e-20
Match length	138
% identity	41
NCBI Description	ATP SYNTHASE DELTA CHAIN, CHLOROPLAST PRECURSOR >gi_280404_pir__S26198 H+-transporting ATP synthase (EC 3.6.1.34) delta chain precursor, chloroplast - common tobacco >gi_19787_emb_CAA45153_ (X63607) chloroplast ATP synthase (delta subunit) [Nicotiana tabacum]

Seq. No.	161322
Seq. ID	LIB3177-017-P1-K2-B2
Method	BLASTN
NCBI GI	g4220643
BLAST score	181
E value	3.0e-97
Match length	245
% identity	93
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MWD22, complete sequence [Arabidopsis thaliana]

Seq. No.	161323
Seq. ID	LIB3177-017-P1-K2-B3
Method	BLASTX
NCBI GI	g2499810
BLAST score	395
E value	1.0e-38
Match length	81
% identity	93
NCBI Description	PROFILIN 1 >gi_2981657_pdb_1A0K_ Profilin I From Arabidopsis Thaliana >gi_1353763 (U43322) profilin 1 [Arabidopsis thaliana] >gi_1353770 (U43325) profilin 1 [Arabidopsis thaliana] >gi_1835878_bbs_179026 (S82691) profilin isoform 1 [Arabidopsis thaliana, Columbia, flowers, Peptide, 131 aa] [Arabidopsis thaliana] >gi_3687242 (AC005169) profilin 1 [Arabidopsis thaliana]

Seq. No.	161324
Seq. ID	LIB3177-017-P1-K2-B4
Method	BLASTX
NCBI GI	g1942179
BLAST score	609
E value	2.0e-63
Match length	130
% identity	92
NCBI Description	Lumen-Side Domain Of Reduced Cytochrome F At -35 Degrees Celsius

Seq. No.	161325
Seq. ID	LIB3177-017-P1-K2-B5
Method	BLASTX
NCBI GI	g4049349
BLAST score	390
E value	7.0e-38
Match length	109
% identity	75
NCBI Description	(AL034567) ubiquinol-cytochrome c reductase-like protein [Arabidopsis thaliana]

Seq. No.	161326
Seq. ID	LIB3177-017-P1-K2-B6
Method	BLASTN
NCBI GI	g2351073
BLAST score	103
E value	1.0e-50
Match length	353
% identity	97
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MYJ24, complete sequence [Arabidopsis thaliana]

Seq. No.	161327
Seq. ID	LIB3177-017-P1-K2-B8
Method	BLASTN
NCBI GI	g1800146
BLAST score	298
E value	1.0e-167
Match length	410
% identity	93

NCBI Description	Arabidopsis thaliana membrane associated protein mRNA, complete cds
Seq. No.	161328
Seq. ID	LIB3177-017-P1-K2-B9
Method	BLASTX
NCBI GI	g1321941
BLAST score	396
E value	2.0e-38
Match length	120
% identity	69
NCBI Description	(Z48564) dihydrolipoamide dehydrogenase [Synechocystis PCC6803]
Seq. No.	161329
Seq. ID	LIB3177-017-P1-K2-C1
Method	BLASTX
NCBI GI	g4741962
BLAST score	439
E value	1.0e-43
Match length	129
% identity	55
NCBI Description	(AF134131) PsbS protein [Arabidopsis thaliana]
Seq. No.	161330
Seq. ID	LIB3177-017-P1-K2-C10
Method	BLASTX
NCBI GI	g2281111
BLAST score	470
E value	4.0e-47
Match length	134
% identity	73
NCBI Description	(AC002333) endochitinase isolog [Arabidopsis thaliana] >gi_2288991 (AC002335) endochitinase isolog [Arabidopsis thaliana]
Seq. No.	161331
Seq. ID	LIB3177-017-P1-K2-C11
Method	BLASTX
NCBI GI	g4587600
BLAST score	258
E value	7.0e-23
Match length	64
% identity	83
NCBI Description	(AC006951) putative translation initiation factor EIF-1A [Arabidopsis thaliana]
Seq. No.	161332
Seq. ID	LIB3177-017-P1-K2-C4
Method	BLASTX
NCBI GI	g3319350
BLAST score	770
E value	3.0e-82
Match length	150
% identity	100
NCBI Description	(AF077407) No definition line found [Arabidopsis thaliana]

Seq. No.	161333
Seq. ID	LIB3177-017-P1-K2-C8
Method	BLASTN
NCBI GI	g2924654
BLAST score	34
E value	1.0e-09
Match length	130
% identity	87
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MHK7, complete sequence [Arabidopsis thaliana]

Seq. No.	161334
Seq. ID	LIB3177-017-P1-K2-D1
Method	BLASTX
NCBI GI	g730526
BLAST score	748
E value	9.0e-80
Match length	145
% identity	99
NCBI Description	60S RIBOSOMAL PROTEIN L13 (BBC1 PROTEIN HOMOLOG) >gi_480787_pir__S37271 ribosomal protein L13 - Arabidopsis thaliana >gi_404166_emb_CAA53005_ (X75162) BBC1 protein [Arabidopsis thaliana]

Seq. No.	161335
Seq. ID	LIB3177-017-P1-K2-D12
Method	BLASTX
NCBI GI	g3859606
BLAST score	47
E value	3.0e-19
Match length	73
% identity	70
NCBI Description	(AF104919) contains similarity to cysteine proteases (Pfam: PF00112, E=1.3e-79, N=1) [Arabidopsis thaliana]

Seq. No.	161336
Seq. ID	LIB3177-017-P1-K2-D2
Method	BLASTX
NCBI GI	g1076385
BLAST score	605
E value	6.0e-63
Match length	114
% identity	100
NCBI Description	protein kinase (EC 2.7.1.37) tousled - Arabidopsis thaliana >gi_433052 (L23985) protein kinase [Arabidopsis thaliana]

Seq. No.	161337
Seq. ID	LIB3177-017-P1-K2-D3
Method	BLASTX
NCBI GI	g1865683
BLAST score	198
E value	1.0e-33
Match length	114
% identity	77
NCBI Description	(Z83321) plastocyanin [Arabidopsis thaliana]

Seq. No. 161338

Seq. ID	LIB3177-017-P1-K2-D4
Method	BLASTX
NCBI GI	g1946362
BLAST score	420
E value	3.0e-41
Match length	123
% identity	68
NCBI Description	(U93215) photosystem II reaction center 6.1KD protein [Arabidopsis thaliana]

Seq. No.	161339
Seq. ID	LIB3177-017-P1-K2-D8
Method	BLASTX
NCBI GI	g1350680
BLAST score	220
E value	2.0e-18
Match length	64
% identity	69
NCBI Description	60S RIBOSOMAL PROTEIN L1

Seq. No.	161340
Seq. ID	LIB3177-017-P1-K2-D9
Method	BLASTX
NCBI GI	g3851636
BLAST score	478
E value	4.0e-48
Match length	123
% identity	72
NCBI Description	(AF098519) unknown [Avicennia marina] >gi_4128206 (AF056316) 40S ribosome protein S7 [Avicennia marina]

Seq. No.	161341
Seq. ID	LIB3177-017-P1-K2-E1
Method	BLASTX
NCBI GI	g1730674
BLAST score	174
E value	2.0e-12
Match length	119
% identity	34
NCBI Description	HYPOTHETICAL 62.7 KD PROTEIN IN SEC12-SSK2 INTERGENIC REGION >gi_2132801_pir__S63361 probable membrane protein YNR030w - yeast (Saccharomyces cerevisiae) >gi_1302525_emb_CAA96310_ (Z71645) ORF YNR030w [Saccharomyces cerevisiae]

Seq. No.	161342
Seq. ID	LIB3177-017-P1-K2-E2
Method	BLASTX
NCBI GI	g3334412
BLAST score	186
E value	1.0e-13
Match length	40
% identity	97
NCBI Description	VACUOLAR ATP SYNTHASE 16 KD PROTEOLIPID SUBUNIT (V-TYPE H+-ATPASE 16 KD SUBUNIT) >gi_1622721 (U16244) V-type H+-ATPase 16 kDa subunit [Kalanchoe daigremontiana]

Seq. No.	161343
Seq. ID	LIB3177-017-P1-K2-E3
Method	BLASTX
NCBI GI	g1363489
BLAST score	700
E value	4.0e-74
Match length	128
% identity	100
NCBI Description	thioglucosidase (EC 3.2.3.1) 3D precursor - Arabidopsis thaliana >gi_984052_emb_CAA61592_ (X89413) thioglucoside glucohydrolase [Arabidopsis thaliana]

Seq. No.	161344
Seq. ID	LIB3177-017-P1-K2-E4
Method	BLASTX
NCBI GI	g2119846
BLAST score	745
E value	2.0e-79
Match length	142
% identity	100
NCBI Description	chlorophyll a/b-binding protein type I precursor Lhb1B2 - Arabidopsis thaliana >gi_16364_emb_CAA45790_ (X64460) photosystem II type I chlorophyll a /b binding protein [Arabidopsis thaliana] >gi_3128230 (AC004077) photosystem II type I chlorophyll a/b binding protein [Arabidopsis thaliana] >gi_3337371 (AC004481) photosystem II type I chlorophyll a/b binding protein [Arabidopsis thaliana]

Seq. No.	161345
Seq. ID	LIB3177-017-P1-K2-E5
Method	BLASTX
NCBI GI	g585536
BLAST score	740
E value	9.0e-79
Match length	135
% identity	100
NCBI Description	MYROSINASE PRECURSOR (SINIGRINASE) (THIOGLUCOSIDASE) >gi_1362006_pir__S56653 thioglucosidase (EC 3.2.3.1) - Arabidopsis thaliana >gi_304115 (L11454) thioglucosidase [Arabidopsis thaliana] >gi_871990_emb_CAA55786_ (X79194) thioglucosidase [Arabidopsis thaliana]

Seq. No.	161346
Seq. ID	LIB3177-017-P1-K2-E7
Method	BLASTX
NCBI GI	g3193296
BLAST score	310
E value	2.0e-28
Match length	107
% identity	55
NCBI Description	(AF069298) similar to pectinesterase [Arabidopsis thaliana]

Seq. No.	161347
Seq. ID	LIB3177-017-P1-K2-E8
Method	BLASTX
NCBI GI	g2369714
BLAST score	697

E value	8.0e-74
Match length	140
% identity	93
NCBI Description	(Z97178) elongation factor 2 [Beta vulgaris]

Seq. No.	161348
Seq. ID	LIB3177-017-P1-K2-F1
Method	BLASTX
NCBI GI	g1175010
BLAST score	599
E value	3.0e-62
Match length	130
% identity	91
NCBI Description	PLASMA MEMBRANE INTRINSIC PROTEIN 1A >gi_629540_pir__S44082 plasma membrane intrinsic protein 1a - Arabidopsis thaliana >gi_472873_emb_CAA53475_ (X75881) plasma membrane intrinsic protein 1a [Arabidopsis thaliana]

Seq. No.	161349
Seq. ID	LIB3177-017-P1-K2-F10
Method	BLASTX
NCBI GI	g4741962
BLAST score	539
E value	3.0e-55
Match length	138
% identity	52
NCBI Description	(AF134131) PsbS protein [Arabidopsis thaliana]

Seq. No.	161350
Seq. ID	LIB3177-017-P1-K2-F2
Method	BLASTX
NCBI GI	g1732570
BLAST score	93
E value	5.0e-73
Match length	139
% identity	100
NCBI Description	(U72153) beta-glucosidase [Arabidopsis thaliana]

Seq. No.	161351
Seq. ID	LIB3177-017-P1-K2-F3
Method	BLASTX
NCBI GI	g1773330
BLAST score	641
E value	3.0e-67
Match length	144
% identity	86
NCBI Description	(U80071) glycolate oxidase [Mesembryanthemum crystallinum]

Seq. No.	161352
Seq. ID	LIB3177-017-P1-K2-F4
Method	BLASTX
NCBI GI	g115767
BLAST score	769
E value	3.0e-82
Match length	149
% identity	98
NCBI Description	CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR

Docket No. 10005.0004-00000

(CAB-165/180) (LHCP) >gi_81603_pir__A29280 chlorophyll a/b-binding protein ab165 - Arabidopsis thaliana >gi_16368_emb_CAA27540_ (X03907) chlorophyll a/b binding protein (LHCP AB 65) [Arabidopsis thaliana] >gi_16372_emb_CAA27541_ (X03908) chlorophyll a/b binding protein (LHCP AB 180) [Arabidopsis thaliana]

Seq. No.	161353
Seq. ID	LIB3177-017-P1-K2-F6
Method	BLASTX
NCBI GI	g2129538
BLAST score	819
E value	5.0e-88
Match length	156
% identity	97
NCBI Description	AT103 protein - Arabidopsis thaliana >gi_1033195 (U38232) AT103 [Arabidopsis thaliana]

Seq. No.	161354
Seq. ID	LIB3177-017-P1-K2-F7
Method	BLASTX
NCBI GI	g267069
BLAST score	215
E value	6.0e-18
Match length	40
% identity	95
NCBI Description	TUBULIN ALPHA-2/ALPHA-4 CHAIN >gi_320183_pir__JQ1594 tubulin alpha chain - Arabidopsis thaliana >gi_166914 (M84696) apha-2 tubulin [Arabidopsis thaliana] >gi_166916 (M84697) alpha-4 tubulin [Arabidopsis thaliana]

Seq. No.	161355
Seq. ID	LIB3177-017-P1-K2-F8
Method	BLASTX
NCBI GI	g2342727
BLAST score	465
E value	1.0e-46
Match length	117
% identity	78
NCBI Description	(AC002341) hypothetical protein [Arabidopsis thaliana]

Seq. No.	161356
Seq. ID	LIB3177-017-P1-K2-G1
Method	BLASTN
NCBI GI	g1086456
BLAST score	33
E value	6.0e-09
Match length	234
% identity	84
NCBI Description	Arabidopsis thaliana Columbia ecotype metallothionein (MT1a) gene, complete cds

Seq. No.	161357
Seq. ID	LIB3177-017-P1-K2-G10
Method	BLASTN
NCBI GI	g4159709
BLAST score	291

E value	1.0e-163
Match length	323
% identity	98
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MLN21, complete sequence

Seq. No.	161358
Seq. ID	LIB3177-017-P1-K2-G12
Method	BLASTX
NCBI GI	g266936
BLAST score	272
E value	6.0e-24
Match length	60
% identity	87
NCBI Description	50S RIBOSOMAL PROTEIN L27, CHLOROPLAST PRECURSOR (CL27) >gi_282960_pir__A42840 ribosomal protein L27 - common tobacco >gi_170306 (M98473) ribosomal protein L27 [Nicotiana tabacum] >gi_170326 (M75731) ribosomal protein L27 [Nicotiana tabacum]

Seq. No.	161359
Seq. ID	LIB3177-017-P1-K2-G2
Method	BLASTX
NCBI GI	g267069
BLAST score	113
E value	3.0e-05
Match length	204
% identity	48
NCBI Description	TUBULIN ALPHA-2/ALPHA-4 CHAIN >gi_320183_pir__JQ1594 tubulin alpha chain - Arabidopsis thaliana >gi_166914 (M84696) apha-2 tubulin [Arabidopsis thaliana] >gi_166916 (M84697) alpha-4 tubulin [Arabidopsis thaliana]

Seq. No.	161360
Seq. ID	LIB3177-017-P1-K2-G3
Method	BLASTX
NCBI GI	g3599968
BLAST score	649
E value	3.0e-68
Match length	132
% identity	98
NCBI Description	(AF032123) clp protease [Arabidopsis thaliana]

Seq. No.	161361
Seq. ID	LIB3177-017-P1-K2-G4
Method	BLASTN
NCBI GI	g2924733
BLAST score	190
E value	1.0e-103
Match length	251
% identity	99
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MUF9, complete sequence [Arabidopsis thaliana]

Seq. No.	161362
Seq. ID	LIB3177-017-P1-K2-G8
Method	BLASTX

NCBI GI	g4583542
BLAST score	546
E value	4.0e-56
Match length	141
% identity	84
NCBI Description	(Y16847) 16 kDa polypeptide of oxygen-evolving complex [Arabidopsis thaliana]

Seq. No.	161363
Seq. ID	LIB3177-017-P1-K2-G9
Method	BLASTX
NCBI GI	g4324967
BLAST score	679
E value	1.0e-71
Match length	141
% identity	95
NCBI Description	(AF114796) ADP-ribosylation factor [Glycine max]

Seq. No.	161364
Seq. ID	LIB3177-017-P1-K2-H1
Method	BLASTX
NCBI GI	g4506223
BLAST score	257
E value	4.0e-22
Match length	118
% identity	42
NCBI Description	proteasome (prosome, macropain) 26S subunit, non-ATPase, 13 >gi_3618343_dbj_BAA33214_ (AB009398) 26S proteasome subunit p40.5 [Homo sapiens]

Seq. No.	161365
Seq. ID	LIB3177-017-P1-K2-H11
Method	BLASTX
NCBI GI	g2129889
BLAST score	469
E value	3.0e-47
Match length	102
% identity	87
NCBI Description	methionine adenosyltransferase (EC 2.5.1.6) 2 - garden pea

Seq. No.	161366
Seq. ID	LIB3177-017-P1-K2-H3
Method	BLASTN
NCBI GI	g4544435
BLAST score	241
E value	1.0e-133
Match length	277
% identity	99
NCBI Description	Arabidopsis thaliana chromosome II BAC F14M13 genomic sequence, complete sequence

Seq. No.	161367
Seq. ID	LIB3177-017-P1-K2-H4
Method	BLASTX
NCBI GI	g3927825
BLAST score	554
E value	5.0e-57

Match length	109
% identity	94
NCBI Description	(AC005727) putative dTDP-glucose 4-6-dehydratase [Arabidopsis thaliana]

Seq. No.	161368
Seq. ID	LIB3177-017-P1-K2-H9
Method	BLASTN
NCBI GI	g1764099
BLAST score	51
E value	6.0e-20
Match length	79
% identity	91
NCBI Description	Arabidopsis thaliana GDP-D-mannose-4,6-dehydratase (MUR1) mRNA, complete cds

Seq. No.	161369
Seq. ID	LIB3177-018-P1-K1-A1
Method	BLASTX
NCBI GI	g166834
BLAST score	219
E value	2.0e-18
Match length	66
% identity	68
NCBI Description	(M86720) ribulose bisphosphate carboxylase/oxygenase activase [Arabidopsis thaliana] >gi_2642155 (AC003000) Rubisco activase [Arabidopsis thaliana]

Seq. No.	161370
Seq. ID	LIB3177-018-P1-K1-A11
Method	BLASTX
NCBI GI	g102278
BLAST score	325
E value	3.0e-30
Match length	112
% identity	9
NCBI Description	ubiquitin 14 - slime mold (Dictyostelium discoideum)

Seq. No.	161371
Seq. ID	LIB3177-018-P1-K1-A4
Method	BLASTX
NCBI GI	g2529665
BLAST score	428
E value	3.0e-42
Match length	115
% identity	71
NCBI Description	(AC002535) putative ribosomal protein L7A [Arabidopsis thaliana]

Seq. No.	161372
Seq. ID	LIB3177-018-P1-K1-A8
Method	BLASTX
NCBI GI	g543841
BLAST score	197
E value	2.0e-15
Match length	69
% identity	62

NCBI Description	ADP-RIBOSYLATION FACTOR 1 >gi_322518_pir__S28875 ADP-ribosylation factor 1 - Arabidopsis thaliana >gi_166586 (M95166) ADP-ribosylation factor [Arabidopsis thaliana] >gi_2275195 (AC002337) ADP-ribosylation factor [Arabidopsis thaliana] >gi_4630747_gb_AAD26597.1_AC007236_2 (AC007236) ADP-ribosylation factor [Arabidopsis thaliana]

Seq. No.	161373
Seq. ID	LIB3177-018-P1-K1-A9
Method	BLASTX
NCBI GI	g3953473
BLAST score	279
E value	5.0e-25
Match length	96
% identity	61
NCBI Description	(AC002328) F22O2.18 [Arabidopsis thaliana]

Seq. No.	161374
Seq. ID	LIB3177-018-P1-K1-B2
Method	BLASTX
NCBI GI	g132074
BLAST score	264
E value	3.0e-23
Match length	96
% identity	61
NCBI Description	RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN 1A PRECURSOR (RUBISCO SMALL SUBUNIT 1A) >gi_68063_pir__RKMUA1 ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain A1 precursor - Arabidopsis thaliana

Seq. No.	161375
Seq. ID	LIB3177-018-P1-K1-B3
Method	BLASTX
NCBI GI	g132074
BLAST score	203
E value	5.0e-16
Match length	83
% identity	49
NCBI Description	RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN 1A PRECURSOR (RUBISCO SMALL SUBUNIT 1A) >gi_68063_pir__RKMUA1 ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain A1 precursor - Arabidopsis thaliana

Seq. No.	161376
Seq. ID	LIB3177-018-P1-K1-C2
Method	BLASTX
NCBI GI	g4538963
BLAST score	320
E value	1.0e-29
Match length	112
% identity	59
NCBI Description	(AL049488) chlorophyll a/b-binding protein-like [Arabidopsis thaliana] >gi_4741958_gb_AAD28776.1_AF134129_1 (AF134129) Lhcb5 protein [Arabidopsis thaliana]

Seq. No.	161377
Seq. ID	LIB3177-018-P1-K1-C8

Method	BLASTN
NCBI GI	g402614
BLAST score	36
E value	6.0e-11
Match length	88
% identity	85
NCBI Description	B.rapa chloroplast mRNA for ribosomal protein L32

Seq. No.	161378
Seq. ID	LIB3177-018-P1-K1-D10
Method	BLASTX
NCBI GI	g1363489
BLAST score	255
E value	6.0e-22
Match length	120
% identity	39
NCBI Description	thioglucosidase (EC 3.2.3.1) 3D precursor - Arabidopsis thaliana >gi_984052_emb_CAA61592_ (X89413) thioglucoside glucohydrolase [Arabidopsis thaliana]

Seq. No.	161379
Seq. ID	LIB3177-018-P1-K1-D11
Method	BLASTX
NCBI GI	g2246621
BLAST score	184
E value	6.0e-14
Match length	69
% identity	61
NCBI Description	(AF004393) salt-stress induced tonoplast intrinsic protein [Arabidopsis thaliana]

Seq. No.	161380
Seq. ID	LIB3177-018-P1-K1-E10
Method	BLASTN
NCBI GI	g4056476
BLAST score	82
E value	2.0e-38
Match length	174
% identity	87
NCBI Description	Arabidopsis thaliana chromosome II BAC F3G5 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	161381
Seq. ID	LIB3177-018-P1-K1-E11
Method	BLASTN
NCBI GI	g3399678
BLAST score	33
E value	3.0e-09
Match length	92
% identity	86
NCBI Description	Arabidopsis thaliana chromosome 1 BAC F13M7 sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	161382
Seq. ID	LIB3177-018-P1-K1-E3
Method	BLASTX
NCBI GI	g1171429

BLAST score	197
E value	1.0e-15
Match length	69
% identity	62
NCBI Description	(U44028) CKC [Arabidopsis thaliana]

Seq. No.	161383
Seq. ID	LIB3177-018-P1-K1-E6
Method	BLASTN
NCBI GI	g2191126
BLAST score	71
E value	1.0e-31
Match length	238
% identity	82
NCBI Description	Arabidopsis thaliana BAC IG002N01

Seq. No.	161384
Seq. ID	LIB3177-018-P1-K1-F1
Method	BLASTX
NCBI GI	g2911085
BLAST score	328
E value	1.0e-30
Match length	95
% identity	72
NCBI Description	(AL021960) photosystem II oxygen-evolving complex protein 3-like [Arabidopsis thaliana] >gi_3402748_emb_CAA20194.1_ (AL031187) photosystem II oxygen-evolving complex protein 3 - like [Arabidopsis thaliana]

Seq. No.	161385
Seq. ID	LIB3177-018-P1-K1-F10
Method	BLASTX
NCBI GI	g2507587
BLAST score	163
E value	4.0e-11
Match length	58
% identity	59
NCBI Description	METALLOTHIONEIN-LIKE PROTEIN 2A (MT-2A) (MT-K) (MT-1G) >gi_1361998_pir__S57861 metallothionein 2a - Arabidopsis thaliana >gi_555976 (U15108) metallothionein-like protein [Arabidopsis thaliana] >gi_1580892_prf__2116236A metallothionein 1 [Arabidopsis thaliana]

Seq. No.	161386
Seq. ID	LIB3177-018-P1-K1-F12
Method	BLASTX
NCBI GI	g3914740
BLAST score	155
E value	2.0e-10
Match length	79
% identity	46
NCBI Description	60S RIBOSOMAL PROTEIN L26 >gi_2160300_dbj_BAA18941_ (D78495) ribosomal protein [Brassica rapa]

Seq. No.	161387
Seq. ID	LIB3177-018-P1-K1-F5
Method	BLASTX

NCBI GI	g2500378
BLAST score	175
E value	9.0e-13
Match length	86
% identity	49
NCBI Description	60S RIBOSOMAL PROTEIN L37

Seq. No.	161388
Seq. ID	LIB3177-018-P1-K1-F8
Method	BLASTX
NCBI GI	g1732570
BLAST score	257
E value	3.0e-22
Match length	99
% identity	57
NCBI Description	(U72153) beta-glucosidase [Arabidopsis thaliana]

Seq. No.	161389
Seq. ID	LIB3177-018-P1-K1-F9
Method	BLASTX
NCBI GI	g3249100
BLAST score	141
E value	7.0e-09
Match length	70
% identity	56
NCBI Description	(AC003114) Match to calreticulin (AtCRTL) mRNA gb_U27698 and DNA gb_U66344. ESTs gb_T45719, gb_T22451, gb_H36323 and gb_AA042519 come from this gene. [Arabidopsis thaliana]

Seq. No.	161390
Seq. ID	LIB3177-018-P1-K1-G10
Method	BLASTX
NCBI GI	g4099408
BLAST score	186
E value	3.0e-14
Match length	85
% identity	46
NCBI Description	(U86763) delta-type tonoplast intrinsic protein [Triticum aestivum]

Seq. No.	161391
Seq. ID	LIB3177-018-P1-K1-H1
Method	BLASTN
NCBI GI	g4199934
BLAST score	83
E value	9.0e-39
Match length	362
% identity	82
NCBI Description	Genomic sequence for Arabidopsis thaliana BAC T3P18, complete sequence [Arabidopsis thaliana]

Seq. No.	161392
Seq. ID	LIB3177-018-P1-K1-H10
Method	BLASTN
NCBI GI	g4757407
BLAST score	57
E value	3.0e-23

Match length	285
% identity	86
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MQD19, complete sequence

Seq. No.	161393
Seq. ID	LIB3177-018-P1-K1-H12
Method	BLASTX
NCBI GI	g1170939
BLAST score	303
E value	1.0e-27
Match length	113
% identity	61
NCBI Description	S-ADENOSYLMETHIONINE SYNTHETASE 3 (METHIONINE ADENOSYLTRANSFERASE 3) (ADOMET SYNTHETASE 3) >gi_1084408_pir__S46540 methionine adenosyltransferase (EC 2.5.1.6) - tomato >gi_429108_emb_CAA80867_ (Z24743) S-adenosyl-L-methionine synthetase [Lycopersicon esculentum]

Seq. No.	161394
Seq. ID	LIB3177-018-P1-K1-H3
Method	BLASTN
NCBI GI	g16192
BLAST score	45
E value	2.0e-16
Match length	125
% identity	84
NCBI Description	A.thaliana ats1B, ats2B and ats3B gene for ribulose-1,5-biphosphate carboxylase small subunit (rbcS) (EC 4.1.1.39)

Seq. No.	161395
Seq. ID	LIB3177-018-P1-K1-H4
Method	BLASTX
NCBI GI	g2809481
BLAST score	385
E value	3.0e-37
Match length	122
% identity	46
NCBI Description	(AF042839) calmodulin [Oryza sativa]

Seq. No.	161396
Seq. ID	LIB3177-018-P1-K1-H6
Method	BLASTN
NCBI GI	g4096078
BLAST score	71
E value	7.0e-32
Match length	208
% identity	83
NCBI Description	Arabidopsis thaliana chromosome I BAC T5A14 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	161397
Seq. ID	LIB3177-018-P1-K2-A1
Method	BLASTX
NCBI GI	g166834

BLAST score	780
E value	2.0e-83
Match length	149
% identity	100
NCBI Description	(M86720) ribulose bisphosphate carboxylase/oxygenase activase [Arabidopsis thaliana] >gi_2642155 (AC003000) Rubisco activase [Arabidopsis thaliana]

Seq. No.	161398
Seq. ID	LIB3177-018-P1-K2-A2
Method	BLASTX
NCBI GI	g1170203
BLAST score	635
E value	2.0e-66
Match length	129
% identity	98
NCBI Description	GLUTAMYL-TRNA REDUCTASE 1 PRECURSOR (GLUTR) >gi_454359 (U03774) glutamyl-tRNA reductase [Arabidopsis thaliana]

Seq. No.	161399
Seq. ID	LIB3177-018-P1-K2-A3
Method	BLASTX
NCBI GI	g4406759
BLAST score	280
E value	7.0e-25
Match length	147
% identity	44
NCBI Description	(AC006836) hypothetical protein [Arabidopsis thaliana]

Seq. No.	161400
Seq. ID	LIB3177-018-P1-K2-A4
Method	BLASTX
NCBI GI	g3603456
BLAST score	422
E value	1.0e-41
Match length	90
% identity	28
NCBI Description	(AF088848) polyubiquitin [Capsicum chinense]

Seq. No.	161401
Seq. ID	LIB3177-018-P1-K2-A8
Method	BLASTX
NCBI GI	g543841
BLAST score	373
E value	8.0e-36
Match length	74
% identity	100
NCBI Description	ADP-RIBOSYLATION FACTOR 1 >gi_322518_pir__S28875 ADP-ribosylation factor 1 - Arabidopsis thaliana >gi_166586 (M95166) ADP-ribosylation factor [Arabidopsis thaliana] >gi_2275195 (AC002337) ADP-ribosylation factor [Arabidopsis thaliana] >gi_4630747_gb_AAD26597.1_AC007236_2 (AC007236) ADP-ribosylation factor [Arabidopsis thaliana]

Seq. No.	161402
Seq. ID	LIB3177-018-P1-K2-A9
Method	BLASTX

NCBI GI	g3953473
BLAST score	721
E value	1.0e-76
Match length	146
% identity	98
NCBI Description	(AC002328) F22O2.18 [Arabidopsis thaliana]

Seq. No.	161403
Seq. ID	LIB3177-018-P1-K2-B1
Method	BLASTX
NCBI GI	g4490737
BLAST score	194
E value	8.0e-15
Match length	53
% identity	68
NCBI Description	(AL035708) putative protein [Arabidopsis thaliana]

Seq. No.	161404
Seq. ID	LIB3177-018-P1-K2-B2
Method	BLASTX
NCBI GI	g132074
BLAST score	712
E value	2.0e-75
Match length	134
% identity	98
NCBI Description	RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN 1A PRECURSOR (RUBISCO SMALL SUBUNIT 1A) >gi_68063_pir__RKMUA1 ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain A1 precursor - Arabidopsis thaliana

Seq. No.	161405
Seq. ID	LIB3177-018-P1-K2-B3
Method	BLASTX
NCBI GI	g2341034
BLAST score	227
E value	3.0e-19
Match length	59
% identity	81
NCBI Description	(AC000104) F19P19.13 [Arabidopsis thaliana]

Seq. No.	161406
Seq. ID	LIB3177-018-P1-K2-B8
Method	BLASTN
NCBI GI	g4589430
BLAST score	121
E value	1.0e-61
Match length	248
% identity	94
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MLD14, complete sequence

Seq. No.	161407
Seq. ID	LIB3177-018-P1-K2-C1
Method	BLASTX
NCBI GI	g1173187
BLAST score	566
E value	2.0e-58

Match length	117
% identity	93
NCBI Description	40S RIBOSOMAL PROTEIN S23 (S12) >gi_1362041_pir__S56673 ribosomal protein S23.e, cytosolic (clone RJ3) - garden strawberry >gi_643074 (U19940) putative 40S ribosomal protein s12 [Fragaria x ananassa]

Seq. No.	161408
Seq. ID	LIB3177-018-P1-K2-C2
Method	BLASTX
NCBI GI	g4538963
BLAST score	539
E value	3.0e-55
Match length	135
% identity	62
NCBI Description	(AL049488) chlorophyll a/b-binding protein-like [Arabidopsis thaliana] >gi_4741958_gb_AAD28776.1_AF134129_1 (AF134129) Lhcb5 protein [Arabidopsis thaliana]

Seq. No.	161409
Seq. ID	LIB3177-018-P1-K2-C3
Method	BLASTX
NCBI GI	g3759184
BLAST score	230
E value	5.0e-19
Match length	103
% identity	48
NCBI Description	(AB018441) phi-1 [Nicotiana tabacum]

Seq. No.	161410
Seq. ID	LIB3177-018-P1-K2-C8
Method	BLASTN
NCBI GI	g402614
BLAST score	79
E value	1.0e-36
Match length	186
% identity	83
NCBI Description	B.rapa chloroplast mRNA for ribosomal protein L32

Seq. No.	161411
Seq. ID	LIB3177-018-P1-K2-D12
Method	BLASTX
NCBI GI	g4056480
BLAST score	517
E value	1.0e-52
Match length	132
% identity	80
NCBI Description	(AC005896) putative adenylate kinase [Arabidopsis thaliana]

Seq. No.	161412
Seq. ID	LIB3177-018-P1-K2-D3
Method	BLASTX
NCBI GI	g1695717
BLAST score	618
E value	2.0e-64
Match length	122
% identity	100

NCBI Description	(D89341) luminal binding protein [Arabidopsis thaliana]

Seq. No.	161413
Seq. ID	LIB3177-018-P1-K2-D4
Method	BLASTX
NCBI GI	g1363489
BLAST score	103
E value	4.0e-54
Match length	138
% identity	86
NCBI Description	thioglucosidase (EC 3.2.3.1) 3D precursor - Arabidopsis thaliana >gi_984052_emb_CAA61592_ (X89413) thioglucoside glucohydrolase [Arabidopsis thaliana]

Seq. No.	161414
Seq. ID	LIB3177-018-P1-K2-D5
Method	BLASTX
NCBI GI	g2246621
BLAST score	274
E value	1.0e-24
Match length	69
% identity	84
NCBI Description	(AF004393) salt-stress induced tonoplast intrinsic protein [Arabidopsis thaliana]

Seq. No.	161415
Seq. ID	LIB3177-018-P1-K2-D6
Method	BLASTN
NCBI GI	g2351068
BLAST score	314
E value	1.0e-176
Match length	362
% identity	97
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MRH10, complete sequence [Arabidopsis thaliana]

Seq. No.	161416
Seq. ID	LIB3177-018-P1-K2-E1
Method	BLASTX
NCBI GI	g1172873
BLAST score	755
E value	1.0e-80
Match length	148
% identity	100
NCBI Description	CYSTEINE PROTEINASE RD21A PRECURSOR >gi_541857_pir__JN0719 drought-inducible cysteine proteinase (EC 3.4.22.-) RD21A precursor - Arabidopsis thaliana >gi_435619_dbj_BAA02374_ (D13043) thiol protease [Arabidopsis thaliana]

Seq. No.	161417
Seq. ID	LIB3177-018-P1-K2-E10
Method	BLASTN
NCBI GI	g3399678
BLAST score	231
E value	1.0e-127
Match length	279
% identity	96

NCBI Description	Arabidopsis thaliana chromosome 1 BAC F13M7 sequence, complete sequence [Arabidopsis thaliana]
Seq. No.	161418
Seq. ID	LIB3177-018-P1-K2-E11
Method	BLASTN
NCBI GI	g2191126
BLAST score	261
E value	1.0e-145
Match length	393
% identity	91
NCBI Description	Arabidopsis thaliana BAC IG002N01
Seq. No.	161419
Seq. ID	LIB3177-018-P1-K2-E12
Method	BLASTX
NCBI GI	g3785996
BLAST score	378
E value	1.0e-36
Match length	77
% identity	57
NCBI Description	(AC005499) putative annexin [Arabidopsis thaliana]
Seq. No.	161420
Seq. ID	LIB3177-018-P1-K2-E3
Method	BLASTX
NCBI GI	g1171429
BLAST score	743
E value	4.0e-79
Match length	141
% identity	58
NCBI Description	(U44028) CKC [Arabidopsis thaliana]
Seq. No.	161421
Seq. ID	LIB3177-018-P1-K2-E4
Method	BLASTX
NCBI GI	g2765081
BLAST score	152
E value	4.0e-10
Match length	38
% identity	79
NCBI Description	(Y10557) g5bf [Arabidopsis thaliana]
Seq. No.	161422
Seq. ID	LIB3177-018-P1-K2-E7
Method	BLASTN
NCBI GI	g16375
BLAST score	114
E value	2.0e-57
Match length	150
% identity	94
NCBI Description	A.thaliana gene (LHCP AB 140) for chlorophyll a/b binding protein
Seq. No.	161423
Seq. ID	LIB3177-018-P1-K2-E8
Method	BLASTN

NCBI GI	g2924505
BLAST score	53
E value	1.0e-21
Match length	57
% identity	98
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone M4E13 (ESSAII project)

Seq. No.	161424
Seq. ID	LIB3177-018-P1-K2-F1
Method	BLASTX
NCBI GI	g2911085
BLAST score	554
E value	5.0e-57
Match length	150
% identity	73
NCBI Description	(AL021960) photosystem II oxygen-evolving complex protein 3-like [Arabidopsis thaliana] >gi_3402748_emb_CAA20194.1_ (AL031187) photosystem II oxygen-evolving complex protein 3 - like [Arabidopsis thaliana]

Seq. No.	161425
Seq. ID	LIB3177-018-P1-K2-F10
Method	BLASTX
NCBI GI	g2500378
BLAST score	169
E value	9.0e-14
Match length	87
% identity	56
NCBI Description	60S RIBOSOMAL PROTEIN L37

Seq. No.	161426
Seq. ID	LIB3177-018-P1-K2-F12
Method	BLASTX
NCBI GI	g3914740
BLAST score	579
E value	7.0e-60
Match length	144
% identity	81
NCBI Description	60S RIBOSOMAL PROTEIN L26 >gi_2160300_dbj_BAA18941_ (D78495) ribosomal protein [Brassica rapa]

Seq. No.	161427
Seq. ID	LIB3177-018-P1-K2-F3
Method	BLASTX
NCBI GI	g2274857
BLAST score	317
E value	1.0e-29
Match length	75
% identity	85
NCBI Description	(AJ000469) glutathione peroxidase [Arabidopsis thaliana] >gi_3482968_emb_CAA20524.1_ (AL031369) glutathione peroxidase precursor [Arabidopsis thaliana]

Seq. No.	161428
Seq. ID	LIB3177-018-P1-K2-F4
Method	BLASTX

NCBI GI	g2507587
BLAST score	294
E value	2.0e-26
Match length	59
% identity	86
NCBI Description	METALLOTHIONEIN-LIKE PROTEIN 2A (MT-2A) (MT-K) (MT-1G) >gi_1361998_pir__S57861 metallothionein 2a - Arabidopsis thaliana >gi_555976 (U15108) metallothionein-like protein [Arabidopsis thaliana] >gi_1580892_prf__2116236A metallothionein 1 [Arabidopsis thaliana]

Seq. No.	161429
Seq. ID	LIB3177-018-P1-K2-F7
Method	BLASTX
NCBI GI	g2529665
BLAST score	303
E value	8.0e-28
Match length	91
% identity	69
NCBI Description	(AC002535) putative ribosomal protein L7A [Arabidopsis thaliana]

Seq. No.	161430
Seq. ID	LIB3177-018-P1-K2-F8
Method	BLASTX
NCBI GI	g1732570
BLAST score	622
E value	4.0e-65
Match length	125
% identity	94
NCBI Description	(U72153) beta-glucosidase [Arabidopsis thaliana]

Seq. No.	161431
Seq. ID	LIB3177-018-P1-K2-F9
Method	BLASTN
NCBI GI	g4757409
BLAST score	387
E value	0.0e+00
Match length	435
% identity	97
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MVC8, complete sequence

Seq. No.	161432
Seq. ID	LIB3177-018-P1-K2-G1
Method	BLASTN
NCBI GI	g4757409
BLAST score	345
E value	0.0e+00
Match length	349
% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MVC8, complete sequence

Seq. No.	161433
Seq. ID	LIB3177-018-P1-K2-G10
Method	BLASTX

NCBI GI	g4099408
BLAST score	282
E value	4.0e-25
Match length	91
% identity	62
NCBI Description	(U86763) delta-type tonoplast intrinsic protein [Triticum aestivum]

Seq. No.	161434
Seq. ID	LIB3177-018-P1-K2-G12
Method	BLASTX
NCBI GI	g1168748
BLAST score	669
E value	2.0e-70
Match length	134
% identity	62
NCBI Description	CALMODULIN-4 >gi_479693_pir__S35185 calmodulin 4 - Arabidopsis thaliana >gi_16223_emb_CAA78057_ (Z12022) calmodulin [Arabidopsis thaliana]

Seq. No.	161435
Seq. ID	LIB3177-018-P1-K2-G2
Method	BLASTX
NCBI GI	g2119848
BLAST score	660
E value	2.0e-69
Match length	124
% identity	99
NCBI Description	chlorophyll a/b-binding protein type I precursor Lhb1B1 - Arabidopsis thaliana >gi_16366_emb_CAA45789_ (X64459) photosystem II type I chlorophyll a /b binding protein [Arabidopsis thaliana] >gi_3128229 (AC004077) putative photosystem II type I chlorophyll a/b binding protein [Arabidopsis thaliana] >gi_3337372 (AC004481) putative photosystem II type I chlorophyll a/b binding protein [Arabidopsis thaliana]

Seq. No.	161436
Seq. ID	LIB3177-018-P1-K2-G3
Method	BLASTX
NCBI GI	g1669387
BLAST score	520
E value	5.0e-53
Match length	95
% identity	100
NCBI Description	(U41998) actin 2 [Arabidopsis thaliana]

Seq. No.	161437
Seq. ID	LIB3177-018-P1-K2-G4
Method	BLASTN
NCBI GI	g4589412
BLAST score	37
E value	2.0e-11
Match length	105
% identity	84
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: F6N7, complete sequence

Seq. No.	161438
Seq. ID	LIB3177-018-P1-K2-G7
Method	BLASTN
NCBI GI	g3702731
BLAST score	369
E value	0.0e+00
Match length	425
% identity	97
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MFC19, complete sequence [Arabidopsis thaliana]

Seq. No.	161439
Seq. ID	LIB3177-018-P1-K2-G8
Method	BLASTN
NCBI GI	g2583106
BLAST score	214
E value	1.0e-117
Match length	378
% identity	90
NCBI Description	Arabidopsis thaliana chromosome II BAC F4L23 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	161440
Seq. ID	LIB3177-018-P1-K2-H10
Method	BLASTN
NCBI GI	g4325340
BLAST score	79
E value	2.0e-36
Match length	143
% identity	89
NCBI Description	Arabidopsis thaliana BAC T1J1

Seq. No.	161441
Seq. ID	LIB3177-018-P1-K2-H11
Method	BLASTX
NCBI GI	g4204270
BLAST score	460
E value	5.0e-46
Match length	103
% identity	88
NCBI Description	(AC005223) branched-chain alpha-keto acid decarboxylase E1 beta subunit [Arabidopsis thaliana]

Seq. No.	161442
Seq. ID	LIB3177-018-P1-K2-H12
Method	BLASTX
NCBI GI	g2129889
BLAST score	44
E value	1.0e-50
Match length	125
% identity	82
NCBI Description	methionine adenosyltransferase (EC 2.5.1.6) 2 - garden pea

Seq. No.	161443
Seq. ID	LIB3177-018-P1-K2-H2
Method	BLASTX

NCBI GI	g132102
BLAST score	186
E value	4.0e-14
Match length	35
% identity	100
NCBI Description	RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN 2B PRECURSOR (RUBISCO SMALL SUBUNIT 2B) >gi_68061_pir__RKMUB2 ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain B2 precursor - Arabidopsis thaliana >gi_16194_emb_CAA32701_ (X14564) ribulose bisphosphate carboxylase [Arabidopsis thaliana]

Seq. No.	161444
Seq. ID	LIB3177-018-P1-K2-H3
Method	BLASTX
NCBI GI	g2529665
BLAST score	653
E value	1.0e-68
Match length	135
% identity	96
NCBI Description	(AC002535) putative ribosomal protein L7A [Arabidopsis thaliana]

Seq. No.	161445
Seq. ID	LIB3177-018-P1-K2-H4
Method	BLASTN
NCBI GI	g4757407
BLAST score	238
E value	1.0e-131
Match length	458
% identity	99
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MQD19, complete sequence

Seq. No.	161446
Seq. ID	LIB3177-018-P1-K2-H5
Method	BLASTN
NCBI GI	g4757407
BLAST score	149
E value	4.0e-78
Match length	305
% identity	94
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MQD19, complete sequence

Seq. No.	161447
Seq. ID	LIB3177-018-P1-K2-H9
Method	BLASTX
NCBI GI	g4160280
BLAST score	234
E value	8.0e-23
Match length	99
% identity	59
NCBI Description	(AJ006224) purple acid phosphatase [Ipomoea batatas]

Seq. No.	161448
Seq. ID	LIB3177-019-P1-K1-A1

Method	BLASTX
NCBI GI	g1769905
BLAST score	450
E value	7.0e-45
Match length	137
% identity	69
NCBI Description	(X98108) 23 kDa polypeptide of oxygen-evolving comlex (OEC) [Arabidopsis thaliana]

Seq. No.	161449
Seq. ID	LIB3177-019-P1-K1-A12
Method	BLASTN
NCBI GI	g166695
BLAST score	42
E value	2.0e-14
Match length	170
% identity	81
NCBI Description	Arabidopsis thaliana recombination and DNA-damage resistance protein (DRT112) mRNA, complete cds

Seq. No.	161450
Seq. ID	LIB3177-019-P1-K1-A2
Method	BLASTX
NCBI GI	g4049401
BLAST score	479
E value	3.0e-48
Match length	130
% identity	73
NCBI Description	(AJ131580) glutathione transferase AtGST 10 [Arabidopsis thaliana]

Seq. No.	161451
Seq. ID	LIB3177-019-P1-K1-A3
Method	BLASTX
NCBI GI	g2583134
BLAST score	194
E value	7.0e-15
Match length	78
% identity	60
NCBI Description	(AC002387) putative proline-rich protein [Arabidopsis thaliana]

Seq. No.	161452
Seq. ID	LIB3177-019-P1-K1-A4
Method	BLASTN
NCBI GI	g4646229
BLAST score	61
E value	1.0e-25
Match length	225
% identity	82
NCBI Description	Arabidopsis thaliana chromosome II BAC F27A10 genomic sequence, complete sequence

Seq. No.	161453
Seq. ID	LIB3177-019-P1-K1-A5
Method	BLASTN
NCBI GI	g11957

BLAST score	97
E value	2.0e-47
Match length	153
% identity	45
NCBI Description	Rice complete chloroplast genome

Seq. No.	161454
Seq. ID	LIB3177-019-P1-K1-A7
Method	BLASTX
NCBI GI	g4454036
BLAST score	415
E value	1.0e-40
Match length	132
% identity	61
NCBI Description	(AL035394) putative major latex protein [Arabidopsis thaliana]

Seq. No.	161455
Seq. ID	LIB3177-019-P1-K1-A8
Method	BLASTX
NCBI GI	g132090
BLAST score	454
E value	3.0e-45
Match length	136
% identity	70
NCBI Description	RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN 1B PRECURSOR (RUBISCO SMALL SUBUNIT 1B) >gi_68062_pir__RKMUB1 ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain B1 precursor - Arabidopsis thaliana >gi_16193_emb_CAA32700_ (X14564) ribulose bisphosphate carboxylase [Arabidopsis thaliana]

Seq. No.	161456
Seq. ID	LIB3177-019-P1-K1-B1
Method	BLASTX
NCBI GI	g1853966
BLAST score	328
E value	1.0e-30
Match length	107
% identity	63
NCBI Description	(D83511) ATMYC1 [Arabidopsis thaliana]

Seq. No.	161457
Seq. ID	LIB3177-019-P1-K1-B2
Method	BLASTX
NCBI GI	g2245079
BLAST score	192
E value	1.0e-14
Match length	101
% identity	43
NCBI Description	(Z97343) hypothetical protein [Arabidopsis thaliana]

Seq. No.	161458
Seq. ID	LIB3177-019-P1-K1-B4
Method	BLASTX
NCBI GI	g2191129
BLAST score	228

E value	9.0e-22
Match length	105
% identity	61
NCBI Description	(AF007269) similar to SPF1 DNA-binding protein [Arabidopsis thaliana]

Seq. No.	161459
Seq. ID	LIB3177-019-P1-K1-B7
Method	BLASTX
NCBI GI	g1709794
BLAST score	362
E value	2.0e-34
Match length	119
% identity	62
NCBI Description	26S PROTEASOME REGULATORY SUBUNIT S5A (MULTIUBIQUITIN CHAIN BINDING PROTEIN) >gi_1165206 (U33269) MBP1 [Arabidopsis thaliana] >gi_4467150_emb_CAB37519_ (AL035540) multiubiquitin chain binding protein (MBP1) [Arabidopsis thaliana]

Seq. No.	161460
Seq. ID	LIB3177-019-P1-K1-B8
Method	BLASTX
NCBI GI	g2501356
BLAST score	268
E value	1.0e-23
Match length	84
% identity	64
NCBI Description	TRANSKETOLASE, CHLOROPLAST PRECURSOR (TK) >gi_1658322_emb_CAA90427_ (Z50099) transketolase precursor [Solanum tuberosum]

Seq. No.	161461
Seq. ID	LIB3177-019-P1-K1-C1
Method	BLASTX
NCBI GI	g2677828
BLAST score	384
E value	4.0e-37
Match length	146
% identity	52
NCBI Description	(U93166) cysteine protease [Prunus armeniaca]

Seq. No.	161462
Seq. ID	LIB3177-019-P1-K1-C11
Method	BLASTX
NCBI GI	g1351272
BLAST score	404
E value	2.0e-39
Match length	130
% identity	65
NCBI Description	TRIOSEPHOSPHATE ISOMERASE, CYTOSOLIC (TIM) >gi_414550 (U02949) cytosolic triose phosphate isomerase [Arabidopsis thaliana] >gi_742408_prf__2009415A triose phosphate isomerase [Arabidopsis thaliana]

Seq. No.	161463
Seq. ID	LIB3177-019-P1-K1-C12

Method	BLASTX
NCBI GI	g4741944
BLAST score	301
E value	5.0e-38
Match length	118
% identity	69
NCBI Description	(AF134122) Lhcb2 protein [Arabidopsis thaliana]

Seq. No.	161464
Seq. ID	LIB3177-019-P1-K1-C3
Method	BLASTX
NCBI GI	g1363489
BLAST score	448
E value	1.0e-44
Match length	122
% identity	73
NCBI Description	thioglucosidase (EC 3.2.3.1) 3D precursor - Arabidopsis thaliana >gi_984052_emb_CAA61592_ (X89413) thioglucoside glucohydrolase [Arabidopsis thaliana]

Seq. No.	161465
Seq. ID	LIB3177-019-P1-K1-C4
Method	BLASTX
NCBI GI	g1170247
BLAST score	381
E value	8.0e-37
Match length	128
% identity	55
NCBI Description	HEVEIN-LIKE PROTEIN PRECURSOR >gi_407248 (U01880) pre-hevein-like protein [Arabidopsis thaliana]

Seq. No.	161466
Seq. ID	LIB3177-019-P1-K1-C8
Method	BLASTN
NCBI GI	g4220510
BLAST score	55
E value	5.0e-22
Match length	249
% identity	84
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F22K18 (ESSAII project)

Seq. No.	161467
Seq. ID	LIB3177-019-P1-K1-D1
Method	BLASTX
NCBI GI	g4741948
BLAST score	362
E value	2.0e-34
Match length	129
% identity	57
NCBI Description	(AF134124) Lhcb2 protein [Arabidopsis thaliana]

Seq. No.	161468
Seq. ID	LIB3177-019-P1-K1-D10
Method	BLASTX
NCBI GI	g4583542
BLAST score	201

E value	1.0e-15
Match length	114
% identity	43
NCBI Description	(Y16847) 16 kDa polypeptide of oxygen-evolving complex [Arabidopsis thaliana]

Seq. No.	161469
Seq. ID	LIB3177-019-P1-K1-D12
Method	BLASTX
NCBI GI	g3250695
BLAST score	260
E value	1.0e-22
Match length	105
% identity	53
NCBI Description	(AL024486) putative protein [Arabidopsis thaliana]

Seq. No.	161470
Seq. ID	LIB3177-019-P1-K1-D3
Method	BLASTX
NCBI GI	g4538913
BLAST score	261
E value	1.0e-22
Match length	89
% identity	57
NCBI Description	(AL049482) putative protein [Arabidopsis thaliana]

Seq. No.	161471
Seq. ID	LIB3177-019-P1-K1-D5
Method	BLASTX
NCBI GI	g3080442
BLAST score	256
E value	4.0e-22
Match length	112
% identity	52
NCBI Description	(AL022605) putative protein [Arabidopsis thaliana]

Seq. No.	161472
Seq. ID	LIB3177-019-P1-K1-D6
Method	BLASTX
NCBI GI	g1773330
BLAST score	291
E value	3.0e-26
Match length	131
% identity	50
NCBI Description	(U80071) glycolate oxidase [Mesembryanthemum crystallinum]

Seq. No.	161473
Seq. ID	LIB3177-019-P1-K1-D8
Method	BLASTX
NCBI GI	g4741954
BLAST score	235
E value	9.0e-20
Match length	87
% identity	60
NCBI Description	(AF134127) Lhcb4.2 protein [Arabidopsis thaliana]

Seq. No.	161474

Seq. ID	LIB3177-019-P1-K1-E1
Method	BLASTN
NCBI GI	g4199934
BLAST score	126
E value	2.0e-64
Match length	392
% identity	82
NCBI Description	Genomic sequence for Arabidopsis thaliana BAC T3P18, complete sequence [Arabidopsis thaliana]

Seq. No.	161475
Seq. ID	LIB3177-019-P1-K1-E11
Method	BLASTX
NCBI GI	g3834325
BLAST score	446
E value	2.0e-44
Match length	139
% identity	65
NCBI Description	(AC005679) Strong similarity to gb_AF067141 gamma-glutamyl hydrolase from Arabidopsis thaliana. ESTs gb_R83955, gb_T45062, gb_T22220, gb_AA586207, gb_AI099851 and gb_AI00672 come from this gene. [Arabidopsis thaliana]

Seq. No.	161476
Seq. ID	LIB3177-019-P1-K1-E2
Method	BLASTX
NCBI GI	g4584548
BLAST score	339
E value	7.0e-32
Match length	131
% identity	57
NCBI Description	(AL049608) putative protein [Arabidopsis thaliana]

Seq. No.	161477
Seq. ID	LIB3177-019-P1-K1-E3
Method	BLASTN
NCBI GI	g469113
BLAST score	126
E value	2.0e-64
Match length	391
% identity	82
NCBI Description	A.thaliana (Columbia) Dr4 mRNA

Seq. No.	161478
Seq. ID	LIB3177-019-P1-K1-E4
Method	BLASTX
NCBI GI	g4165488
BLAST score	267
E value	2.0e-23
Match length	74
% identity	72
NCBI Description	(AJ132399) alpha-tubulin 3 [Hordeum vulgare]

Seq. No.	161479
Seq. ID	LIB3177-019-P1-K1-E5
Method	BLASTX
NCBI GI	g466044

BLAST score	143
E value	8.0e-09
Match length	90
% identity	36
NCBI Description	HYPOTHETICAL ZINC FINGER PROTEIN ZK686.4 IN CHROMOSOME III >gi_630780_pir__S44909 ZK686.4 protein - Caenorhabditis elegans >gi_304346 (L17337) coded for by C. elegans cDNAs GenBank:M88869 and T01933; putative [Caenorhabditis elegans]

Seq. No.	161480
Seq. ID	LIB3177-019-P1-K1-E6
Method	BLASTX
NCBI GI	g2576361
BLAST score	236
E value	9.0e-20
Match length	91
% identity	51
NCBI Description	(U39782) lysine and histidine specific transporter [Arabidopsis thaliana]

Seq. No.	161481
Seq. ID	LIB3177-019-P1-K1-E9
Method	BLASTX
NCBI GI	g4263525
BLAST score	366
E value	6.0e-35
Match length	130
% identity	59
NCBI Description	(AC004044) putative photosystem I reaction center subunit II precursor [Arabidopsis thaliana]

Seq. No.	161482
Seq. ID	LIB3177-019-P1-K1-F1
Method	BLASTX
NCBI GI	g1709825
BLAST score	190
E value	2.0e-14
Match length	85
% identity	48
NCBI Description	PHOTOSYSTEM I REACTION CENTRE SUBUNIT PSAN PRECURSOR (PSI-N) >gi_1237124 (U32176) PSI-N [Arabidopsis thaliana]

Seq. No.	161483
Seq. ID	LIB3177-019-P1-K1-F2
Method	BLASTX
NCBI GI	g113026
BLAST score	534
E value	1.0e-54
Match length	135
% identity	73
NCBI Description	ISOCITRATE LYASE (ISOCITRASE) (ISOCITRATASE) (ICL) >gi_68211_pir__WZRPI isocitrate lyase (EC 4.1.3.1) - rape >gi_255220_bbs_112862 isocitrate lyase, threo-D S-isocitrate glyoxylate-lyase, IL {EC 4.1.3.1} [Brassica napus, seedlings, Peptide, 576 aa] >gi_167144 (L08482) isocitrate lyase [Brassica napus] >gi_447142_prf__1913424A

isocitrate lyase [Brassica napus]

Seq. No.	161484
Seq. ID	LIB3177-019-P1-K1-F3
Method	BLASTX
NCBI GI	g3273743
BLAST score	320
E value	1.0e-29
Match length	108
% identity	61
NCBI Description	(AF057357) lipid transfer protein 2 precursor [Arabidopsis thaliana] >gi_3786019 (AC005499) unknown protein [Arabidopsis thaliana]

Seq. No.	161485
Seq. ID	LIB3177-019-P1-K1-F5
Method	BLASTX
NCBI GI	g1710780
BLAST score	290
E value	4.0e-26
Match length	114
% identity	52
NCBI Description	40S RIBOSOMAL PROTEIN S9 (S7) >gi_1321917_emb_CAA65433_ (X96613) cytoplasmic ribosomal protein S7 [Podospora anserina]

Seq. No.	161486
Seq. ID	LIB3177-019-P1-K1-F7
Method	BLASTX
NCBI GI	g115767
BLAST score	334
E value	3.0e-31
Match length	108
% identity	64
NCBI Description	CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR (CAB-165/180) (LHCP) >gi_81603_pir__A29280 chlorophyll a/b-binding protein ab165 - Arabidopsis thaliana >gi_16368_emb_CAA27540_ (X03907) chlorophyll a/b binding protein (LHCP AB 65) [Arabidopsis thaliana] >gi_16372_emb_CAA27541_ (X03908) chlorophyll a/b binding protein (LHCP AB 180) [Arabidopsis thaliana]

Seq. No.	161487
Seq. ID	LIB3177-019-P1-K1-F9
Method	BLASTN
NCBI GI	g2264318
BLAST score	58
E value	5.0e-24
Match length	114
% identity	88
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MUP24, complete sequence [Arabidopsis thaliana]

Seq. No.	161488
Seq. ID	LIB3177-019-P1-K1-G1
Method	BLASTX
NCBI GI	g421826

BLAST score	285
E value	2.0e-25
Match length	85
% identity	67
NCBI Description	chlorophyll a/b-binding protein CP29 - Arabidopsis thaliana >gi_298036_emb_CAA50712_ (X71878) CP29 [Arabidopsis thaliana]

Seq. No.	161489
Seq. ID	LIB3177-019-P1-K1-G11
Method	BLASTX
NCBI GI	g1946331
BLAST score	302
E value	2.0e-27
Match length	124
% identity	53
NCBI Description	(U69155) prohibitin [Arabidopsis thaliana] >gi_4097692 (U66593) prohibitin 3 [Arabidopsis thaliana]

Seq. No.	161490
Seq. ID	LIB3177-019-P1-K1-G2
Method	BLASTN
NCBI GI	g4589445
BLAST score	103
E value	1.0e-50
Match length	349
% identity	86
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MWL2, complete sequence

Seq. No.	161491
Seq. ID	LIB3177-019-P1-K1-G3
Method	BLASTX
NCBI GI	g4510395
BLAST score	460
E value	5.0e-46
Match length	130
% identity	64
NCBI Description	(AC006587) putative beta-galactosidase precursor [Arabidopsis thaliana]

Seq. No.	161492
Seq. ID	LIB3177-019-P1-K1-G4
Method	BLASTX
NCBI GI	g2827662
BLAST score	273
E value	4.0e-24
Match length	107
% identity	50
NCBI Description	(AL021637) Phosphoribosylanthranilate transferase [Arabidopsis thaliana]

Seq. No.	161493
Seq. ID	LIB3177-019-P1-K1-G7
Method	BLASTX
NCBI GI	g400983
BLAST score	146

E value	4.0e-09
Match length	111
% identity	39
NCBI Description	50S RIBOSOMAL PROTEIN L11, CHLOROPLAST PRECURSOR (CL11) >gi_279648_pir__R5SP11 ribosomal protein L11 precursor - spinach >gi_21313_emb_CAA39950_ (X56615) ribosomal protein L11 [Spinacia oleracea]

Seq. No.	161494
Seq. ID	LIB3177-019-P1-K1-G8
Method	BLASTX
NCBI GI	g2499810
BLAST score	283
E value	3.0e-25
Match length	104
% identity	53
NCBI Description	PROFILIN 1 >gi_2981657_pdb_1A0K_ Profilin I From Arabidopsis Thaliana >gi_1353763 (U43322) profilin 1 [Arabidopsis thaliana] >gi_1353770 (U43325) profilin 1 [Arabidopsis thaliana] >gi_1835878_bbs_179026 (S82691) profilin isoform 1 [Arabidopsis thaliana, Columbia, flowers, Peptide, 131 aa] [Arabidopsis thaliana] >gi_3687242 (AC005169) profilin 1 [Arabidopsis thaliana]

Seq. No.	161495
Seq. ID	LIB3177-019-P1-K1-G9
Method	BLASTX
NCBI GI	g4586103
BLAST score	230
E value	5.0e-19
Match length	116
% identity	53
NCBI Description	(AL049638) putative protein [Arabidopsis thaliana]

Seq. No.	161496
Seq. ID	LIB3177-019-P1-K1-H1
Method	BLASTX
NCBI GI	g2344892
BLAST score	153
E value	3.0e-10
Match length	72
% identity	53
NCBI Description	(AC002388) unknown protein [Arabidopsis thaliana]

Seq. No.	161497
Seq. ID	LIB3177-019-P1-K1-H10
Method	BLASTX
NCBI GI	g730645
BLAST score	267
E value	2.0e-23
Match length	83
% identity	65
NCBI Description	40S RIBOSOMAL PROTEIN S15 >gi_629556_pir__S43412 ribosomal protein S15 - Arabidopsis thaliana >gi_313152_emb_CAA80679_ (Z23161) ribosomal protein S15 [Arabidopsis thaliana] >gi_313188_emb_CAA80681_ (Z23162) ribosomal protein S15 [Arabidopsis thaliana] >gi_1903366_gb_AAB70449_ (AC000104)

Strong similarity to Oryza 40S ribosomal protein S15. ESTs gb_R29788,gb_ATTS0365 come from this gene. [Arabidopsis thaliana]

Seq. No.	161498
Seq. ID	LIB3177-019-P1-K1-H2
Method	BLASTN
NCBI GI	g3869067
BLAST score	81
E value	2.0e-37
Match length	386
% identity	87
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MCK7, complete sequence [Arabidopsis thaliana]

Seq. No.	161499
Seq. ID	LIB3177-019-P1-K1-H3
Method	BLASTX
NCBI GI	g3193313
BLAST score	272
E value	6.0e-24
Match length	126
% identity	46
NCBI Description	(AF069299) contains similarity to pectinesterase [Arabidopsis thaliana]

Seq. No.	161500
Seq. ID	LIB3177-019-P1-K1-H4
Method	BLASTN
NCBI GI	g2854069
BLAST score	150
E value	9.0e-79
Match length	366
% identity	85
NCBI Description	Arabidopsis thaliana putative histone deacetylase (HD2) mRNA, complete cds

Seq. No.	161501
Seq. ID	LIB3177-019-P1-K1-H7
Method	BLASTX
NCBI GI	g267070
BLAST score	434
E value	5.0e-43
Match length	127
% identity	69
NCBI Description	TUBULIN ALPHA-6 CHAIN >gi_282852_pir__JQ1597 tubulin alpha-6 chain - Arabidopsis thaliana >gi_166920 (M84699) TUA6 [Arabidopsis thaliana] >gi_2244853_emb_CAB10275_ (Z97337) tubulin alpha-6 chain (TUA6) [Arabidopsis thaliana]

Seq. No.	161502
Seq. ID	LIB3177-019-P1-K1-H9
Method	BLASTX
NCBI GI	g127041
BLAST score	257
E value	3.0e-22

Match length	91
% identity	60
NCBI Description	S-ADENOSYLMETHIONINE SYNTHETASE 1 (METHIONINE ADENOSYLTRANSFERASE 1) (ADOMET SYNTHETASE 1) >gi_81647_pir__JN0131 methionine adenosyltransferase (EC 2.5.1.6) - Arabidopsis thaliana >gi_166872 (M55077) S-adenosylmethionine synthetase [Arabidopsis thaliana]

Seq. No.	161503
Seq. ID	LIB3177-019-P1-K2-A1
Method	BLASTX
NCBI GI	g1769905
BLAST score	669
E value	1.0e-70
Match length	131
% identity	98
NCBI Description	(X98108) 23 kDa polypeptide of oxygen-evolving comlex (OEC) [Arabidopsis thaliana]

Seq. No.	161504
Seq. ID	LIB3177-019-P1-K2-A10
Method	BLASTN
NCBI GI	g4646229
BLAST score	201
E value	1.0e-109
Match length	265
% identity	93
NCBI Description	Arabidopsis thaliana chromosome II BAC F27A10 genomic sequence, complete sequence

Seq. No.	161505
Seq. ID	LIB3177-019-P1-K2-A11
Method	BLASTX
NCBI GI	g1335862
BLAST score	360
E value	2.0e-34
Match length	83
% identity	77
NCBI Description	(U42608) clathrin heavy chain [Glycine max]

Seq. No.	161506
Seq. ID	LIB3177-019-P1-K2-A12
Method	BLASTX
NCBI GI	g3461828
BLAST score	235
E value	9.0e-20
Match length	91
% identity	48
NCBI Description	(AC004138) unknown protein [Arabidopsis thaliana]

Seq. No.	161507
Seq. ID	LIB3177-019-P1-K2-A2
Method	BLASTX
NCBI GI	g4049401
BLAST score	598
E value	2.0e-62
Match length	116

% identity	99
NCBI Description	(AJ131580) glutathione transferase AtGST 10 [Arabidopsis thaliana]

Seq. No.	161508
Seq. ID	LIB3177-019-P1-K2-A4
Method	BLASTX
NCBI GI	g127041
BLAST score	538
E value	3.0e-55
Match length	104
% identity	99
NCBI Description	S-ADENOSYLMETHIONINE SYNTHETASE 1 (METHIONINE ADENOSYLTRANSFERASE 1) (ADOMET SYNTHETASE 1) >gi_81647_pir__JN0131 methionine adenosyltransferase (EC 2.5.1.6) - Arabidopsis thaliana >gi_166872 (M55077) S-adenosylmethionine synthetase [Arabidopsis thaliana]

Seq. No.	161509
Seq. ID	LIB3177-019-P1-K2-A5
Method	BLASTX
NCBI GI	g131398
BLAST score	150
E value	7.0e-10
Match length	60
% identity	55
NCBI Description	PHOTOSYSTEM II 10 KD POLYPEPTIDE PRECURSOR >gi_72714_pir__F2MU10 photosystem II 10K protein precursor - Arabidopsis thaliana >gi_16447_emb_CAA39441_ (X55970) photosystem II 10 kDa polypeptide [Arabidopsis thaliana] >gi_3152571 (AC002986) Match to photosystem II 10kDa polypeptide gb_X55970. ESTs gb_Z17693, gb_N37616, gb_T41858, gb_T88021, gb_R37531, gb_T04679, gb_N37520, gb_N64965, gb_Z17592 and gb_N65338, gb_N37466 and gb_T45400 come from this gene. [Arabidopsis

Seq. No.	161510
Seq. ID	LIB3177-019-P1-K2-A7
Method	BLASTX
NCBI GI	g4454036
BLAST score	492
E value	6.0e-50
Match length	93
% identity	97
NCBI Description	(AL035394) putative major latex protein [Arabidopsis thaliana]

Seq. No.	161511
Seq. ID	LIB3177-019-P1-K2-A8
Method	BLASTX
NCBI GI	g132090
BLAST score	625
E value	2.0e-65
Match length	117
% identity	98
NCBI Description	RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN 1B PRECURSOR (RUBISCO SMALL SUBUNIT 1B) >gi_68062_pir__RKMUB1

	ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain B1 precursor - Arabidopsis thaliana >gi_16193_emb_CAA32700_ (X14564) ribulose bisphosphate carboxylase [Arabidopsis thaliana]
Seq. No.	161512
Seq. ID	LIB3177-019-P1-K2-B10
Method	BLASTX
NCBI GI	g2191129
BLAST score	80
E value	1.0e-27
Match length	106
% identity	64
NCBI Description	(AF007269) similar to SPF1 DNA-binding protein [Arabidopsis thaliana]
Seq. No.	161513
Seq. ID	LIB3177-019-P1-K2-B12
Method	BLASTN
NCBI GI	g4559375
BLAST score	170
E value	9.0e-91
Match length	317
% identity	96
NCBI Description	Arabidopsis thaliana chromosome II BAC F11C10 genomic sequence, complete sequence
Seq. No.	161514
Seq. ID	LIB3177-019-P1-K2-B3
Method	BLASTX
NCBI GI	g2583125
BLAST score	437
E value	2.0e-68
Match length	137
% identity	91
NCBI Description	(AC002387) putative transketolase precursor [Arabidopsis thaliana]
Seq. No.	161515
Seq. ID	LIB3177-019-P1-K2-B4
Method	BLASTN
NCBI GI	g166695
BLAST score	74
E value	1.0e-33
Match length	102
% identity	96
NCBI Description	Arabidopsis thaliana recombination and DNA-damage resistance protein (DRT112) mRNA, complete cds
Seq. No.	161516
Seq. ID	LIB3177-019-P1-K2-B5
Method	BLASTX
NCBI GI	g2660671
BLAST score	592
E value	2.0e-61
Match length	116
% identity	99

NCBI Description	(AC002342) hypothetical protein [Arabidopsis thaliana]
Seq. No.	161517
Seq. ID	LIB3177-019-P1-K2-B7
Method	BLASTX
NCBI GI	g3047112
BLAST score	518
E value	5.0e-53
Match length	102
% identity	98
NCBI Description	(AF058919) No definition line found [Arabidopsis thaliana]
Seq. No.	161518
Seq. ID	LIB3177-019-P1-K2-B8
Method	BLASTX
NCBI GI	g2245079
BLAST score	193
E value	7.0e-15
Match length	66
% identity	61
NCBI Description	(Z97343) hypothetical protein [Arabidopsis thaliana]
Seq. No.	161519
Seq. ID	LIB3177-019-P1-K2-C3
Method	BLASTN
NCBI GI	g4220510
BLAST score	420
E value	0.0e+00
Match length	440
% identity	99
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F22K18 (ESSAII project)
Seq. No.	161520
Seq. ID	LIB3177-019-P1-K2-C4
Method	BLASTX
NCBI GI	g4741952
BLAST score	205
E value	3.0e-16
Match length	91
% identity	55
NCBI Description	(AF134126) Lhcb3 protein [Arabidopsis thaliana]
Seq. No.	161521
Seq. ID	LIB3177-019-P1-K2-C5
Method	BLASTX
NCBI GI	g2369766
BLAST score	385
E value	2.0e-37
Match length	97
% identity	74
NCBI Description	(AJ001304) hypothetical protein [Citrus x paradisi]
Seq. No.	161522
Seq. ID	LIB3177-019-P1-K2-C6
Method	BLASTX
NCBI GI	g1351272

BLAST score	43
E value	4.0e-60
Match length	129
% identity	93
NCBI Description	TRIOSEPHOSPHATE ISOMERASE, CYTOSOLIC (TIM) >gi_414550 (U02949) cytosolic triose phosphate isomerase [Arabidopsis thaliana] >gi_742408_prf__2009415A triose phosphate isomerase [Arabidopsis thaliana]

Seq. No.	161523
Seq. ID	LIB3177-019-P1-K2-C9
Method	BLASTX
NCBI GI	g1363489
BLAST score	745
E value	2.0e-79
Match length	143
% identity	97
NCBI Description	thioglucosidase (EC 3.2.3.1) 3D precursor - Arabidopsis thaliana >gi_984052_emb_CAA61592_ (X89413) thioglucoside glucohydrolase [Arabidopsis thaliana]

Seq. No.	161524
Seq. ID	LIB3177-019-P1-K2-D11
Method	BLASTX
NCBI GI	g3080442
BLAST score	759
E value	5.0e-81
Match length	146
% identity	95
NCBI Description	(AL022605) putative protein [Arabidopsis thaliana]

Seq. No.	161525
Seq. ID	LIB3177-019-P1-K2-D12
Method	BLASTX
NCBI GI	g2501812
BLAST score	598
E value	3.0e-62
Match length	142
% identity	83
NCBI Description	(U91509) glycolate oxidase [Arabidopsis thaliana]

Seq. No.	161526
Seq. ID	LIB3177-019-P1-K2-D4
Method	BLASTX
NCBI GI	g4741944
BLAST score	727
E value	2.0e-77
Match length	135
% identity	99
NCBI Description	(AF134122) Lhcb2 protein [Arabidopsis thaliana]

Seq. No.	161527
Seq. ID	LIB3177-019-P1-K2-D5
Method	BLASTX
NCBI GI	g4583542
BLAST score	458
E value	1.0e-45

Match length	150
% identity	65
NCBI Description	(Y16847) 16 kDa polypeptide of oxygen-evolving complex [Arabidopsis thaliana]

Seq. No.	161528
Seq. ID	LIB3177-019-P1-K2-D7
Method	BLASTX
NCBI GI	g4741944
BLAST score	45
E value	8.0e-56
Match length	108
% identity	99
NCBI Description	(AF134122) Lhcb2 protein [Arabidopsis thaliana]

Seq. No.	161529
Seq. ID	LIB3177-019-P1-K2-E1
Method	BLASTN
NCBI GI	g3851706
BLAST score	57
E value	3.0e-23
Match length	241
% identity	82
NCBI Description	Arabidopsis thaliana actin depolymerizing factor 1 (ADF1) gene, complete cds

Seq. No.	161530
Seq. ID	LIB3177-019-P1-K2-E10
Method	BLASTX
NCBI GI	g267069
BLAST score	492
E value	7.0e-50
Match length	92
% identity	99
NCBI Description	TUBULIN ALPHA-2/ALPHA-4 CHAIN >gi_320183_pir__JQ1594 tubulin alpha chain - Arabidopsis thaliana >gi_166914 (M84696) apha-2 tubulin [Arabidopsis thaliana] >gi_166916 (M84697) alpha-4 tubulin [Arabidopsis thaliana]

Seq. No.	161531
Seq. ID	LIB3177-019-P1-K2-E11
Method	BLASTX
NCBI GI	g466044
BLAST score	215
E value	3.0e-17
Match length	65
% identity	57
NCBI Description	HYPOTHETICAL ZINC FINGER PROTEIN ZK686.4 IN CHROMOSOME III >gi_630780_pir__S44909 ZK686.4 protein - Caenorhabditis elegans >gi_304346 (L17337) coded for by C. elegans cDNAs GenBank:M88869 and T01933; putative [Caenorhabditis elegans]

Seq. No.	161532
Seq. ID	LIB3177-019-P1-K2-E12
Method	BLASTX
NCBI GI	g2576361

BLAST score	380
E value	9.0e-37
Match length	103
% identity	71
NCBI Description	(U39782) lysine and histidine specific transporter [Arabidopsis thaliana]

Seq. No.	161533
Seq. ID	LIB3177-019-P1-K2-E2
Method	BLASTX
NCBI GI	g2129634
BLAST score	200
E value	1.0e-15
Match length	84
% identity	49
NCBI Description	lectin-like protein - Arabidopsis thaliana >gi_995619_emb_CAA62665_ (X91259) lectin like protein [Arabidopsis thaliana]

Seq. No.	161534
Seq. ID	LIB3177-019-P1-K2-E4
Method	BLASTN
NCBI GI	g3250673
BLAST score	276
E value	1.0e-154
Match length	453
% identity	95
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone T16H5 (ESSAII project)

Seq. No.	161535
Seq. ID	LIB3177-019-P1-K2-E6
Method	BLASTX
NCBI GI	g3169656
BLAST score	553
E value	4.0e-57
Match length	107
% identity	97
NCBI Description	(AF067141) gamma-glutamyl hydrolase [Arabidopsis thaliana]

Seq. No.	161536
Seq. ID	LIB3177-019-P1-K2-E7
Method	BLASTX
NCBI GI	g629670
BLAST score	383
E value	6.0e-37
Match length	153
% identity	46
NCBI Description	hypothetical protein - tomato

Seq. No.	161537
Seq. ID	LIB3177-019-P1-K2-E8
Method	BLASTX
NCBI GI	g4584548
BLAST score	678
E value	1.0e-71
Match length	141

% identity	93
NCBI Description	(AL049608) putative protein [Arabidopsis thaliana]

Seq. No.	161538
Seq. ID	LIB3177-019-P1-K2-E9
Method	BLASTX
NCBI GI	g1084338
BLAST score	629
E value	8.0e-66
Match length	122
% identity	98
NCBI Description	drought-induced protein Dr4 - Arabidopsis thaliana >gi_469114_emb_CAA55323_ (X78586) Dr4 [Arabidopsis thaliana]

Seq. No.	161539
Seq. ID	LIB3177-019-P1-K2-F1
Method	BLASTX
NCBI GI	g4263525
BLAST score	309
E value	1.0e-28
Match length	84
% identity	74
NCBI Description	(AC004044) putative photosystem I reaction center subunit II precursor [Arabidopsis thaliana]

Seq. No.	161540
Seq. ID	LIB3177-019-P1-K2-F11
Method	BLASTX
NCBI GI	g1710780
BLAST score	285
E value	8.0e-26
Match length	75
% identity	72
NCBI Description	40S RIBOSOMAL PROTEIN S9 (S7) >gi_1321917_emb_CAA65433_ (X96613) cytoplasmic ribosomal protein S7 [Podospora anserina]

Seq. No.	161541
Seq. ID	LIB3177-019-P1-K2-F12
Method	BLASTX
NCBI GI	g2190554
BLAST score	286
E value	1.0e-25
Match length	120
% identity	44
NCBI Description	(AC001229) Similar to Arabidopsis cytochrome P450 CYP90 (gb_X87367). [Arabidopsis thaliana]

Seq. No.	161542
Seq. ID	LIB3177-019-P1-K2-F2
Method	BLASTX
NCBI GI	g115783
BLAST score	319
E value	8.0e-30
Match length	63
% identity	95

NCBI Description	CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR (CAB-140) (LHCP) >gi_16376_emb_CAA27543_ (X03909) chlorophyll a/b binding protein (LHCP AB 140) [Arabidopsis thaliana]
Seq. No.	161543
Seq. ID	LIB3177-019-P1-K2-F4
Method	BLASTX
NCBI GI	g115832
BLAST score	152
E value	9.0e-18
Match length	92
% identity	60
NCBI Description	CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR (CAB) (LHCP) >gi_81414_pir__JS0171 chlorophyll a/b-binding protein precursor - moss (Physcomitrella patens) >gi_169020 (M23532) major chlorophyll binding protein [Physcomitrella patens]
Seq. No.	161544
Seq. ID	LIB3177-019-P1-K2-F5
Method	BLASTX
NCBI GI	g2129662
BLAST score	349
E value	5.0e-33
Match length	142
% identity	51
NCBI Description	ovule-specific homeotic protein homolog A20 - Arabidopsis thaliana >gi_1881536 (U37589) A20 [Arabidopsis thaliana]
Seq. No.	161545
Seq. ID	LIB3177-019-P1-K2-F8
Method	BLASTX
NCBI GI	g113026
BLAST score	747
E value	1.0e-79
Match length	145
% identity	94
NCBI Description	ISOCITRATE LYASE (ISOCITRASE) (ISOCITRATASE) (ICL) >gi_68211_pir__WZRPI isocitrate lyase (EC 4.1.3.1) - rape >gi_255220_bbs_112862 isocitrate lyase, threo-D S-isocitrate glyoxylate-lyase, IL {EC 4.1.3.1} [Brassica napus, seedlings, Peptide, 576 aa] >gi_167144 (L08482) isocitrate lyase [Brassica napus] >gi_447142_prf__1913424A isocitrate lyase [Brassica napus]
Seq. No.	161546
Seq. ID	LIB3177-019-P1-K2-G1
Method	BLASTN
NCBI GI	g2264318
BLAST score	163
E value	1.0e-86
Match length	203
% identity	95
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MUP24, complete sequence [Arabidopsis thaliana]

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Seq. No.	161547
Seq. ID	LIB3177-019-P1-K2-G10
Method	BLASTX
NCBI GI	g2827662
BLAST score	389
E value	9.0e-38
Match length	109
% identity	64
NCBI Description	(AL021637) Phosphoribosylanthranilate transferase [Arabidopsis thaliana]

Seq. No.	161548
Seq. ID	LIB3177-019-P1-K2-G11
Method	BLASTN
NCBI GI	g3985952
BLAST score	36
E value	9.0e-11
Match length	128
% identity	82
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MRC8, complete sequence [Arabidopsis thaliana]

Seq. No.	161549
Seq. ID	LIB3177-019-P1-K2-G2
Method	BLASTX
NCBI GI	g400983
BLAST score	281
E value	4.0e-25
Match length	105
% identity	63
NCBI Description	50S RIBOSOMAL PROTEIN L11, CHLOROPLAST PRECURSOR (CL11) >gi_279648_pir__R5SP11 ribosomal protein L11 precursor - spinach >gi_21313_emb_CAA39950_ (X56615) ribosomal protein L11 [Spinacia oleracea]

Seq. No.	161550
Seq. ID	LIB3177-019-P1-K2-G3
Method	BLASTX
NCBI GI	g2499810
BLAST score	386
E value	1.0e-37
Match length	86
% identity	81
NCBI Description	PROFILIN 1 >gi_2981657_pdb_1A0K_ Profilin I From Arabidopsis Thaliana >gi_1353763 (U43322) profilin 1 [Arabidopsis thaliana] >gi_1353770 (U43325) profilin 1 [Arabidopsis thaliana] >gi_1835878_bbs_179026 (S82691) profilin isoform 1 [Arabidopsis thaliana, Columbia, flowers, Peptide, 131 aa] [Arabidopsis thaliana] >gi_3687242 (AC005169) profilin 1 [Arabidopsis thaliana]

Seq. No.	161551
Seq. ID	LIB3177-019-P1-K2-G6
Method	BLASTX
NCBI GI	g1946331
BLAST score	493
E value	4.0e-50

Match length	122
% identity	82
NCBI Description	(U69155) prohibitin [Arabidopsis thaliana] >gi_4097692 (U66593) prohibitin 3 [Arabidopsis thaliana]

Seq. No.	161552
Seq. ID	LIB3177-019-P1-K2-G7
Method	BLASTX
NCBI GI	g421826
BLAST score	406
E value	8.0e-40
Match length	117
% identity	67
NCBI Description	chlorophyll a/b-binding protein CP29 - Arabidopsis thaliana >gi_298036_emb_CAA50712_ (X71878) CP29 [Arabidopsis thaliana]

Seq. No.	161553
Seq. ID	LIB3177-019-P1-K2-G8
Method	BLASTX
NCBI GI	g2827561
BLAST score	172
E value	2.0e-12
Match length	94
% identity	35
NCBI Description	(AL021635) predicted protein [Arabidopsis thaliana] >gi_3292809_emb_CAA19799_ (AL031018) putative protein [Arabidopsis thaliana]

Seq. No.	161554
Seq. ID	LIB3177-019-P1-K2-G9
Method	BLASTX
NCBI GI	g4510395
BLAST score	764
E value	1.0e-81
Match length	132
% identity	100
NCBI Description	(AC006587) putative beta-galactosidase precursor [Arabidopsis thaliana]

Seq. No.	161555
Seq. ID	LIB3177-019-P1-K2-H1
Method	BLASTX
NCBI GI	g4586103
BLAST score	491
E value	9.0e-50
Match length	122
% identity	86
NCBI Description	(AL049638) putative protein [Arabidopsis thaliana]

Seq. No.	161556
Seq. ID	LIB3177-019-P1-K2-H10
Method	BLASTN
NCBI GI	g2854069
BLAST score	355
E value	0.0e+00
Match length	371

% identity	99
NCBI Description	Arabidopsis thaliana putative histone deacetylase (HD2) mRNA, complete cds
Seq. No.	161557
Seq. ID	LIB3177-019-P1-K2-H12
Method	BLASTX
NCBI GI	g2924520
BLAST score	80
E value	1.0e-13
Match length	65
% identity	71
NCBI Description	(AL022023) plasma membrane intrinsic protein (SIMIP) [Arabidopsis thaliana]
Seq. No.	161558
Seq. ID	LIB3177-019-P1-K2-H2
Method	BLASTX
NCBI GI	g267069
BLAST score	570
E value	4.0e-59
Match length	108
% identity	98
NCBI Description	TUBULIN ALPHA-2/ALPHA-4 CHAIN >gi_320183_pir__JQ1594 tubulin alpha chain - Arabidopsis thaliana >gi_166914 (M84696) apha-2 tubulin [Arabidopsis thaliana] >gi_166916 (M84697) alpha-4 tubulin [Arabidopsis thaliana]
Seq. No.	161559
Seq. ID	LIB3177-019-P1-K2-H5
Method	BLASTX
NCBI GI	g730645
BLAST score	472
E value	2.0e-47
Match length	94
% identity	98
NCBI Description	40S RIBOSOMAL PROTEIN S15 >gi_629556_pir__S43412 ribosomal protein S15 - Arabidopsis thaliana >gi_313152_emb_CAA80679_ (Z23161) ribosomal protein S15 [Arabidopsis thaliana] >gi_313188_emb_CAA80681_ (Z23162) ribosomal protein S15 [Arabidopsis thaliana] >gi_1903366_gb_AAB70449_ (AC000104) Strong similarity to Oryza 40S ribosomal protein S15. ESTs gb_R29788,gb_ATTS0365 come from this gene. [Arabidopsis thaliana]
Seq. No.	161560
Seq. ID	LIB3177-019-P1-K2-H6
Method	BLASTX
NCBI GI	g113026
BLAST score	196
E value	1.0e-15
Match length	53
% identity	77
NCBI Description	ISOCITRATE LYASE (ISOCITRASE) (ISOCITRATASE) (ICL) >gi_68211_pir__WZRPI isocitrate lyase (EC 4.1.3.1) - rape >gi_255220_bbs_112862 isocitrate lyase, threo-D S-isocitrate glyoxylate-lyase, IL (EC 4.1.3.1) [Brassica

napus, seedlings, Peptide, 576 aa] >gi_167144 (L08482) isocitrate lyase [Brassica napus] >gi_447142_prf__1913424A isocitrate lyase [Brassica napus]

Seq. No.	161561
Seq. ID	LIB3177-019-P1-K2-H8
Method	BLASTN
NCBI GI	g3869067
BLAST score	156
E value	9.0e-83
Match length	156
% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MCK7, complete sequence [Arabidopsis thaliana]

Seq. No.	161562
Seq. ID	LIB3177-019-P1-K2-H9
Method	BLASTX
NCBI GI	g1213629
BLAST score	325
E value	3.0e-30
Match length	119
% identity	55
NCBI Description	(X95991) pectinesterase [Prunus persica]

Seq. No.	161563
Seq. ID	LIB3177-020-P1-K1-A10
Method	BLASTX
NCBI GI	g3540195
BLAST score	327
E value	2.0e-30
Match length	118
% identity	35
NCBI Description	(AC004260) Unknown protein [Arabidopsis thaliana]

Seq. No.	161564
Seq. ID	LIB3177-020-P1-K1-A12
Method	BLASTX
NCBI GI	g132074
BLAST score	382
E value	7.0e-37
Match length	127
% identity	61
NCBI Description	RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN 1A PRECURSOR (RUBISCO SMALL SUBUNIT 1A) >gi_68063_pir__RKMUA1 ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain A1 precursor - Arabidopsis thaliana

Seq. No.	161565
Seq. ID	LIB3177-020-P1-K1-A2
Method	BLASTX
NCBI GI	g1172977
BLAST score	104
E value	3.0e-20
Match length	70
% identity	62
NCBI Description	60S RIBOSOMAL PROTEIN L18 >gi_606970 (U15741) cytoplasmic

ribosomal protein L18 [Arabidopsis thaliana]

Seq. No.	161566
Seq. ID	LIB3177-020-P1-K1-A3
Method	BLASTX
NCBI GI	g3859112
BLAST score	189
E value	2.0e-14
Match length	74
% identity	53
NCBI Description	(AF031607) male sterility MS5 [Arabidopsis thaliana]

Seq. No.	161567
Seq. ID	LIB3177-020-P1-K1-A4
Method	BLASTN
NCBI GI	g1490552
BLAST score	187
E value	1.0e-101
Match length	299
% identity	91
NCBI Description	Arabidopsis thaliana S-adenosylmethionine decarboxylase (SAMdc) mRNA, complete cds

Seq. No.	161568
Seq. ID	LIB3177-020-P1-K1-A5
Method	BLASTX
NCBI GI	g2129629
BLAST score	274
E value	3.0e-24
Match length	99
% identity	60
NCBI Description	L-ascorbate peroxidase (EC 1.11.1.11) - Arabidopsis thaliana >gi_1332439_emb_CAA66640_ (X98003) ascorbate peroxidase [Arabidopsis thaliana] >gi_1523791_emb_CAA66926_ (X98276) L-ascorbate peroxidase [Arabidopsis thaliana] >gi_2444019 (U69138) ascorbate peroxidase 3 [Arabidopsis thaliana] >gi_2924511_emb_CAA17765.1_ (AL022023) L-ascorbate peroxidase [Arabidopsis thaliana]

Seq. No.	161569
Seq. ID	LIB3177-020-P1-K1-A6
Method	BLASTX
NCBI GI	g4741960
BLAST score	412
E value	2.0e-40
Match length	113
% identity	71
NCBI Description	(AF134130) Lhcb6 protein [Arabidopsis thaliana]

Seq. No.	161570
Seq. ID	LIB3177-020-P1-K1-A9
Method	BLASTX
NCBI GI	g133729
BLAST score	264
E value	3.0e-23
Match length	70
% identity	70

NCBI Description	CHLOROPLAST 30S RIBOSOMAL PROTEIN S11 >gi_70941_pir__R3NT11 ribosomal protein S11 - common tobacco chloroplast >gi_11861_emb_CAA77377_ (Z00044) ribosomal protein S11 [Nicotiana tabacum] >gi_225229_prf__1211235BL ribosomal protein S11 [Nicotiana tabacum]
Seq. No.	161571
Seq. ID	LIB3177-020-P1-K1-B1
Method	BLASTX
NCBI GI	g3860258
BLAST score	219
E value	8.0e-18
Match length	102
% identity	44
NCBI Description	(AC005824) unknown protein [Arabidopsis thaliana]
Seq. No.	161572
Seq. ID	LIB3177-020-P1-K1-B10
Method	BLASTX
NCBI GI	g115767
BLAST score	285
E value	1.0e-25
Match length	106
% identity	55
NCBI Description	CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR (CAB-165/180) (LHCP) >gi_81603_pir__A29280 chlorophyll a/b-binding protein ab165 - Arabidopsis thaliana >gi_16368_emb_CAA27540_ (X03907) chlorophyll a/b binding protein (LHCP AB 65) [Arabidopsis thaliana] >gi_16372_emb_CAA27541_ (X03908) chlorophyll a/b binding protein (LHCP AB 180) [Arabidopsis thaliana]
Seq. No.	161573
Seq. ID	LIB3177-020-P1-K1-B2
Method	BLASTX
NCBI GI	g3152613
BLAST score	199
E value	4.0e-18
Match length	95
% identity	58
NCBI Description	(AC004482) hypothetical protein [Arabidopsis thaliana]
Seq. No.	161574
Seq. ID	LIB3177-020-P1-K1-B3
Method	BLASTX
NCBI GI	g3608147
BLAST score	284
E value	2.0e-25
Match length	112
% identity	61
NCBI Description	(AC005314) putative chloroplast 31 kDa ribonucleoprotein precursor [Arabidopsis thaliana]
Seq. No.	161575
Seq. ID	LIB3177-020-P1-K1-B4
Method	BLASTX
NCBI GI	g3924615

BLAST score	148
E value	2.0e-09
Match length	123
% identity	31
NCBI Description	(AF069442) hypothetical protein [Arabidopsis thaliana]

Seq. No.	161576
Seq. ID	LIB3177-020-P1-K1-B5
Method	BLASTX
NCBI GI	g2119848
BLAST score	343
E value	2.0e-32
Match length	112
% identity	65
NCBI Description	chlorophyll a/b-binding protein type I precursor Lhb1B1 - Arabidopsis thaliana >gi_16366_emb_CAA45789_ (X64459) photosystem II type I chlorophyll a /b binding protein [Arabidopsis thaliana] >gi_3128229 (AC004077) putative photosystem II type I chlorophyll a/b binding protein [Arabidopsis thaliana] >gi_3337372 (AC004481) putative photosystem II type I chlorophyll a/b binding protein [Arabidopsis thaliana]

Seq. No.	161577
Seq. ID	LIB3177-020-P1-K1-B8
Method	BLASTN
NCBI GI	g2924651
BLAST score	58
E value	6.0e-24
Match length	130
% identity	86
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K2A18, complete sequence [Arabidopsis thaliana]

Seq. No.	161578
Seq. ID	LIB3177-020-P1-K1-C12
Method	BLASTN
NCBI GI	g4757410
BLAST score	125
E value	6.0e-64
Match length	336
% identity	87
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MVE11, complete sequence

Seq. No.	161579
Seq. ID	LIB3177-020-P1-K1-C2
Method	BLASTX
NCBI GI	g4454036
BLAST score	231
E value	3.0e-19
Match length	105
% identity	49
NCBI Description	(AL035394) putative major latex protein [Arabidopsis thaliana]

Seq. No. 161580

Seq. ID	LIB3177-020-P1-K1-C3
Method	BLASTX
NCBI GI	g543841
BLAST score	261
E value	7.0e-23
Match length	76
% identity	70
NCBI Description	ADP-RIBOSYLATION FACTOR 1 >gi_322518_pir__S28875 ADP-ribosylation factor 1 - Arabidopsis thaliana >gi_166586 (M95166) ADP-ribosylation factor [Arabidopsis thaliana] >gi_2275195 (AC002337) ADP-ribosylation factor [Arabidopsis thaliana] >gi_4630747_gb_AAD26597.1_AC007236_2 (AC007236) ADP-ribosylation factor [Arabidopsis thaliana]

Seq. No.	161581
Seq. ID	LIB3177-020-P1-K1-C4
Method	BLASTX
NCBI GI	g2827529
BLAST score	271
E value	6.0e-24
Match length	106
% identity	56
NCBI Description	(AL021633) putative protein [Arabidopsis thaliana]

Seq. No.	161582
Seq. ID	LIB3177-020-P1-K1-D1
Method	BLASTX
NCBI GI	g3702351
BLAST score	210
E value	9.0e-17
Match length	109
% identity	50
NCBI Description	(AC005397) putative desiccation protectant protein [Arabidopsis thaliana]

Seq. No.	161583
Seq. ID	LIB3177-020-P1-K1-D12
Method	BLASTX
NCBI GI	g3309082
BLAST score	411
E value	3.0e-40
Match length	131
% identity	67
NCBI Description	(AF076251) calcineurin B-like protein 1 [Arabidopsis thaliana]

Seq. No.	161584
Seq. ID	LIB3177-020-P1-K1-D3
Method	BLASTX
NCBI GI	g99696
BLAST score	503
E value	5.0e-51
Match length	142
% identity	67
NCBI Description	glutamate--ammonia ligase (EC 6.3.1.2) precursor, chloroplast (clone lambdaAtgsl1) - Arabidopsis thaliana >gi_240070_bbs_69728 (S69727) light-regulated glutamine

synthetase isoenzyme [Arabidopsis thaliana, Peptide, 430 aa] [Arabidopsis thaliana] >gi_228453_prf__1804333A Gln synthetase [Arabidopsis thaliana]

Seq. No.	161585
Seq. ID	LIB3177-020-P1-K1-E1
Method	BLASTX
NCBI GI	g3929364
BLAST score	306
E value	6.0e-42
Match length	126
% identity	71
NCBI Description	NADH-UBIQUINONE OXIDOREDUCTASE 23 KD SUBUNIT PRECURSOR (COMPLEX I-23KD) (CI-23KD) >gi_1076356_pir__S52380 NADH dehydrogenase (EC 1.6.99.3) - Arabidopsis thaliana >gi_666977_emb_CAA59061_ (X84318) NADH dehydrogenase [Arabidopsis thaliana] >gi_3152573 (AC002986) Match to NADH:ubiquinone oxidoreductase gb_X84318 from A.thaliana. ESTs gb_Z27005, gb_T04711, gb_T45078 and gb_Z28689 come from this gene. [Arabidopsis thaliana]

Seq. No.	161586
Seq. ID	LIB3177-020-P1-K1-E10
Method	BLASTX
NCBI GI	g2506443
BLAST score	217
E value	2.0e-17
Match length	104
% identity	50
NCBI Description	GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE A PRECURSOR, CHLOROPLAST >gi_2117520_pir__JQ1285 glyceraldehyde-3-phosphate dehydrogenase (NADP+) (phosphorylating) (EC 1.2.1.13) A precursor, chloroplast - Arabidopsis thaliana >gi_166704 (M64117) glyceraldehyde 3-phosphate dehydrogenase [Arabidopsis thaliana] >gi_1402885_emb_CAA66816_ (X98130) glyceraldehyde-3-phosphate dehydrogenase (NADP+) (phosphorylating) [Arabidopsis thaliana]

Seq. No.	161587
Seq. ID	LIB3177-020-P1-K1-E2
Method	BLASTX
NCBI GI	g3273196
BLAST score	422
E value	1.0e-41
Match length	114
% identity	75
NCBI Description	(AB010915) responce regulator1 [Arabidopsis thaliana] >gi_3323583 (AF057282) two-component response regulator homolog [Arabidopsis thaliana] >gi_3953597_dbj_BAA34726_ (AB008487) response regulator 4 [Arabidopsis thaliana]

Seq. No.	161588
Seq. ID	LIB3177-020-P1-K1-E4
Method	BLASTN
NCBI GI	g3873174
BLAST score	108

E value	1.0e-53
Match length	380
% identity	82
NCBI Description	Genomic sequence for Arabidopsis thaliana BAC F14N23, complete sequence [Arabidopsis thaliana]

Seq. No.	161589
Seq. ID	LIB3177-020-P1-K1-F1
Method	BLASTX
NCBI GI	g2499327
BLAST score	268
E value	1.0e-23
Match length	102
% identity	59
NCBI Description	NADH-UBIQUINONE OXIDOREDUCTASE 20 KD SUBUNIT PRECURSOR (COMPLEX I-20KD) (CI-20KD) >gi_1084345_pir__S52286 NADH dehydrogenase (EC 1.6.99.3) - Arabidopsis thaliana >gi_643090_emb_CAA58887.1_ (X84078) NADH dehydrogenase [Arabidopsis thaliana]

Seq. No.	161590
Seq. ID	LIB3177-020-P1-K1-F12
Method	BLASTX
NCBI GI	g132074
BLAST score	128
E value	8.0e-28
Match length	110
% identity	65
NCBI Description	RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN 1A PRECURSOR (RUBISCO SMALL SUBUNIT 1A) >gi_68063_pir__RKMUA1 ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain A1 precursor - Arabidopsis thaliana

Seq. No.	161591
Seq. ID	LIB3177-020-P1-K1-F2
Method	BLASTX
NCBI GI	g115783
BLAST score	267
E value	2.0e-23
Match length	95
% identity	62
NCBI Description	CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR (CAB-140) (LHCP) >gi_16376_emb_CAA27543_ (X03909) chlorophyll a/b binding protein (LHCP AB 140) [Arabidopsis thaliana]

Seq. No.	161592
Seq. ID	LIB3177-020-P1-K1-F7
Method	BLASTX
NCBI GI	g2506443
BLAST score	287
E value	8.0e-26
Match length	122
% identity	54
NCBI Description	GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE A PRECURSOR, CHLOROPLAST >gi_2117520_pir__JQ1285 glyceraldehyde-3-phosphate dehydrogenase (NADP+)

	(phosphorylating) (EC 1.2.1.13) A precursor, chloroplast - Arabidopsis thaliana >gi_166704 (M64117) glyceraldehyde 3-phosphate dehydrogenase [Arabidopsis thaliana] >gi_1402885_emb_CAA66816_ (X98130) glyceraldehyde-3-phosphate dehydrogenase (NADP+) (phosphorylating) [Arabidopsis thaliana]
Seq. No.	161593
Seq. ID	LIB3177-020-P1-K1-G1
Method	BLASTX
NCBI GI	g1621268
BLAST score	178
E value	5.0e-13
Match length	79
% identity	49
NCBI Description	(Z81012) unknown [Ricinus communis]
Seq. No.	161594
Seq. ID	LIB3177-020-P1-K1-G12
Method	BLASTN
NCBI GI	g2244991
BLAST score	38
E value	6.0e-12
Match length	139
% identity	86
NCBI Description	Arabidopsis thaliana DNA chromosome 4, ESSA I contig fragment No
Seq. No.	161595
Seq. ID	LIB3177-020-P1-K1-G2
Method	BLASTX
NCBI GI	g3273743
BLAST score	337
E value	1.0e-31
Match length	93
% identity	74
NCBI Description	(AF057357) lipid transfer protein 2 precursor [Arabidopsis thaliana] >gi_3786019 (AC005499) unknown protein [Arabidopsis thaliana]
Seq. No.	161596
Seq. ID	LIB3177-020-P1-K1-G3
Method	BLASTN
NCBI GI	g4741961
BLAST score	59
E value	1.0e-24
Match length	204
% identity	85
NCBI Description	Arabidopsis thaliana PsbS protein (PsbS) mRNA, complete cds
Seq. No.	161597
Seq. ID	LIB3177-020-P1-K1-G4
Method	BLASTX
NCBI GI	g124224
BLAST score	374
E value	6.0e-36
Match length	120

% identity	61
NCBI Description	INITIATION FACTOR 5A-1 (EIF-5A) (EIF-4D) >gi_100345_pir__S21060 translation initiation factor eIF-5A - common tobacco >gi_19887_emb_CAA45105_ (X63543) eukaryotic initiatin factor 5A (3) [Nicotiana tabacum]
Seq. No.	161598
Seq. ID	LIB3177-020-P1-K1-G8
Method	BLASTX
NCBI GI	g131398
BLAST score	67
E value	1.0e-19
Match length	102
% identity	53
NCBI Description	PHOTOSYSTEM II 10 KD POLYPEPTIDE PRECURSOR >gi_72714_pir__F2MU10 photosystem II 10K protein precursor - Arabidopsis thaliana >gi_16447_emb_CAA39441_ (X55970) photosystem II 10 kDa polypeptide [Arabidopsis thaliana] >gi_3152571 (AC002986) Match to photosystem II 10kDa polypeptide gb_X55970. ESTs gb_Z17693, gb_N37616, gb_T41858, gb_T88021, gb_R37531, gb_T04679, gb_N37520, gb_N64965, gb_Z17592 and gb_N65338, gb_N37466 and gb_T45400 come from this gene. [Arabidopsis
Seq. No.	161599
Seq. ID	LIB3177-020-P1-K1-H1
Method	BLASTN
NCBI GI	g2656031
BLAST score	42
E value	2.0e-14
Match length	245
% identity	82
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MXC20
Seq. No.	161600
Seq. ID	LIB3177-020-P1-K1-H11
Method	BLASTN
NCBI GI	g4733953
BLAST score	93
E value	7.0e-45
Match length	229
% identity	85
NCBI Description	Arabidopsis thaliana chromosome I BAC F13O11 genomic sequence, complete sequence
Seq. No.	161601
Seq. ID	LIB3177-020-P1-K1-H4
Method	BLASTX
NCBI GI	g3169173
BLAST score	78
E value	2.8e-01
Match length	94
% identity	34
NCBI Description	(AC004401) putative serine carboxypeptidase I [Arabidopsis thaliana] >gi_3445215 (AC004786) putative serine carboxypeptidase I [Arabidopsis thaliana]

Seq. No.	161602
Seq. ID	LIB3177-020-P1-K1-H5
Method	BLASTX
NCBI GI	g1350930
BLAST score	312
E value	1.0e-28
Match length	111
% identity	63
NCBI Description	40S RIBOSOMAL PROTEIN S13

Seq. No.	161603
Seq. ID	LIB3177-020-P1-K1-H7
Method	BLASTN
NCBI GI	g4371278
BLAST score	131
E value	2.0e-67
Match length	295
% identity	86
NCBI Description	Arabidopsis thaliana chromosome II BAC T2N18 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	161604
Seq. ID	LIB3177-020-P1-K1-H9
Method	BLASTX
NCBI GI	g730449
BLAST score	273
E value	4.0e-24
Match length	118
% identity	52
NCBI Description	60S RIBOSOMAL PROTEIN L13-1 (COLD INDUCED PROTEIN C24A) >gi_480647_pir__S37132 ribosomal protein L13.A - rape >gi_398918_emb_CAA80341_ (Z22618) cold induced protein (BnC24A) [Brassica napus]

Seq. No.	161605
Seq. ID	LIB3177-020-P1-K2-A10
Method	BLASTN
NCBI GI	g3176694
BLAST score	224
E value	1.0e-123
Match length	417
% identity	83
NCBI Description	Arabidopsis thaliana chromosome I BAC T14N5 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	161606
Seq. ID	LIB3177-020-P1-K2-A12
Method	BLASTX
NCBI GI	g132074
BLAST score	698
E value	6.0e-74
Match length	134
% identity	96
NCBI Description	RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN 1A PRECURSOR (RUBISCO SMALL SUBUNIT 1A) >gi_68063_pir__RKMUA1 ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain

A1 precursor - Arabidopsis thaliana

Seq. No.	161607
Seq. ID	LIB3177-020-P1-K2-A2
Method	BLASTX
NCBI GI	g1172977
BLAST score	623
E value	3.0e-65
Match length	126
% identity	98
NCBI Description	60S RIBOSOMAL PROTEIN L18 >gi_606970 (U15741) cytoplasmic ribosomal protein L18 [Arabidopsis thaliana]

Seq. No.	161608
Seq. ID	LIB3177-020-P1-K2-A3
Method	BLASTX
NCBI GI	g3859116
BLAST score	464
E value	2.0e-46
Match length	133
% identity	68
NCBI Description	(AF031609) unknown [Oryza sativa]

Seq. No.	161609
Seq. ID	LIB3177-020-P1-K2-A4
Method	BLASTN
NCBI GI	g1490552
BLAST score	213
E value	1.0e-116
Match length	249
% identity	97
NCBI Description	Arabidopsis thaliana S-adenosylmethionine decarboxylase (SAMdc) mRNA, complete cds

Seq. No.	161610
Seq. ID	LIB3177-020-P1-K2-A5
Method	BLASTX
NCBI GI	g2129629
BLAST score	238
E value	1.0e-20
Match length	48
% identity	98
NCBI Description	L-ascorbate peroxidase (EC 1.11.1.11) - Arabidopsis thaliana >gi_1332439_emb_CAA66640_ (X98003) ascorbate peroxidase [Arabidopsis thaliana] >gi_1523791_emb_CAA66926_ (X98276) L-ascorbate peroxidase [Arabidopsis thaliana] >gi_2444019 (U69138) ascorbate peroxidase 3 [Arabidopsis thaliana] >gi_2924511_emb_CAA17765.1_ (AL022023) L-ascorbate peroxidase [Arabidopsis thaliana]

Seq. No.	161611
Seq. ID	LIB3177-020-P1-K2-A6
Method	BLASTX
NCBI GI	g4741960
BLAST score	561
E value	8.0e-58
Match length	126

% identity	86
NCBI Description	(AF134130) Lhcb6 protein [Arabidopsis thaliana]

Seq. No.	161612
Seq. ID	LIB3177-020-P1-K2-A9
Method	BLASTX
NCBI GI	g133729
BLAST score	312
E value	1.0e-28
Match length	88
% identity	75
NCBI Description	CHLOROPLAST 30S RIBOSOMAL PROTEIN S11 >gi_70941_pir__R3NT11 ribosomal protein S11 - common tobacco chloroplast >gi_11861_emb_CAA77377_ (Z00044) ribosomal protein S11 [Nicotiana tabacum] >gi_225229_prf__1211235BL ribosomal protein S11 [Nicotiana tabacum]

Seq. No.	161613
Seq. ID	LIB3177-020-P1-K2-B1
Method	BLASTX
NCBI GI	g4581141
BLAST score	367
E value	5.0e-35
Match length	104
% identity	83
NCBI Description	(AC006919) unknown protein [Arabidopsis thaliana]

Seq. No.	161614
Seq. ID	LIB3177-020-P1-K2-B10
Method	BLASTX
NCBI GI	g115767
BLAST score	338
E value	5.0e-32
Match length	83
% identity	84
NCBI Description	CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR (CAB-165/180) (LHCP) >gi_81603_pir__A29280 chlorophyll a/b-binding protein ab165 - Arabidopsis thaliana >gi_16368_emb_CAA27540_ (X03907) chlorophyll a/b binding protein (LHCP AB 65) [Arabidopsis thaliana] >gi_16372_emb_CAA27541_ (X03908) chlorophyll a/b binding protein (LHCP AB 180) [Arabidopsis thaliana]

Seq. No.	161615
Seq. ID	LIB3177-020-P1-K2-B2
Method	BLASTN
NCBI GI	g3152602
BLAST score	156
E value	1.0e-82
Match length	242
% identity	100
NCBI Description	Arabidopsis thaliana chromosome II BAC F27L4 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	161616
Seq. ID	LIB3177-020-P1-K2-B3
Method	BLASTX

NCBI GI	g3608147
BLAST score	564
E value	4.0e-58
Match length	133
% identity	57
NCBI Description	(AC005314) putative chloroplast 31 kDa ribonucleoprotein precursor [Arabidopsis thaliana]

Seq. No.	161617
Seq. ID	LIB3177-020-P1-K2-B4
Method	BLASTX
NCBI GI	g3924615
BLAST score	279
E value	9.0e-25
Match length	149
% identity	37
NCBI Description	(AF069442) hypothetical protein [Arabidopsis thaliana]

Seq. No.	161618
Seq. ID	LIB3177-020-P1-K2-B5
Method	BLASTX
NCBI GI	g2119848
BLAST score	436
E value	1.0e-52
Match length	131
% identity	82
NCBI Description	chlorophyll a/b-binding protein type I precursor Lhb1B1 - Arabidopsis thaliana >gi_16366_emb_CAA45789_ (X64459) photosystem II type I chlorophyll a /b binding protein [Arabidopsis thaliana] >gi_3128229 (AC004077) putative photosystem II type I chlorophyll a/b binding protein [Arabidopsis thaliana] >gi_3337372 (AC004481) putative photosystem II type I chlorophyll a/b binding protein [Arabidopsis thaliana]

Seq. No.	161619
Seq. ID	LIB3177-020-P1-K2-B8
Method	BLASTN
NCBI GI	g2924651
BLAST score	434
E value	0.0e+00
Match length	459
% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K2A18, complete sequence [Arabidopsis thaliana]

Seq. No.	161620
Seq. ID	LIB3177-020-P1-K2-B9
Method	BLASTN
NCBI GI	g2924651
BLAST score	238
E value	1.0e-131
Match length	330
% identity	93
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K2A18, complete sequence [Arabidopsis thaliana]

Seq. No.	161621
Seq. ID	LIB3177-020-P1-K2-C12
Method	BLASTN
NCBI GI	g3355463
BLAST score	75
E value	3.0e-34
Match length	179
% identity	85
NCBI Description	Arabidopsis thaliana chromosome II BAC F12L6 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	161622
Seq. ID	LIB3177-020-P1-K2-C2
Method	BLASTX
NCBI GI	g4454036
BLAST score	744
E value	3.0e-79
Match length	136
% identity	99
NCBI Description	(AL035394) putative major latex protein [Arabidopsis thaliana]

Seq. No.	161623
Seq. ID	LIB3177-020-P1-K2-C3
Method	BLASTX
NCBI GI	g543841
BLAST score	639
E value	6.0e-67
Match length	125
% identity	100
NCBI Description	ADP-RIBOSYLATION FACTOR 1 >gi_322518_pir__S28875 ADP-ribosylation factor 1 - Arabidopsis thaliana >gi_166586 (M95166) ADP-ribosylation factor [Arabidopsis thaliana] >gi_2275195 (AC002337) ADP-ribosylation factor [Arabidopsis thaliana] >gi_4630747_gb_AAD26597.1_AC007236_2 (AC007236) ADP-ribosylation factor [Arabidopsis thaliana]

Seq. No.	161624
Seq. ID	LIB3177-020-P1-K2-C4
Method	BLASTX
NCBI GI	g4337210
BLAST score	547
E value	3.0e-56
Match length	148
% identity	71
NCBI Description	(AC006403) hypothetical protein [Arabidopsis thaliana]

Seq. No.	161625
Seq. ID	LIB3177-020-P1-K2-D1
Method	BLASTX
NCBI GI	g3702351
BLAST score	536
E value	7.0e-55
Match length	111
% identity	95
NCBI Description	(AC005397) putative desiccation protectant protein [Arabidopsis thaliana]

Seq. No.	161626
Seq. ID	LIB3177-020-P1-K2-D4
Method	BLASTN
NCBI GI	g4757410
BLAST score	223
E value	1.0e-122
Match length	428
% identity	99
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MVE11, complete sequence

Seq. No.	161627
Seq. ID	LIB3177-020-P1-K2-D7
Method	BLASTN
NCBI GI	g3702315
BLAST score	62
E value	1.0e-26
Match length	99
% identity	89
NCBI Description	Arabidopsis thaliana chromosome II BAC T3F17 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	161628
Seq. ID	LIB3177-020-P1-K2-E1
Method	BLASTX
NCBI GI	g3929364
BLAST score	809
E value	7.0e-87
Match length	153
% identity	99
NCBI Description	NADH-UBIQUINONE OXIDOREDUCTASE 23 KD SUBUNIT PRECURSOR (COMPLEX I-23KD) (CI-23KD) >gi_1076356_pir__S52380 NADH dehydrogenase (EC 1.6.99.3) - Arabidopsis thaliana >gi_666977_emb_CAA59061_ (X84318) NADH dehydrogenase [Arabidopsis thaliana] >gi_3152573 (AC002986) Match to NADH:ubiquinone oxidoreductase gb_X84318 from A.thaliana. ESTs gb_Z27005, gb_T04711, gb_T45078 and gb_Z28689 come from this gene. [Arabidopsis thaliana]

Seq. No.	161629
Seq. ID	LIB3177-020-P1-K2-E10
Method	BLASTN
NCBI GI	g3873174
BLAST score	415
E value	0.0e+00
Match length	440
% identity	98
NCBI Description	Genomic sequence for Arabidopsis thaliana BAC F14N23, complete sequence [Arabidopsis thaliana]

Seq. No.	161630
Seq. ID	LIB3177-020-P1-K2-E2
Method	BLASTX
NCBI GI	g3273196
BLAST score	759
E value	5.0e-81

Match length	151
% identity	100
NCBI Description	(AB010915) responce regulator1 [Arabidopsis thaliana] >gi_3323583 (AF057282) two-component response regulator homolog [Arabidopsis thaliana] >gi_3953597_dbj_BAA34726_ (AB008487) response regulator 4 [Arabidopsis thaliana]

Seq. No.	161631
Seq. ID	LIB3177-020-P1-K2-E3
Method	BLASTX
NCBI GI	g3510256
BLAST score	210
E value	1.0e-16
Match length	81
% identity	47
NCBI Description	(AC005310) unknown protein [Arabidopsis thaliana]

Seq. No.	161632
Seq. ID	LIB3177-020-P1-K2-E4
Method	BLASTX
NCBI GI	g3309082
BLAST score	662
E value	1.0e-69
Match length	131
% identity	98
NCBI Description	(AF076251) calcineurin B-like protein 1 [Arabidopsis thaliana]

Seq. No.	161633
Seq. ID	LIB3177-020-P1-K2-E5
Method	BLASTX
NCBI GI	g2506443
BLAST score	574
E value	2.0e-59
Match length	153
% identity	76
NCBI Description	GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE A PRECURSOR, CHLOROPLAST >gi_2117520_pir__JQ1285 glyceraldehyde-3-phosphate dehydrogenase (NADP+) (phosphorylating) (EC 1.2.1.13) A precursor, chloroplast - Arabidopsis thaliana >gi_166704 (M64117) glyceraldehyde 3-phosphate dehydrogenase [Arabidopsis thaliana] >gi_1402885_emb_CAA66816_ (X98130) glyceraldehyde-3-phosphate dehydrogenase (NADP+) (phosphorylating) [Arabidopsis thaliana]

Seq. No.	161634
Seq. ID	LIB3177-020-P1-K2-E6
Method	BLASTN
NCBI GI	g4455168
BLAST score	134
E value	3.0e-69
Match length	303
% identity	90
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F10M10 (ESSAII project)

Seq. No.	161635
Seq. ID	LIB3177-020-P1-K2-E7
Method	BLASTX
NCBI GI	g4689034
BLAST score	198
E value	3.0e-15
Match length	69
% identity	59
NCBI Description	(AJ133751) chloroplast ribosome recycling factor protein [Spinacia oleracea]

Seq. No.	161636
Seq. ID	LIB3177-020-P1-K2-F1
Method	BLASTX
NCBI GI	g2499327
BLAST score	315
E value	4.0e-29
Match length	113
% identity	58
NCBI Description	NADH-UBIQUINONE OXIDOREDUCTASE 20 KD SUBUNIT PRECURSOR (COMPLEX I-20KD) (CI-20KD) >gi_1084345_pir__S52286 NADH dehydrogenase (EC 1.6.99.3) - Arabidopsis thaliana >gi_643090_emb_CAA58887.1_ (X84078) NADH dehydrogenase [Arabidopsis thaliana]

Seq. No.	161637
Seq. ID	LIB3177-020-P1-K2-F12
Method	BLASTX
NCBI GI	g3212879
BLAST score	271
E value	9.0e-26
Match length	108
% identity	65
NCBI Description	(AC004005) putative ribosomal protein L7 [Arabidopsis thaliana]

Seq. No.	161638
Seq. ID	LIB3177-020-P1-K2-F2
Method	BLASTX
NCBI GI	g115783
BLAST score	689
E value	8.0e-73
Match length	132
% identity	99
NCBI Description	CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR (CAB-140) (LHCP) >gi_16376_emb_CAA27543_ (X03909) chlorophyll a/b binding protein (LHCP AB 140) [Arabidopsis thaliana]

Seq. No.	161639
Seq. ID	LIB3177-020-P1-K2-F3
Method	BLASTX
NCBI GI	g4262156
BLAST score	153
E value	2.0e-43
Match length	144
% identity	66

NCBI Description	(AC005275) putative component of cytochrome B6-F complex [Arabidopsis thaliana]
Seq. No.	161640
Seq. ID	LIB3177-020-P1-K2-F6
Method	BLASTX
NCBI GI	g1071913
BLAST score	47
E value	4.0e-12
Match length	108
% identity	42
NCBI Description	cysteine synthase (EC 4.2.99.8) C precursor, mitochondrial - spinach >gi_1066153_dbj_BAA07177_ (D37963) cysteine synthase [Spinacia oleracea]
Seq. No.	161641
Seq. ID	LIB3177-020-P1-K2-F7
Method	BLASTX
NCBI GI	g166702
BLAST score	612
E value	8.0e-64
Match length	151
% identity	81
NCBI Description	(M64114) glyceraldehyde 3-phosphate dehydrogenase A subunit [Arabidopsis thaliana]
Seq. No.	161642
Seq. ID	LIB3177-020-P1-K2-F8
Method	BLASTX
NCBI GI	g927575
BLAST score	260
E value	2.0e-22
Match length	92
% identity	54
NCBI Description	(U12926) alpha galactosidase [Glycine max]
Seq. No.	161643
Seq. ID	LIB3177-020-P1-K2-G1
Method	BLASTX
NCBI GI	g1621268
BLAST score	497
E value	2.0e-50
Match length	131
% identity	70
NCBI Description	(Z81012) unknown [Ricinus communis]
Seq. No.	161644
Seq. ID	LIB3177-020-P1-K2-G10
Method	BLASTX
NCBI GI	g3024022
BLAST score	597
E value	5.0e-62
Match length	134
% identity	84
NCBI Description	INITIATION FACTOR 5A-5 (EIF-5A) (EIF-4D) >gi_2225885_dbj_BAA20879_ (AB004826) eukaryotic initiation factor 5A5 [Solanum tuberosum]

Seq. No.	161645
Seq. ID	LIB3177-020-P1-K2-G11
Method	BLASTX
NCBI GI	g1749546
BLAST score	232
E value	3.0e-19
Match length	81
% identity	58
NCBI Description	(D89169) similar to Saccharomyces cerevisiae SCD6 protein, SWISS-PROT Accession Number P45978 [Schizosaccharomyces pombe]

Seq. No.	161646
Seq. ID	LIB3177-020-P1-K2-G2
Method	BLASTX
NCBI GI	g3273743
BLAST score	616
E value	3.0e-64
Match length	118
% identity	99
NCBI Description	(AF057357) lipid transfer protein 2 precursor [Arabidopsis thaliana] >gi_3786019 (AC005499) unknown protein [Arabidopsis thaliana]

Seq. No.	161647
Seq. ID	LIB3177-020-P1-K2-G3
Method	BLASTX
NCBI GI	g4741962
BLAST score	330
E value	9.0e-31
Match length	139
% identity	39
NCBI Description	(AF134131) PsbS protein [Arabidopsis thaliana]

Seq. No.	161648
Seq. ID	LIB3177-020-P1-K2-G4
Method	BLASTX
NCBI GI	g132074
BLAST score	754
E value	2.0e-80
Match length	137
% identity	100
NCBI Description	RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN 1A PRECURSOR (RUBISCO SMALL SUBUNIT 1A) >gi_68063_pir__RKMUA1 ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain A1 precursor - Arabidopsis thaliana

Seq. No.	161649
Seq. ID	LIB3177-020-P1-K2-G8
Method	BLASTX
NCBI GI	g131398
BLAST score	112
E value	4.0e-41
Match length	124
% identity	77
NCBI Description	PHOTOSYSTEM II 10 KD POLYPEPTIDE PRECURSOR

	>gi_72714_pir__F2MU10 photosystem II 10K protein precursor - Arabidopsis thaliana >gi_16447_emb_CAA39441_ (X55970) photosystem II 10 kDa polypeptide [Arabidopsis thaliana] >gi_3152571 (AC002986) Match to photosystem II 10kDa polypeptide gb_X55970. ESTs gb_Z17693, gb_N37616, gb_T41858, gb_T88021, gb_R37531, gb_T04679, gb_N37520, gb_N64965, gb_Z17592 and gb_N65338, gb_N37466 and gb_T45400 come from this gene. [Arabidopsis
Seq. No.	161650
Seq. ID	LIB3177-020-P1-K2-G9
Method	BLASTX
NCBI GI	g131398
BLAST score	231
E value	3.0e-19
Match length	73
% identity	66
NCBI Description	PHOTOSYSTEM II 10 KD POLYPEPTIDE PRECURSOR
	>gi_72714_pir__F2MU10 photosystem II 10K protein precursor - Arabidopsis thaliana >gi_16447_emb_CAA39441_ (X55970) photosystem II 10 kDa polypeptide [Arabidopsis thaliana] >gi_3152571 (AC002986) Match to photosystem II 10kDa polypeptide gb_X55970. ESTs gb_Z17693, gb_N37616, gb_T41858, gb_T88021, gb_R37531, gb_T04679, gb_N37520, gb_N64965, gb_Z17592 and gb_N65338, gb_N37466 and gb_T45400 come from this gene. [Arabidopsis
Seq. No.	161651
Seq. ID	LIB3177-020-P1-K2-H1
Method	BLASTN
NCBI GI	g2656031
BLAST score	386
E value	0.0e+00
Match length	419
% identity	98
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MXC20
Seq. No.	161652
Seq. ID	LIB3177-020-P1-K2-H11
Method	BLASTX
NCBI GI	g1350930
BLAST score	725
E value	5.0e-77
Match length	147
% identity	96
NCBI Description	40S RIBOSOMAL PROTEIN S13
Seq. No.	161653
Seq. ID	LIB3177-020-P1-K2-H2
Method	BLASTX
NCBI GI	g2499973
BLAST score	298
E value	6.0e-27
Match length	87
% identity	71
NCBI Description	PHOTOSYSTEM II 5 KD PROTEIN PRECURSOR (PSII-T)

>gi_1465366_emb_CAA66701_ (X98078) photosystem II [Arabidopsis thaliana]

Seq. No.	161654
Seq. ID	LIB3177-020-P1-K2-H4
Method	BLASTN
NCBI GI	g2244991
BLAST score	311
E value	1.0e-175
Match length	463
% identity	91
NCBI Description	Arabidopsis thaliana DNA chromosome 4, ESSA I contig fragment No

Seq. No.	161655
Seq. ID	LIB3177-020-P1-K2-H6
Method	BLASTN
NCBI GI	g4733953
BLAST score	230
E value	1.0e-126
Match length	340
% identity	91
NCBI Description	Arabidopsis thaliana chromosome I BAC F13O11 genomic sequence, complete sequence

Seq. No.	161656
Seq. ID	LIB3177-020-P1-K2-H7
Method	BLASTN
NCBI GI	g4371278
BLAST score	340
E value	0.0e+00
Match length	405
% identity	99
NCBI Description	Arabidopsis thaliana chromosome II BAC T2N18 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	161657
Seq. ID	LIB3177-020-P1-K2-H9
Method	BLASTX
NCBI GI	g730526
BLAST score	599
E value	3.0e-62
Match length	131
% identity	88
NCBI Description	60S RIBOSOMAL PROTEIN L13 (BBC1 PROTEIN HOMOLOG) >gi_480787_pir__S37271 ribosomal protein L13 - Arabidopsis thaliana >gi_404166_emb_CAA53005_ (X75162) BBC1 protein [Arabidopsis thaliana]

Seq. No.	161658
Seq. ID	LIB3177-021-P1-K1-A1
Method	BLASTN
NCBI GI	g2160155
BLAST score	109
E value	2.0e-54
Match length	269
% identity	84

NCBI Description	Sequence of BAC F21M12 from Arabidopsis thaliana chromosome 1, complete sequence [Arabidopsis thaliana]
Seq. No.	161659
Seq. ID	LIB3177-021-P1-K1-A11
Method	BLASTX
NCBI GI	g2119846
BLAST score	363
E value	9.0e-35
Match length	101
% identity	72
NCBI Description	chlorophyll a/b-binding protein type I precursor Lhb1B2 - Arabidopsis thaliana >gi_16364_emb_CAA45790_ (X64460) photosystem II type I chlorophyll a /b binding protein [Arabidopsis thaliana] >gi_3128230 (AC004077) photosystem II type I chlorophyll a/b binding protein [Arabidopsis thaliana] >gi_3337371 (AC004481) photosystem II type I chlorophyll a/b binding protein [Arabidopsis thaliana]
Seq. No.	161660
Seq. ID	LIB3177-021-P1-K1-A2
Method	BLASTX
NCBI GI	g4056479
BLAST score	185
E value	3.0e-14
Match length	59
% identity	66
NCBI Description	(AC005896) unknown protein [Arabidopsis thaliana]
Seq. No.	161661
Seq. ID	LIB3177-021-P1-K1-A4
Method	BLASTX
NCBI GI	g119975
BLAST score	238
E value	4.0e-20
Match length	105
% identity	57
NCBI Description	FERREDOXIN PRECURSOR >gi_99692_pir__S09979 ferredoxin [2Fe-2S] precursor - Arabidopsis thaliana >gi_16437_emb_CAA35754_ (X51370) ferredoxin precursor [Arabidopsis thaliana] >gi_166698 (M35868) ferrodoxin A [Arabidopsis thaliana]
Seq. No.	161662
Seq. ID	LIB3177-021-P1-K1-A6
Method	BLASTX
NCBI GI	g2529665
BLAST score	135
E value	6.0e-08
Match length	132
% identity	46
NCBI Description	(AC002535) putative ribosomal protein L7A [Arabidopsis thaliana]
Seq. No.	161663
Seq. ID	LIB3177-021-P1-K1-A7
Method	BLASTX

NCBI GI	g115470
BLAST score	159
E value	4.0e-11
Match length	67
% identity	54
NCBI Description	CARBONIC ANHYDRASE, CHLOROPLAST PRECURSOR (CARBONATE DEHYDRATASE) >gi_320554_pir__S28412 carbonate dehydratase (EC 4.2.1.1) precursor - Arabidopsis thaliana >gi_14343_emb_CAA46508_ (X65541) carbonic anhydrase [Arabidopsis thaliana]

Seq. No.	161664
Seq. ID	LIB3177-021-P1-K1-A9
Method	BLASTN
NCBI GI	g4454022
BLAST score	39
E value	1.0e-12
Match length	186
% identity	83
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F9D16 (ESSAII project)

Seq. No.	161665
Seq. ID	LIB3177-021-P1-K1-B2
Method	BLASTX
NCBI GI	g3122753
BLAST score	244
E value	1.0e-20
Match length	87
% identity	52
NCBI Description	60S RIBOSOMAL PROTEIN L44 >gi_2244789_emb_CAB10211.1_ (Z97336) ribosomal protein [Arabidopsis thaliana]

Seq. No.	161666
Seq. ID	LIB3177-021-P1-K1-B3
Method	BLASTX
NCBI GI	g4490705
BLAST score	296
E value	7.0e-27
Match length	119
% identity	55
NCBI Description	(AL035680) ribosomal protein L14-like protein [Arabidopsis thaliana]

Seq. No.	161667
Seq. ID	LIB3177-021-P1-K1-B4
Method	BLASTX
NCBI GI	g115767
BLAST score	340
E value	5.0e-32
Match length	120
% identity	62
NCBI Description	CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR (CAB-165/180) (LHCP) >gi_81603_pir__A29280 chlorophyll a/b-binding protein ab165 - Arabidopsis thaliana >gi_16368_emb_CAA27540_ (X03907) chlorophyll a/b binding protein (LHCP AB 65) [Arabidopsis thaliana]

>gi_16372_emb_CAA27541_ (X03908) chlorophyll a/b binding protein (LHCP AB 180) [Arabidopsis thaliana]

Seq. No.	161668
Seq. ID	LIB3177-021-P1-K1-B5
Method	BLASTX
NCBI GI	g2369714
BLAST score	209
E value	7.0e-17
Match length	89
% identity	51
NCBI Description	(Z97178) elongation factor 2 [Beta vulgaris]

Seq. No.	161669
Seq. ID	LIB3177-021-P1-K1-B6
Method	BLASTN
NCBI GI	g2829274
BLAST score	89
E value	2.0e-42
Match length	205
% identity	86
NCBI Description	Arabidopsis thaliana nucleoside diphosphate kinase 3 (ndpk3) mRNA, complete cds

Seq. No.	161670
Seq. ID	LIB3177-021-P1-K1-B7
Method	BLASTX
NCBI GI	g115385
BLAST score	203
E value	4.0e-16
Match length	67
% identity	67
NCBI Description	CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR (CAB-4) (LHCP) >gi_166646 (M63931) light-harvesting chlorophyll a/b binding protein [Arabidopsis thaliana]

Seq. No.	161671
Seq. ID	LIB3177-021-P1-K1-C11
Method	BLASTN
NCBI GI	g4757414
BLAST score	80
E value	4.0e-37
Match length	312
% identity	81
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MYF24, complete sequence

Seq. No.	161672
Seq. ID	LIB3177-021-P1-K1-C12
Method	BLASTN
NCBI GI	g2980757
BLAST score	41
E value	7.0e-14
Match length	153
% identity	82
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F6I18 (ESSAII project)

Seq. No.	161673
Seq. ID	LIB3177-021-P1-K1-C3
Method	BLASTX
NCBI GI	g115385
BLAST score	335
E value	2.0e-31
Match length	93
% identity	74
NCBI Description	CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR (CAB-4) (LHCP) >gi_166646 (M63931) light-harvesting chlorophyll a/b binding protein [Arabidopsis thaliana]

Seq. No.	161674
Seq. ID	LIB3177-021-P1-K1-C4
Method	BLASTX
NCBI GI	g132110
BLAST score	308
E value	2.0e-28
Match length	101
% identity	61
NCBI Description	RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN 3B PRECURSOR (RUBISCO SMALL SUBUNIT 3B) >gi_68060_pir__RKMUB3 ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain B3 precursor - Arabidopsis thaliana >gi_16195_emb_CAA32702_ (X14564) ribulose bisphosphate carboxylase [Arabidopsis thaliana]

Seq. No.	161675
Seq. ID	LIB3177-021-P1-K1-C5
Method	BLASTN
NCBI GI	g3249094
BLAST score	53
E value	6.0e-21
Match length	147
% identity	88
NCBI Description	Arabidopsis thaliana chromosome 1 BAC T12M4 sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	161676
Seq. ID	LIB3177-021-P1-K1-C6
Method	BLASTN
NCBI GI	g4589445
BLAST score	61
E value	1.0e-25
Match length	336
% identity	82
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MWL2, complete sequence

Seq. No.	161677
Seq. ID	LIB3177-021-P1-K1-C7
Method	BLASTX
NCBI GI	g1706772
BLAST score	357
E value	4.0e-34
Match length	104

% identity	68
NCBI Description	FARNESYL-DIPHOSPHATE FARNESYLTRANSFERASE (SQUALENE SYNTHETASE) (SQS) (SS) (FPP:FPP FARNESYLTRANSFERASE) >gi_1076324_pir__S54251 farnesyl-diphosphate farnesyltransferase (EC 2.5.1.21) - Arabidopsis thaliana >gi_798820_emb_CAA60385_ (X86692) farnesyl-diphosphate farnesyltransferase [Arabidopsis thaliana] >gi_806325_dbj_BAA06103_ (D29017) squalene synthase [Arabidopsis thaliana] >gi_2232212 (AF004560) squalene synthase 1 [Arabidopsis thaliana] >gi_3096933_emb_CAA18843.1_ (AL023094) farnesyl-diphosphate farnesyltransferase [Arabidopsis thaliana] >gi_4098519 (U79159) squalene synthase [Arabidopsis thaliana]

Seq. No.	161678
Seq. ID	LIB3177-021-P1-K1-D1
Method	BLASTN
NCBI GI	g2924733
BLAST score	33
E value	6.0e-09
Match length	41
% identity	95
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MUF9, complete sequence [Arabidopsis thaliana]

Seq. No.	161679
Seq. ID	LIB3177-021-P1-K1-D2
Method	BLASTX
NCBI GI	g4589962
BLAST score	264
E value	4.0e-23
Match length	85
% identity	68
NCBI Description	(AC007169) putative fructokinase [Arabidopsis thaliana]

Seq. No.	161680
Seq. ID	LIB3177-021-P1-K1-D3
Method	BLASTX
NCBI GI	g2262164
BLAST score	191
E value	1.0e-14
Match length	85
% identity	49
NCBI Description	(AC002329) putative obtusifoliol 14-alpha demethylase [Arabidopsis thaliana]

Seq. No.	161681
Seq. ID	LIB3177-021-P1-K1-D4
Method	BLASTX
NCBI GI	g3193287
BLAST score	294
E value	1.0e-26
Match length	110
% identity	54
NCBI Description	(AF069298) Arabidopsis predicted protein of unknown function T10P11.19 (GB:AC002330) [Arabidopsis thaliana]

Seq. No.	161682
Seq. ID	LIB3177-021-P1-K1-D5
Method	BLASTX
NCBI GI	g3834325
BLAST score	284
E value	2.0e-25
Match length	110
% identity	52
NCBI Description	(AC005679) Strong similarity to gb_AF067141 gamma-glutamyl hydrolase from Arabidopsis thaliana. ESTs gb_R83955, gb_T45062, gb_T22220, gb_AA586207, gb_AI099851 and gb_AI00672 come from this gene. [Arabidopsis thaliana]

Seq. No.	161683
Seq. ID	LIB3177-021-P1-K1-D8
Method	BLASTX
NCBI GI	g115385
BLAST score	393
E value	3.0e-38
Match length	123
% identity	68
NCBI Description	CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR (CAB-4) (LHCP) >gi_166646 (M63931) light-harvesting chlorophyll a/b binding protein [Arabidopsis thaliana]

Seq. No.	161684
Seq. ID	LIB3177-021-P1-K1-E1
Method	BLASTX
NCBI GI	g4678262
BLAST score	269
E value	1.0e-23
Match length	105
% identity	69
NCBI Description	(AL049657) argininosuccinate synthase-like protein [Arabidopsis thaliana]

Seq. No.	161685
Seq. ID	LIB3177-021-P1-K1-E10
Method	BLASTN
NCBI GI	g4519195
BLAST score	73
E value	8.0e-33
Match length	329
% identity	83
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MQC12, complete sequence

Seq. No.	161686
Seq. ID	LIB3177-021-P1-K1-E12
Method	BLASTX
NCBI GI	g2244750
BLAST score	317
E value	3.0e-29
Match length	111
% identity	60
NCBI Description	(Z97335) adenosylhomocysteinase [Arabidopsis thaliana] >gi_3088579 (AF059581) S-adenosyl-L-homocysteine hydrolase

[Arabidopsis thaliana]

Seq. No.	161687
Seq. ID	LIB3177-021-P1-K1-E2
Method	BLASTX
NCBI GI	g1542941
BLAST score	219
E value	9.0e-18
Match length	80
% identity	61
NCBI Description	(X78116) Acetoacetyl-coenzyme A thiolase [Raphanus sativus]

Seq. No.	161688
Seq. ID	LIB3177-021-P1-K1-E3
Method	BLASTX
NCBI GI	g1709825
BLAST score	174
E value	5.0e-13
Match length	61
% identity	64
NCBI Description	PHOTOSYSTEM I REACTION CENTRE SUBUNIT PSAN PRECURSOR (PSI-N) >gi_1237124 (U32176) PSI-N [Arabidopsis thaliana]

Seq. No.	161689
Seq. ID	LIB3177-021-P1-K1-E4
Method	BLASTX
NCBI GI	g2052379
BLAST score	174
E value	1.0e-12
Match length	100
% identity	43
NCBI Description	(U66343) calreticulin [Arabidopsis thaliana]

Seq. No.	161690
Seq. ID	LIB3177-021-P1-K1-E5
Method	BLASTX
NCBI GI	g2497886
BLAST score	239
E value	4.0e-20
Match length	66
% identity	68
NCBI Description	METALLOTHIONEIN-LIKE PROTEIN 2B (MT-2B) >gi_1361999_pir__S57862 metallothionein 2b - Arabidopsis thaliana >gi_1086463 (U11256) metallothionein [Arabidopsis thaliana]

Seq. No.	161691
Seq. ID	LIB3177-021-P1-K1-E7
Method	BLASTN
NCBI GI	g4220640
BLAST score	49
E value	2.0e-18
Match length	170
% identity	81
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MPE11, complete sequence [Arabidopsis thaliana]

Seq. No.	161692
Seq. ID	LIB3177-021-P1-K1-E8
Method	BLASTX
NCBI GI	g461550
BLAST score	232
E value	3.0e-19
Match length	124
% identity	49
NCBI Description	ATP SYNTHASE GAMMA CHAIN 1, CHLOROPLAST PRECURSOR >gi_81635_pir__B39732 H+-transporting ATP synthase (EC 3.6.1.34) gamma-1 chain precursor, chloroplast - Arabidopsis thaliana >gi_166632 (M61741) ATP synthase gamma-subunit [Arabidopsis thaliana]

Seq. No.	161693
Seq. ID	LIB3177-021-P1-K1-E9
Method	BLASTX
NCBI GI	g3236476
BLAST score	145
E value	4.0e-09
Match length	73
% identity	51
NCBI Description	(AF071195) 26S protease regulatory subunit [Gossypium hirsutum]

Seq. No.	161694
Seq. ID	LIB3177-021-P1-K1-F1
Method	BLASTN
NCBI GI	g2264311
BLAST score	80
E value	5.0e-37
Match length	288
% identity	82
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MLN1, complete sequence [Arabidopsis thaliana]

Seq. No.	161695
Seq. ID	LIB3177-021-P1-K1-F10
Method	BLASTX
NCBI GI	g2088654
BLAST score	256
E value	3.0e-22
Match length	108
% identity	55
NCBI Description	(AF002109) 60S acidic ribosomal protein P0 isolog [Arabidopsis thaliana]

Seq. No.	161696
Seq. ID	LIB3177-021-P1-K1-F4
Method	BLASTN
NCBI GI	g2618601
BLAST score	64
E value	1.0e-27
Match length	208
% identity	83
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MHJ24, complete sequence [Arabidopsis thaliana]

Seq. No.	161697
Seq. ID	LIB3177-021-P1-K1-F7
Method	BLASTX
NCBI GI	g3582341
BLAST score	176
E value	8.0e-13
Match length	108
% identity	41
NCBI Description	(AC005496) putative flavonol 3-o-glucosyltransferase [Arabidopsis thaliana]

Seq. No.	161698
Seq. ID	LIB3177-021-P1-K1-G1
Method	BLASTX
NCBI GI	g4510395
BLAST score	258
E value	2.0e-22
Match length	124
% identity	53
NCBI Description	(AC006587) putative beta-galactosidase precursor [Arabidopsis thaliana]

Seq. No.	161699
Seq. ID	LIB3177-021-P1-K1-G3
Method	BLASTX
NCBI GI	g4049349
BLAST score	181
E value	3.0e-13
Match length	108
% identity	40
NCBI Description	(AL034567) ubiquinol-cytochrome c reductase-like protein [Arabidopsis thaliana]

Seq. No.	161700
Seq. ID	LIB3177-021-P1-K1-G5
Method	BLASTX
NCBI GI	g115767
BLAST score	298
E value	3.0e-27
Match length	88
% identity	69
NCBI Description	CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR (CAB-165/180) (LHCP) >gi_81603_pir__A29280 chlorophyll a/b-binding protein ab165 - Arabidopsis thaliana >gi_16368_emb_CAA27540_ (X03907) chlorophyll a/b binding protein (LHCP AB 65) [Arabidopsis thaliana] >gi_16372_emb_CAA27541_ (X03908) chlorophyll a/b binding protein (LHCP AB 180) [Arabidopsis thaliana]

Seq. No.	161701
Seq. ID	LIB3177-021-P1-K1-G8
Method	BLASTN
NCBI GI	g3849811
BLAST score	42
E value	3.0e-14
Match length	327

% identity	81
NCBI Description	Arabidopsis thaliana chromosome I BAC T2P11 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	161702
Seq. ID	LIB3177-021-P1-K1-H10
Method	BLASTN
NCBI GI	g2252848
BLAST score	68
E value	8.0e-30
Match length	356
% identity	81
NCBI Description	Arabidopsis thaliana BAC TM018A10

Seq. No.	161703
Seq. ID	LIB3177-021-P1-K1-H12
Method	BLASTX
NCBI GI	g132102
BLAST score	316
E value	4.0e-29
Match length	111
% identity	61
NCBI Description	RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN 2B PRECURSOR (RUBISCO SMALL SUBUNIT 2B) >gi_68061_pir__RKMUB2 ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain B2 precursor - Arabidopsis thaliana >gi_16194_emb_CAA32701_ (X14564) ribulose bisphosphate carboxylase [Arabidopsis thaliana]

Seq. No.	161704
Seq. ID	LIB3177-021-P1-K1-H4
Method	BLASTX
NCBI GI	g2499811
BLAST score	169
E value	4.0e-12
Match length	56
% identity	55
NCBI Description	PROFILIN 2 >gi_1353766 (U43323) profilin 2 [Arabidopsis thaliana] >gi_1353772 (U43326) profilin 2 [Arabidopsis thaliana]

Seq. No.	161705
Seq. ID	LIB3177-021-P1-K1-H5
Method	BLASTX
NCBI GI	g2864615
BLAST score	177
E value	8.0e-13
Match length	58
% identity	57
NCBI Description	(AL021811) putative protein [Arabidopsis thaliana]

Seq. No.	161706
Seq. ID	LIB3177-021-P1-K1-H6
Method	BLASTX
NCBI GI	g2996158
BLAST score	165
E value	2.0e-11

Match length	44
% identity	66
NCBI Description	(AF051753) GASA5-like protein [Picea mariana] >gi_2996160 (AF051754) GASA5-like protein [Picea mariana]

Seq. No.	161707
Seq. ID	LIB3177-021-P1-K1-H7
Method	BLASTX
NCBI GI	g132102
BLAST score	146
E value	8.0e-10
Match length	55
% identity	64
NCBI Description	RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN 2B PRECURSOR (RUBISCO SMALL SUBUNIT 2B) >gi_68061_pir__RKMUB2 ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain B2 precursor - Arabidopsis thaliana >gi_16194_emb_CAA32701_ (X14564) ribulose bisphosphate carboxylase [Arabidopsis thaliana]

Seq. No.	161708
Seq. ID	LIB3177-021-P1-K1-H9
Method	BLASTX
NCBI GI	g132102
BLAST score	396
E value	2.0e-38
Match length	114
% identity	70
NCBI Description	RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN 2B PRECURSOR (RUBISCO SMALL SUBUNIT 2B) >gi_68061_pir__RKMUB2 ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain B2 precursor - Arabidopsis thaliana >gi_16194_emb_CAA32701_ (X14564) ribulose bisphosphate carboxylase [Arabidopsis thaliana]

Seq. No.	161709
Seq. ID	LIB3177-021-P1-K2-A1
Method	BLASTX
NCBI GI	g2160158
BLAST score	420
E value	2.0e-41
Match length	130
% identity	65
NCBI Description	(AC000132) Similar to elongation factor 1-gamma (gb_EF1G_XENLA). ESTs gb_T20564,gb_T45940,gb_T04527 come from this gene. [Arabidopsis thaliana]

Seq. No.	161710
Seq. ID	LIB3177-021-P1-K2-A11
Method	BLASTX
NCBI GI	g2119846
BLAST score	668
E value	2.0e-70
Match length	130
% identity	98
NCBI Description	chlorophyll a/b-binding protein type I precursor Lhb1B2 - Arabidopsis thaliana >gi_16364_emb_CAA45790_ (X64460)

	photosystem II type I chlorophyll a /b binding protein [Arabidopsis thaliana] >gi_3128230 (AC004077) photosystem II type I chlorophyll a/b binding protein [Arabidopsis thaliana] >gi_3337371 (AC004481) photosystem II type I chlorophyll a/b binding protein [Arabidopsis thaliana]
Seq. No.	161711
Seq. ID	LIB3177-021-P1-K2-A12
Method	BLASTX
NCBI GI	g82040
BLAST score	461
E value	3.0e-46
Match length	103
% identity	23
NCBI Description	ubiquitin precursor - flax (fragment) >gi_168304 (M57895) ubiquitin [Linum usitatissimum]
Seq. No.	161712
Seq. ID	LIB3177-021-P1-K2-A2
Method	BLASTN
NCBI GI	g4056476
BLAST score	90
E value	5.0e-43
Match length	231
% identity	94
NCBI Description	Arabidopsis thaliana chromosome II BAC F3G5 genomic sequence, complete sequence [Arabidopsis thaliana]
Seq. No.	161713
Seq. ID	LIB3177-021-P1-K2-A3
Method	BLASTX
NCBI GI	g1419090
BLAST score	45
E value	5.0e-18
Match length	102
% identity	55
NCBI Description	(X94968) 37kDa chloroplast inner envelope membrane polypeptide precursor [Nicotiana tabacum]
Seq. No.	161714
Seq. ID	LIB3177-021-P1-K2-A4
Method	BLASTX
NCBI GI	g119975
BLAST score	539
E value	3.0e-55
Match length	128
% identity	88
NCBI Description	FERREDOXIN PRECURSOR >gi_99692_pir__S09979 ferredoxin [2Fe-2S] precursor - Arabidopsis thaliana >gi_16437_emb_CAA35754_ (X51370) ferredoxin precursor [Arabidopsis thaliana] >gi_166698 (M35868) ferrodoxin A [Arabidopsis thaliana]
Seq. No.	161715
Seq. ID	LIB3177-021-P1-K2-A6
Method	BLASTX
NCBI GI	g1350768

BLAST score	150
E value	2.0e-43
Match length	121
% identity	86
NCBI Description	60S RIBOSOMAL PROTEIN L7A

Seq. No.	161716
Seq. ID	LIB3177-021-P1-K2-A7
Method	BLASTX
NCBI GI	g115470
BLAST score	330
E value	8.0e-31
Match length	66
% identity	95
NCBI Description	CARBONIC ANHYDRASE, CHLOROPLAST PRECURSOR (CARBONATE DEHYDRATASE) >gi_320554_pir__S28412 carbonate dehydratase (EC 4.2.1.1) precursor - Arabidopsis thaliana >gi_14343_emb_CAA46508_ (X65541) carbonic anhydrase [Arabidopsis thaliana]

Seq. No.	161717
Seq. ID	LIB3177-021-P1-K2-A8
Method	BLASTN
NCBI GI	g2914688
BLAST score	54
E value	6.0e-22
Match length	106
% identity	92
NCBI Description	Arabidopsis thaliana chromosome II BAC F24L7 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	161718
Seq. ID	LIB3177-021-P1-K2-A9
Method	BLASTX
NCBI GI	g4454036
BLAST score	479
E value	3.0e-48
Match length	89
% identity	100
NCBI Description	(AL035394) putative major latex protein [Arabidopsis thaliana]

Seq. No.	161719
Seq. ID	LIB3177-021-P1-K2-B1
Method	BLASTX
NCBI GI	g1781348
BLAST score	159
E value	1.0e-10
Match length	59
% identity	63
NCBI Description	(Y10380) homologous to plastidic aldolases [Solanum tuberosum]

Seq. No.	161720
Seq. ID	LIB3177-021-P1-K2-B2
Method	BLASTX
NCBI GI	g3122753

BLAST score	457
E value	1.0e-45
Match length	87
% identity	98
NCBI Description	60S RIBOSOMAL PROTEIN L44 >gi_2244789_emb_CAB10211.1_ (Z97336) ribosomal protein [Arabidopsis thaliana]

Seq. No.	161721
Seq. ID	LIB3177-021-P1-K2-B3
Method	BLASTN
NCBI GI	g4490701
BLAST score	45
E value	1.0e-16
Match length	65
% identity	94
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone T24A18 (ESSA project)

Seq. No.	161722
Seq. ID	LIB3177-021-P1-K2-B7
Method	BLASTX
NCBI GI	g115385
BLAST score	284
E value	4.0e-34
Match length	81
% identity	96
NCBI Description	CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR (CAB-4) (LHCP) >gi_166646 (M63931) light-harvesting chlorophyll a/b binding protein [Arabidopsis thaliana]

Seq. No.	161723
Seq. ID	LIB3177-021-P1-K2-C1
Method	BLASTN
NCBI GI	g2760165
BLAST score	144
E value	4.0e-75
Match length	439
% identity	98
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MAC9, complete sequence [Arabidopsis thaliana]

Seq. No.	161724
Seq. ID	LIB3177-021-P1-K2-C12
Method	BLASTX
NCBI GI	g2980781
BLAST score	291
E value	2.0e-26
Match length	65
% identity	88
NCBI Description	(AL022198) putative protein [Arabidopsis thaliana]

Seq. No.	161725
Seq. ID	LIB3177-021-P1-K2-C3
Method	BLASTX
NCBI GI	g115385
BLAST score	568
E value	1.0e-58

Match length	109
% identity	100
NCBI Description	CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR (CAB-4) (LHCP) >gi_166646 (M63931) light-harvesting chlorophyll a/b binding protein [Arabidopsis thaliana]

Seq. No.	161726
Seq. ID	LIB3177-021-P1-K2-C7
Method	BLASTX
NCBI GI	g1706772
BLAST score	380
E value	4.0e-40
Match length	134
% identity	70
NCBI Description	FARNESYL-DIPHOSPHATE FARNESYLTRANSFERASE (SQUALENE SYNTHETASE) (SQS) (SS) (FPP:FPP FARNESYLTRANSFERASE) >gi_1076324_pir__S54251 farnesyl-diphosphate farnesyltransferase (EC 2.5.1.21) - Arabidopsis thaliana >gi_798820_emb_CAA60385_ (X86692) farnesyl-diphosphate farnesyltransferase [Arabidopsis thaliana] >gi_806325_dbj_BAA06103_ (D29017) squalene synthase [Arabidopsis thaliana] >gi_2232212 (AF004560) squalene synthase 1 [Arabidopsis thaliana] >gi_3096933_emb_CAA18843.1_ (AL023094) farnesyl-diphosphate farnesyltransferase [Arabidopsis thaliana] >gi_4098519 (U79159) squalene synthase [Arabidopsis thaliana]

Seq. No.	161727
Seq. ID	LIB3177-021-P1-K2-D1
Method	BLASTX
NCBI GI	g2677828
BLAST score	406
E value	1.0e-39
Match length	121
% identity	65
NCBI Description	(U93166) cysteine protease [Prunus armeniaca]

Seq. No.	161728
Seq. ID	LIB3177-021-P1-K2-D2
Method	BLASTX
NCBI GI	g4589962
BLAST score	432
E value	8.0e-43
Match length	88
% identity	98
NCBI Description	(AC007169) putative fructokinase [Arabidopsis thaliana]

Seq. No.	161729
Seq. ID	LIB3177-021-P1-K2-D5
Method	BLASTX
NCBI GI	g2497886
BLAST score	284
E value	2.0e-25
Match length	53
% identity	96
NCBI Description	METALLOTHIONEIN-LIKE PROTEIN 2B (MT-2B) >gi_1361999_pir__S57862 metallothionein 2b - Arabidopsis

	thaliana >gi_1086463 (U11256) metallothionein [Arabidopsis thaliana]
Seq. No.	161730
Seq. ID	LIB3177-021-P1-K2-E1
Method	BLASTN
NCBI GI	g4678258
BLAST score	142
E value	5.0e-74
Match length	399
% identity	99
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F6I7 (ESSA project)
Seq. No.	161731
Seq. ID	LIB3177-021-P1-K2-E12
Method	BLASTX
NCBI GI	g2244750
BLAST score	420
E value	3.0e-41
Match length	112
% identity	73
NCBI Description	(Z97335) adenosylhomocysteinase [Arabidopsis thaliana] >gi_3088579 (AF059581) S-adenosyl-L-homocysteine hydrolase [Arabidopsis thaliana]
Seq. No.	161732
Seq. ID	LIB3177-021-P1-K2-E2
Method	BLASTX
NCBI GI	g461550
BLAST score	150
E value	7.0e-10
Match length	85
% identity	42
NCBI Description	ATP SYNTHASE GAMMA CHAIN 1, CHLOROPLAST PRECURSOR >gi_81635_pir__B39732 H+-transporting ATP synthase (EC 3.6.1.34) gamma-1 chain precursor, chloroplast - Arabidopsis thaliana >gi_166632 (M61741) ATP synthase gamma-subunit [Arabidopsis thaliana]
Seq. No.	161733
Seq. ID	LIB3177-021-P1-K2-E4
Method	BLASTX
NCBI GI	g2052379
BLAST score	458
E value	9.0e-46
Match length	126
% identity	73
NCBI Description	(U66343) calreticulin [Arabidopsis thaliana]
Seq. No.	161734
Seq. ID	LIB3177-021-P1-K2-E5
Method	BLASTN
NCBI GI	g1086462
BLAST score	45
E value	8.0e-17
Match length	53

% identity	96
NCBI Description	Arabidopsis thaliana Columbia ecotype metallothionein (MT2b) gene, complete cds

Seq. No.	161735
Seq. ID	LIB3177-021-P1-K2-E6
Method	BLASTN
NCBI GI	g2244991
BLAST score	60
E value	2.0e-25
Match length	99
% identity	90
NCBI Description	Arabidopsis thaliana DNA chromosome 4, ESSA I contig fragment No

Seq. No.	161736
Seq. ID	LIB3177-021-P1-K2-E8
Method	BLASTX
NCBI GI	g3510256
BLAST score	182
E value	2.0e-13
Match length	71
% identity	45
NCBI Description	(AC005310) unknown protein [Arabidopsis thaliana]

Seq. No.	161737
Seq. ID	LIB3177-021-P1-K2-E9
Method	BLASTN
NCBI GI	g2264311
BLAST score	306
E value	1.0e-172
Match length	347
% identity	97
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MLN1, complete sequence [Arabidopsis thaliana]

Seq. No.	161738
Seq. ID	LIB3177-021-P1-K2-F10
Method	BLASTX
NCBI GI	g2088654
BLAST score	625
E value	2.0e-65
Match length	141
% identity	91
NCBI Description	(AF002109) 60S acidic ribosomal protein P0 isolog [Arabidopsis thaliana]

Seq. No.	161739
Seq. ID	LIB3177-021-P1-K2-F12
Method	BLASTX
NCBI GI	g1703108
BLAST score	639
E value	5.0e-67
Match length	119
% identity	99
NCBI Description	ACTIN 2/7 >gi_2129525_pir__S71210 actin 2 - Arabidopsis thaliana >gi_2129528_pir__S68107 actin 7 - Arabidopsis

	thaliana >gi_1049307 (U37281) actin-2 [Arabidopsis thaliana] >gi_1943863 (U27811) actin7 [Arabidopsis thaliana]
Seq. No.	161740
Seq. ID	LIB3177-021-P1-K2-F2
Method	BLASTX
NCBI GI	g2654122
BLAST score	208
E value	2.0e-16
Match length	90
% identity	53
NCBI Description	(AF034694) ribosomal protein L23a [Arabidopsis thaliana]
Seq. No.	161741
Seq. ID	LIB3177-021-P1-K2-F7
Method	BLASTN
NCBI GI	g2264316
BLAST score	92
E value	4.0e-44
Match length	428
% identity	35
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MRO11, complete sequence [Arabidopsis thaliana]
Seq. No.	161742
Seq. ID	LIB3177-021-P1-K2-F9
Method	BLASTN
NCBI GI	g4510392
BLAST score	33
E value	4.0e-09
Match length	84
% identity	85
NCBI Description	Arabidopsis thaliana chromosome II BAC T17D12 genomic sequence, complete sequence
Seq. No.	161743
Seq. ID	LIB3177-021-P1-K2-G1
Method	BLASTX
NCBI GI	g4510395
BLAST score	613
E value	6.0e-64
Match length	136
% identity	92
NCBI Description	(AC006587) putative beta-galactosidase precursor [Arabidopsis thaliana]
Seq. No.	161744
Seq. ID	LIB3177-021-P1-K2-G2
Method	BLASTX
NCBI GI	g2911060
BLAST score	164
E value	3.0e-11
Match length	136
% identity	22
NCBI Description	(AL021961) putative protein [Arabidopsis thaliana] >gi_3297826_emb_CAA19884.1_ (AL031032) putative protein

[Arabidopsis thaliana]

Seq. No.	161745
Seq. ID	LIB3177-021-P1-K2-G5
Method	BLASTX
NCBI GI	g16374
BLAST score	425
E value	6.0e-42
Match length	88
% identity	93
NCBI Description	(X03908) chlorophyll a/b binding protein (LHCP AB 180) [Arabidopsis thaliana]

Seq. No.	161746
Seq. ID	LIB3177-021-P1-K2-G7
Method	BLASTX
NCBI GI	g231660
BLAST score	148
E value	2.0e-09
Match length	132
% identity	39
NCBI Description	HYPOTHETICAL 226 KD PROTEIN (ORF 1901)

Seq. No.	161747
Seq. ID	LIB3177-021-P1-K2-G8
Method	BLASTN
NCBI GI	g3849811
BLAST score	199
E value	1.0e-108
Match length	281
% identity	98
NCBI Description	Arabidopsis thaliana chromosome I BAC T2P11 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	161748
Seq. ID	LIB3177-021-P1-K2-H10
Method	BLASTN
NCBI GI	g2252848
BLAST score	255
E value	1.0e-141
Match length	437
% identity	99
NCBI Description	Arabidopsis thaliana BAC TM018A10

Seq. No.	161749
Seq. ID	LIB3177-021-P1-K2-H12
Method	BLASTX
NCBI GI	g132102
BLAST score	544
E value	6.0e-56
Match length	113
% identity	96
NCBI Description	RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN 2B PRECURSOR (RUBISCO SMALL SUBUNIT 2B) >gi_68061_pir__RKMUB2 ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain B2 precursor - Arabidopsis thaliana >gi_16194_emb_CAA32701_ (X14564) ribulose bisphosphate carboxylase [Arabidopsis

thaliana]

Seq. No.	161750
Seq. ID	LIB3177-021-P1-K2-H2
Method	BLASTX
NCBI GI	g2499973
BLAST score	407
E value	9.0e-40
Match length	102
% identity	80
NCBI Description	PHOTOSYSTEM II 5 KD PROTEIN PRECURSOR (PSII-T) >gi_1465366_emb_CAA66701_ (X98078) photosystem II [Arabidopsis thaliana]

Seq. No.	161751
Seq. ID	LIB3177-021-P1-K2-H4
Method	BLASTX
NCBI GI	g2499811
BLAST score	616
E value	3.0e-64
Match length	121
% identity	96
NCBI Description	PROFILIN 2 >gi_1353766 (U43323) profilin 2 [Arabidopsis thaliana] >gi_1353772 (U43326) profilin 2 [Arabidopsis thaliana]

Seq. No.	161752
Seq. ID	LIB3177-021-P1-K2-H5
Method	BLASTX
NCBI GI	g2864615
BLAST score	265
E value	4.0e-23
Match length	71
% identity	76
NCBI Description	(AL021811) putative protein [Arabidopsis thaliana]

Seq. No.	161753
Seq. ID	LIB3177-021-P1-K2-H6
Method	BLASTX
NCBI GI	g2982285
BLAST score	352
E value	3.0e-33
Match length	69
% identity	80
NCBI Description	(AF051227) GASA5-like protein [Picea mariana]

Seq. No.	161754
Seq. ID	LIB3177-021-P1-K2-H7
Method	BLASTX
NCBI GI	g132102
BLAST score	699
E value	5.0e-74
Match length	134
% identity	97
NCBI Description	RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN 2B PRECURSOR (RUBISCO SMALL SUBUNIT 2B) >gi_68061_pir__RKMUB2 ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain

B2 precursor - Arabidopsis thaliana >gi_16194_emb_CAA32701_ (X14564) ribulose bisphosphate carboxylase [Arabidopsis thaliana]

Seq. No.	161755
Seq. ID	LIB3177-021-P1-K2-H9
Method	BLASTX
NCBI GI	g132102
BLAST score	628
E value	9.0e-66
Match length	121
% identity	98
NCBI Description	RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN 2B PRECURSOR (RUBISCO SMALL SUBUNIT 2B) >gi_68061_pir__RKMUB2 ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain B2 precursor - Arabidopsis thaliana >gi_16194_emb_CAA32701_ (X14564) ribulose bisphosphate carboxylase [Arabidopsis thaliana]

Seq. No.	161756
Seq. ID	LIB3177-022-P1-K2-A1
Method	BLASTX
NCBI GI	g117238
BLAST score	451
E value	5.0e-45
Match length	129
% identity	76
NCBI Description	MAGNESIUM-CHELATASE SUBUNIT CHLI PRECURSOR (PROTEIN CS/CH-42) (MG-PROTOPORPHYRIN IX CHELATASE) >gi_81656_pir__S12785 protein ch-42 precursor, chloroplast - Arabidopsis thaliana >gi_1020100_emb_CAA62754_ (X91411) protoporphyrin-IX Mg-chetalase [Arabidopsis thaliana] >gi_2832653_emb_CAA16728_ (AL021710) protein ch-42 precursor, chloroplast [Arabidopsis thaliana] >gi_4490290_emb_CAB38561.1_ (X51799) chloroplast protein [Arabidopsis thaliana] >gi_228771_prf__1811226A ccsA gene [Euglena gracilis]

Seq. No.	161757
Seq. ID	LIB3177-022-P1-K2-A2
Method	BLASTN
NCBI GI	g4757662
BLAST score	79
E value	2.0e-36
Match length	277
% identity	87
NCBI Description	Genomic sequence for Arabidopsis thaliana BAC F10B6 from chromosome I, complete sequence

Seq. No.	161758
Seq. ID	LIB3177-022-P1-K2-A4
Method	BLASTX
NCBI GI	g3212869
BLAST score	436
E value	3.0e-43
Match length	94
% identity	85

NCBI Description	(AC004005) unknown protein [Arabidopsis thaliana]

Seq. No.	161759
Seq. ID	LIB3177-022-P1-K2-A5
Method	BLASTX
NCBI GI	g3688162
BLAST score	630
E value	7.0e-66
Match length	124
% identity	66
NCBI Description	(AJ009672) centrin [Arabidopsis thaliana]

Seq. No.	161760
Seq. ID	LIB3177-022-P1-K2-A6
Method	BLASTX
NCBI GI	g2443887
BLAST score	234
E value	1.0e-19
Match length	104
% identity	49
NCBI Description	(AC002294) Similar to transcription factor gb_Z46606_1658307 and others [Arabidopsis thaliana]

Seq. No.	161761
Seq. ID	LIB3177-022-P1-K2-A7
Method	BLASTX
NCBI GI	g2119846
BLAST score	540
E value	2.0e-55
Match length	123
% identity	85
NCBI Description	chlorophyll a/b-binding protein type I precursor Lhb1B2 - Arabidopsis thaliana >gi_16364_emb_CAA45790_ (X64460) photosystem II type I chlorophyll a /b binding protein [Arabidopsis thaliana] >gi_3128230 (AC004077) photosystem II type I chlorophyll a/b binding protein [Arabidopsis thaliana] >gi_3337371 (AC004481) photosystem II type I chlorophyll a/b binding protein [Arabidopsis thaliana]

Seq. No.	161762
Seq. ID	LIB3177-022-P1-K2-A8
Method	BLASTX
NCBI GI	g2829899
BLAST score	291
E value	3.0e-26
Match length	94
% identity	60
NCBI Description	(AC002311) similar to ripening-induced protein, gp_AJ001449_2465015 and major#latex protein, gp_X91961_1107495 [Arabidopsis thaliana]

Seq. No.	161763
Seq. ID	LIB3177-022-P1-K2-B3
Method	BLASTX
NCBI GI	g2506443
BLAST score	407
E value	7.0e-40

Match length	117
% identity	72
NCBI Description	GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE A PRECURSOR, CHLOROPLAST >gi_2117520_pir__JQ1285 glyceraldehyde-3-phosphate dehydrogenase (NADP+) (phosphorylating) (EC 1.2.1.13) A precursor, chloroplast - Arabidopsis thaliana >gi_166704 (M64117) glyceraldehyde 3-phosphate dehydrogenase [Arabidopsis thaliana] >gi_1402885_emb_CAA66816_ (X98130) glyceraldehyde-3-phosphate dehydrogenase (NADP+) (phosphorylating) [Arabidopsis thaliana]

Seq. No.	161764
Seq. ID	LIB3177-022-P1-K2-B8
Method	BLASTN
NCBI GI	g2852453
BLAST score	81
E value	1.0e-37
Match length	121
% identity	92
NCBI Description	Arabidopsis thaliana gene for cystathionine gamma-synthase, complete cds

Seq. No.	161765
Seq. ID	LIB3177-022-P1-K2-C1
Method	BLASTN
NCBI GI	g2760165
BLAST score	114
E value	3.0e-57
Match length	437
% identity	93
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MAC9, complete sequence [Arabidopsis thaliana]

Seq. No.	161766
Seq. ID	LIB3177-022-P1-K2-C11
Method	BLASTX
NCBI GI	g99696
BLAST score	178
E value	3.0e-52
Match length	139
% identity	78
NCBI Description	glutamate--ammonia ligase (EC 6.3.1.2) precursor, chloroplast (clone lambdaAtgs11) - Arabidopsis thaliana >gi_240070_bbs_69728 (S69727) light-regulated glutamine synthetase isoenzyme [Arabidopsis thaliana, Peptide, 430 aa] [Arabidopsis thaliana] >gi_228453_prf__1804333A Gln synthetase [Arabidopsis thaliana]

Seq. No.	161767
Seq. ID	LIB3177-022-P1-K2-C12
Method	BLASTN
NCBI GI	g4079614
BLAST score	209
E value	1.0e-114
Match length	371
% identity	89

NCBI Description	Arabidopsis thaliana chromosome I BAC F21M11 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	161768
Seq. ID	LIB3177-022-P1-K2-C3
Method	BLASTX
NCBI GI	g3859599
BLAST score	440
E value	1.0e-43
Match length	105
% identity	76
NCBI Description	(AF104919) similar to class I chitinases (Pfam: PF00182, E=1.2e-142, N=1) [Arabidopsis thaliana]

Seq. No.	161769
Seq. ID	LIB3177-022-P1-K2-C4
Method	BLASTX
NCBI GI	g1170895
BLAST score	697
E value	9.0e-74
Match length	150
% identity	89
NCBI Description	MALATE DEHYDROGENASE (NADP), CHLOROPLAST PRECURSOR (NADP-MDH) >gi_725262 (L40958) NADP-malate dehydrogenase [Flaveria bidentis]

Seq. No.	161770
Seq. ID	LIB3177-022-P1-K2-C5
Method	BLASTX
NCBI GI	g481223
BLAST score	192
E value	7.0e-15
Match length	86
% identity	52
NCBI Description	malate dehydrogenase (NADP+) (EC 1.1.1.82) - garden pea

Seq. No.	161771
Seq. ID	LIB3177-022-P1-K2-C6
Method	BLASTX
NCBI GI	g493224
BLAST score	53
E value	2.0e-17
Match length	119
% identity	42
NCBI Description	(D14581) fatty-acid desaturase [Anabaena variabilis]

Seq. No.	161772
Seq. ID	LIB3177-022-P1-K2-C9
Method	BLASTX
NCBI GI	g586339
BLAST score	150
E value	1.0e-09
Match length	67
% identity	42
NCBI Description	PEROXISOMAL-COENZYME A SYNTHETASE >gi_626794_pir__S46098 probable AMP-binding protein - yeast (Saccharomyces cerevisiae) >gi_536615_emb_CAA85185_ (Z36091) ORF YBR222c

[Saccharomyces cerevisiae]

Seq. No.	161773
Seq. ID	LIB3177-022-P1-K2-D1
Method	BLASTN
NCBI GI	g2924733
BLAST score	35
E value	3.0e-10
Match length	115
% identity	89
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MUF9, complete sequence [Arabidopsis thaliana]

Seq. No.	161774
Seq. ID	LIB3177-022-P1-K2-D10
Method	BLASTN
NCBI GI	g469113
BLAST score	173
E value	2.0e-92
Match length	332
% identity	88
NCBI Description	A.thaliana (Columbia) Dr4 mRNA

Seq. No.	161775
Seq. ID	LIB3177-022-P1-K2-D3
Method	BLASTX
NCBI GI	g99696
BLAST score	555
E value	3.0e-57
Match length	118
% identity	86
NCBI Description	glutamate--ammonia ligase (EC 6.3.1.2) precursor, chloroplast (clone lambdaAtgs11) - Arabidopsis thaliana >gi_240070_bbs_69728 (S69727) light-regulated glutamine synthetase isoenzyme [Arabidopsis thaliana, Peptide, 430 aa] [Arabidopsis thaliana] >gi_228453_prf__1804333A Gln synthetase [Arabidopsis thaliana]

Seq. No.	161776
Seq. ID	LIB3177-022-P1-K2-D4
Method	BLASTN
NCBI GI	g3688798
BLAST score	246
E value	1.0e-136
Match length	293
% identity	96
NCBI Description	Arabidopsis thaliana gamma tonoplast intrinsic protein 2 (TIP2) mRNA, complete cds

Seq. No.	161777
Seq. ID	LIB3177-022-P1-K2-D9
Method	BLASTX
NCBI GI	g2642215
BLAST score	332
E value	6.0e-31
Match length	79
% identity	78

NCBI Description	(AF030386) NOI protein [Arabidopsis thaliana]
Seq. No.	161778
Seq. ID	LIB3177-022-P1-K2-E1
Method	BLASTX
NCBI GI	g1389699
BLAST score	139
E value	2.0e-16
Match length	81
% identity	59
NCBI Description	(U38845) nitrilase 1 [Arabidopsis thaliana]
Seq. No.	161779
Seq. ID	LIB3177-022-P1-K2-E10
Method	BLASTX
NCBI GI	g3193289
BLAST score	572
E value	4.0e-59
Match length	137
% identity	86
NCBI Description	(AF069298) similar to several small proteins (~100 aa) that are induced by heat, auxin, ethylene and wounding such as Phaseolus aureus indole-3-acetic acid induced protein ARG (SW:32292) [Arabidopsis thaliana]
Seq. No.	161780
Seq. ID	LIB3177-022-P1-K2-E2
Method	BLASTX
NCBI GI	g4204274
BLAST score	96
E value	2.0e-28
Match length	98
% identity	72
NCBI Description	(AC004146) ribulose bisphosphate carboxylase, small subunit [Arabidopsis thaliana]
Seq. No.	161781
Seq. ID	LIB3177-022-P1-K2-E4
Method	BLASTX
NCBI GI	g1169598
BLAST score	725
E value	5.0e-77
Match length	148
% identity	91
NCBI Description	OMEGA-6 FATTY ACID DESATURASE, ENDOPLASMIC RETICULUM (DELTA-12 DESATURASE) >gi_438451 (L26296) delta-12 desaturase [Arabidopsis thaliana]
Seq. No.	161782
Seq. ID	LIB3177-022-P1-K2-E5
Method	BLASTX
NCBI GI	g3687243
BLAST score	245
E value	9.0e-21
Match length	66
% identity	77
NCBI Description	(AC005169) putative ribosomal protein [Arabidopsis

thaliana]

Seq. No.	161783
Seq. ID	LIB3177-022-P1-K2-E7
Method	BLASTX
NCBI GI	g3096935
BLAST score	223
E value	3.0e-18
Match length	88
% identity	53
NCBI Description	(AL023094) putative protein [Arabidopsis thaliana]

Seq. No.	161784
Seq. ID	LIB3177-022-P1-K2-E9
Method	BLASTN
NCBI GI	g4455168
BLAST score	179
E value	5.0e-96
Match length	453
% identity	99
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F10M10 (ESSAII project)

Seq. No.	161785
Seq. ID	LIB3177-022-P1-K2-F10
Method	BLASTX
NCBI GI	g629541
BLAST score	504
E value	4.0e-51
Match length	124
% identity	79
NCBI Description	plasma membrane intrinsic protein 1c - Arabidopsis thaliana >gi_472875_emb_CAA53476_ (X75882) plasma membrane intrinsic protein 1c [Arabidopsis thaliana]

Seq. No.	161786
Seq. ID	LIB3177-022-P1-K2-F11
Method	BLASTN
NCBI GI	g2281081
BLAST score	89
E value	2.0e-42
Match length	300
% identity	72
NCBI Description	Arabidopsis thaliana chromosome II BAC F18O19 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	161787
Seq. ID	LIB3177-022-P1-K2-F4
Method	BLASTX
NCBI GI	g115916
BLAST score	467
E value	2.0e-47
Match length	106
% identity	92
NCBI Description	CELL DIVISION CONTROL PROTEIN 2 HOMOLOG A >gi_282863_pir__S23095 protein kinase (EC 2.7.1.37) cdc2 - Arabidopsis thaliana >gi_251888_bbs_109461 p34cdc2 protein

kinase [Arabidopsis thaliana, flower, Peptide, 294 aa] >gi_16219_emb_CAA40971_ (X57839) p34(cdc2) [Arabidopsis thaliana] >gi_166784 (M59198) protein kinase [Arabidopsis thaliana] >gi_217849_dbj_BAA01623_ (D10850) p32 protein serine/threonine kinase [Arabidopsis thaliana] >gi_257374_bbs_115411 (S45387) Aracdc2=p34cdc2 protein kinase homolog [Arabidopsis thaliana, ecotype Columbia, flowers, Peptide, 294 aa] [Arabidopsis thaliana]

Seq. No.	161788
Seq. ID	LIB3177-022-P1-K2-F6
Method	BLASTN
NCBI GI	g3241917
BLAST score	312
E value	1.0e-175
Match length	400
% identity	98
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K19B1, complete sequence [Arabidopsis thaliana]

Seq. No.	161789
Seq. ID	LIB3177-022-P1-K2-F7
Method	BLASTX
NCBI GI	g133917
BLAST score	172
E value	9.0e-63
Match length	143
% identity	88
NCBI Description	CHLOROPLAST 30S RIBOSOMAL PROTEIN S2 >gi_70856_pir__R3NT2 ribosomal protein S2 - common tobacco chloroplast >gi_11814_emb_CAA77345_ (Z00044) ribosomal protein S2 [Nicotiana tabacum] >gi_225274_prf__1211235J ribosomal protein S2 [Nicotiana tabacum]

Seq. No.	161790
Seq. ID	LIB3177-022-P1-K2-F8
Method	BLASTX
NCBI GI	g4586256
BLAST score	361
E value	1.0e-34
Match length	104
% identity	73
NCBI Description	(AL049640) probable photosystem I chain XI precursor [Arabidopsis thaliana]

Seq. No.	161791
Seq. ID	LIB3177-022-P1-K2-F9
Method	BLASTX
NCBI GI	g3152618
BLAST score	400
E value	6.0e-39
Match length	113
% identity	63
NCBI Description	(AC004482) putative pectinesterase [Arabidopsis thaliana] >gi_3242724 (AC003040) putative pectinesterase [Arabidopsis thaliana]

Seq. No.	161792
Seq. ID	LIB3177-022-P1-K2-G1
Method	BLASTX
NCBI GI	g2129577
BLAST score	244
E value	1.0e-20
Match length	60
% identity	82
NCBI Description	DnaJ homolog protein - Arabidopsis thaliana >gi_727357 (U22340) DnaJ homolog [Arabidopsis thaliana]

Seq. No.	161793
Seq. ID	LIB3177-022-P1-K2-G12
Method	BLASTX
NCBI GI	g1363484
BLAST score	258
E value	2.0e-22
Match length	57
% identity	89
NCBI Description	IAA13 protein - Arabidopsis thaliana >gi_972929 (U18415) IAA13 [Arabidopsis thaliana] >gi_2459414 (AC002332) auxin inducible protein, IAA13 [Arabidopsis thaliana]

Seq. No.	161794
Seq. ID	LIB3177-022-P1-K2-G2
Method	BLASTX
NCBI GI	g132110
BLAST score	192
E value	4.0e-60
Match length	124
% identity	92
NCBI Description	RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN 3B PRECURSOR (RUBISCO SMALL SUBUNIT 3B) >gi_68060_pir__RKMUB3 ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain B3 precursor - Arabidopsis thaliana >gi_16195_emb_CAA32702_ (X14564) ribulose bisphosphate carboxylase [Arabidopsis thaliana]

Seq. No.	161795
Seq. ID	LIB3177-022-P1-K2-G3
Method	BLASTN
NCBI GI	g1669598
BLAST score	191
E value	1.0e-103
Match length	219
% identity	97
NCBI Description	Arabidopsis thaliana mRNA for AR791, complete cds

Seq. No.	161796
Seq. ID	LIB3177-022-P1-K2-G4
Method	BLASTX
NCBI GI	g166708
BLAST score	578
E value	8.0e-60
Match length	133
% identity	87
NCBI Description	(M64118) glyceraldehyde-3-phosphate dehydrogenase

[Arabidopsis thaliana]

Seq. No.	161797
Seq. ID	LIB3177-022-P1-K2-H10
Method	BLASTX
NCBI GI	g4567207
BLAST score	423
E value	1.0e-41
Match length	116
% identity	71
NCBI Description	(AC007168) unknown protein [Arabidopsis thaliana]

Seq. No.	161798
Seq. ID	LIB3177-022-P1-K2-H4
Method	BLASTN
NCBI GI	g4691223
BLAST score	37
E value	7.0e-12
Match length	124
% identity	82
NCBI Description	Arabidopsis thaliana DNA chromosome 3, BAC clone F4F15 (ESSA project)

Seq. No.	161799
Seq. ID	LIB3177-024-P1-K1-A1
Method	BLASTX
NCBI GI	g1350930
BLAST score	309
E value	2.0e-28
Match length	99
% identity	65
NCBI Description	40S RIBOSOMAL PROTEIN S13

Seq. No.	161800
Seq. ID	LIB3177-024-P1-K1-A10
Method	BLASTX
NCBI GI	g1363489
BLAST score	455
E value	2.0e-45
Match length	137
% identity	66
NCBI Description	thioglucosidase (EC 3.2.3.1) 3D precursor - Arabidopsis thaliana >gi_984052_emb_CAA61592_ (X89413) thioglucoside glucohydrolase [Arabidopsis thaliana]

Seq. No.	161801
Seq. ID	LIB3177-024-P1-K1-A12
Method	BLASTX
NCBI GI	g4741960
BLAST score	370
E value	2.0e-35
Match length	94
% identity	78
NCBI Description	(AF134130) Lhcb6 protein [Arabidopsis thaliana]

Seq. No.	161802
Seq. ID	LIB3177-024-P1-K1-A6

Method	BLASTX
NCBI GI	g120667
BLAST score	393
E value	3.0e-38
Match length	125
% identity	66
NCBI Description	GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE, CYTOSOLIC >gi_81622_pir__JQ1287 glyceraldehyde-3-phosphate dehydrogenase (EC 1.2.1.12), cytosolic - Arabidopsis thaliana >gi_166706 (M64116) cystolic glyceraldehyde-3-phosphate dehydrogenase [Arabidopsis thaliana] >gi_166710 (M64119) glyceraldehyde-3-phosphate dehydrogenase [Arabidopsis thaliana]

Seq. No.	161803
Seq. ID	LIB3177-024-P1-K1-A7
Method	BLASTX
NCBI GI	g99688
BLAST score	192
E value	6.0e-36
Match length	129
% identity	67
NCBI Description	translation elongation factor eEF-1 alpha chain (gene A4) - Arabidopsis thaliana >gi_295789_emb_CAA34456_ (X16432) elongation factor 1-alpha [Arabidopsis thaliana]

Seq. No.	161804
Seq. ID	LIB3177-024-P1-K1-A9
Method	BLASTX
NCBI GI	g266936
BLAST score	265
E value	3.0e-23
Match length	101
% identity	58
NCBI Description	50S RIBOSOMAL PROTEIN L27, CHLOROPLAST PRECURSOR (CL27) >gi_282960_pir__A42840 ribosomal protein L27 - common tobacco >gi_170306 (M98473) ribosomal protein L27 [Nicotiana tabacum] >gi_170326 (M75731) ribosomal protein L27 [Nicotiana tabacum]

Seq. No.	161805
Seq. ID	LIB3177-024-P1-K1-B2
Method	BLASTN
NCBI GI	g4521999
BLAST score	78
E value	9.0e-36
Match length	262
% identity	82
NCBI Description	Arabidopsis thaliana chromosome II BAC F2G1 genomic sequence, complete sequence

Seq. No.	161806
Seq. ID	LIB3177-024-P1-K1-B3
Method	BLASTX
NCBI GI	g1172969
BLAST score	195
E value	4.0e-15

Match length	92
% identity	52
NCBI Description	60S RIBOSOMAL PROTEIN L11 (L16) >gi_629552_pir__S49033 ribosomal protein L11.e - Arabidopsis thaliana >gi_550544_emb_CAA57394_ (X81798) ribosomal protein L16 [Arabidopsis thaliana]

Seq. No.	161807
Seq. ID	LIB3177-024-P1-K1-B4
Method	BLASTX
NCBI GI	g3913640
BLAST score	323
E value	5.0e-30
Match length	128
% identity	59
NCBI Description	FRUCTOSE-1,6-BISPHOSPHATASE, CYTOSOLIC (D-FRUCTOSE-1,6-BISPHOSPHATE 1-PHOSPHOHYDROLASE) (FBPASE) >gi_3041775_dbj_BAA25422_ (AB007193) fructose-1,6-bisphosphatase [Oryza sativa]

Seq. No.	161808
Seq. ID	LIB3177-024-P1-K1-B5
Method	BLASTX
NCBI GI	g3983125
BLAST score	217
E value	9.0e-18
Match length	89
% identity	56
NCBI Description	(AF097648) phosphate/triose-phosphate translocator precursor [Arabidopsis thaliana]

Seq. No.	161809
Seq. ID	LIB3177-024-P1-K1-B6
Method	BLASTX
NCBI GI	g1865683
BLAST score	239
E value	3.0e-20
Match length	89
% identity	64
NCBI Description	(Z83321) plastocyanin [Arabidopsis thaliana]

Seq. No.	161810
Seq. ID	LIB3177-024-P1-K1-B7
Method	BLASTX
NCBI GI	g115767
BLAST score	271
E value	5.0e-24
Match length	67
% identity	78
NCBI Description	CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR (CAB-165/180) (LHCP) >gi_81603_pir__A29280 chlorophyll a/b-binding protein ab165 - Arabidopsis thaliana >gi_16368_emb_CAA27540_ (X03907) chlorophyll a/b binding protein (LHCP AB 65) [Arabidopsis thaliana] >gi_16372_emb_CAA27541_ (X03908) chlorophyll a/b binding protein (LHCP AB 180) [Arabidopsis thaliana]

Seq. No.	161811
Seq. ID	LIB3177-024-P1-K1-B9
Method	BLASTX
NCBI GI	g115767
BLAST score	380
E value	1.0e-36
Match length	118
% identity	67
NCBI Description	CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR (CAB-165/180) (LHCP) >gi_81603_pir__A29280 chlorophyll a/b-binding protein ab165 - Arabidopsis thaliana >gi_16368_emb_CAA27540_ (X03907) chlorophyll a/b binding protein (LHCP AB 65) [Arabidopsis thaliana] >gi_16372_emb_CAA27541_ (X03908) chlorophyll a/b binding protein (LHCP AB 180) [Arabidopsis thaliana]

Seq. No.	161812
Seq. ID	LIB3177-024-P1-K1-C12
Method	BLASTN
NCBI GI	g3421122
BLAST score	108
E value	1.0e-53
Match length	310
% identity	84
NCBI Description	Arabidopsis thaliana 20S proteasome beta subunit PBG1 (PBG1) mRNA, complete cds

Seq. No.	161813
Seq. ID	LIB3177-024-P1-K1-C4
Method	BLASTX
NCBI GI	g1938424
BLAST score	169
E value	5.0e-12
Match length	98
% identity	38
NCBI Description	(U97002) similar to acyl-CoA dehydrogenases and epoxide hydrolases [Caenorhabditis elegans]

Seq. No.	161814
Seq. ID	LIB3177-024-P1-K1-C5
Method	BLASTX
NCBI GI	g132110
BLAST score	298
E value	4.0e-27
Match length	97
% identity	65
NCBI Description	RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN 3B PRECURSOR (RUBISCO SMALL SUBUNIT 3B) >gi_68060_pir__RKMUB3 ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain B3 precursor - Arabidopsis thaliana >gi_16195_emb_CAA32702_ (X14564) ribulose bisphosphate carboxylase [Arabidopsis thaliana]

Seq. No.	161815
Seq. ID	LIB3177-024-P1-K1-C8
Method	BLASTX
NCBI GI	g3043536

BLAST score	180
E value	4.0e-13
Match length	78
% identity	55
NCBI Description	(AB000708) SAUR [Raphanus sativus]

Seq. No.	161816
Seq. ID	LIB3177-024-P1-K1-C9
Method	BLASTX
NCBI GI	g2924520
BLAST score	298
E value	5.0e-27
Match length	113
% identity	54
NCBI Description	(AL022023) plasma membrane intrinsic protein (SIMIP) [Arabidopsis thaliana]

Seq. No.	161817
Seq. ID	LIB3177-024-P1-K1-D4
Method	BLASTX
NCBI GI	g1170503
BLAST score	49
E value	3.0e-26
Match length	113
% identity	60
NCBI Description	EUKARYOTIC INITIATION FACTOR 4A-1 (EIF-4A-1) >gi_322503_pir__JC1452 translation initiation factor eIF-4A1 - Arabidopsis thaliana >gi_16554_emb_CAA46188_ (X65052) eukaryotic translation initiation factor 4A-1 [Arabidopsis thaliana]

Seq. No.	161818
Seq. ID	LIB3177-024-P1-K1-D6
Method	BLASTX
NCBI GI	g4585935
BLAST score	415
E value	8.0e-41
Match length	122
% identity	66
NCBI Description	(AC007211) putative chlorophyll A/B binding protein [Arabidopsis thaliana] >gi_4741946_gb_AAD28770.1_AF134123_1 (AF134123) Lhcb2 protein [Arabidopsis thaliana]

Seq. No.	161819
Seq. ID	LIB3177-024-P1-K1-D7
Method	BLASTX
NCBI GI	g3157947
BLAST score	480
E value	2.0e-48
Match length	126
% identity	41
NCBI Description	(AC002131) Similar to protein gb_Z74962 from Brassica oleracea which is similar to bacterial YRN1 and HEAHIO proteins. ESTs gb_T21954, gb_T04283, gb_Z37609, gb_N37366, gb_R90704, gb_F15500 and gb_F14353 come from this gene. [Arabidopsis tha

Seq. No.	161820
Seq. ID	LIB3177-024-P1-K1-D8
Method	BLASTN
NCBI GI	g3985952
BLAST score	68
E value	8.0e-30
Match length	343
% identity	83
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MRC8, complete sequence [Arabidopsis thaliana]

Seq. No.	161821
Seq. ID	LIB3177-024-P1-K1-D9
Method	BLASTX
NCBI GI	g3858935
BLAST score	286
E value	1.0e-25
Match length	128
% identity	50
NCBI Description	(AL021636) synaptobrevin-like protein [Arabidopsis thaliana] >gi_4103357 (AF025332) vesicle-associated membrane protein 7C; synaptobrevin 7C [Arabidopsis thaliana]

Seq. No.	161822
Seq. ID	LIB3177-024-P1-K1-E4
Method	BLASTX
NCBI GI	g2586125
BLAST score	269
E value	1.0e-23
Match length	69
% identity	81
NCBI Description	(U89512) b-keto acyl reductase [Arabidopsis thaliana]

Seq. No.	161823
Seq. ID	LIB3177-024-P1-K1-E5
Method	BLASTX
NCBI GI	g4539308
BLAST score	322
E value	4.0e-30
Match length	94
% identity	69
NCBI Description	(AL049480) possible apospory-associated like protein [Arabidopsis thaliana]

Seq. No.	161824
Seq. ID	LIB3177-024-P1-K1-E7
Method	BLASTX
NCBI GI	g123601
BLAST score	221
E value	3.0e-18
Match length	83
% identity	57
NCBI Description	HEAT SHOCK 70 KD PROTEIN >gi_99913_pir__S14992 heat shock protein, 70K - soybean >gi_18663_emb_CAA44620_ (X62799) Heat Shock 70kD protein [Glycine max]

Seq. No.	161825
Seq. ID	LIB3177-024-P1-K1-E8
Method	BLASTN
NCBI GI	g3449326
BLAST score	79
E value	2.0e-36
Match length	367
% identity	80
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K19M22, complete sequence [Arabidopsis thaliana]

Seq. No.	161826
Seq. ID	LIB3177-024-P1-K1-E9
Method	BLASTX
NCBI GI	g267073
BLAST score	251
E value	2.0e-21
Match length	97
% identity	58
NCBI Description	TUBULIN BETA-2/BETA-3 CHAIN >gi_320184_pir__JQ1587 tubulin beta chain - Arabidopsis thaliana >gi_166898 (M84700) beta-2 tubulin [Arabidopsis thaliana] >gi_166900 (M84701) beta-3 tubulin [Arabidopsis thaliana]

Seq. No.	161827
Seq. ID	LIB3177-024-P1-K1-F2
Method	BLASTN
NCBI GI	g3292807
BLAST score	45
E value	4.0e-16
Match length	192
% identity	90
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F7H19 (ESSAII project)

Seq. No.	161828
Seq. ID	LIB3177-024-P1-K1-F4
Method	BLASTN
NCBI GI	g3449314
BLAST score	88
E value	8.0e-42
Match length	329
% identity	81
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K22F20, complete sequence [Arabidopsis thaliana]

Seq. No.	161829
Seq. ID	LIB3177-024-P1-K1-F6
Method	BLASTN
NCBI GI	g4589434
BLAST score	67
E value	3.0e-29
Match length	159
% identity	91
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MNJ7, complete sequence

Seq. No.	161830
Seq. ID	LIB3177-024-P1-K1-F9
Method	BLASTN
NCBI GI	g2351071
BLAST score	78
E value	5.0e-36
Match length	210
% identity	85
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MVA3, complete sequence [Arabidopsis thaliana]

Seq. No.	161831
Seq. ID	LIB3177-024-P1-K1-G10
Method	BLASTX
NCBI GI	g1710581
BLAST score	290
E value	3.0e-26
Match length	101
% identity	62
NCBI Description	60S RIBOSOMAL PROTEIN L9 >gi_2129720_pir__S71255 ribosomal protein L9 - Arabidopsis thaliana >gi_1107489_emb_CAA63024_ (X91958) 60S ribosomal protein L9 [Arabidopsis thaliana]

Seq. No.	161832
Seq. ID	LIB3177-024-P1-K1-G12
Method	BLASTX
NCBI GI	g132110
BLAST score	154
E value	2.0e-10
Match length	69
% identity	49
NCBI Description	RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN 3B PRECURSOR (RUBISCO SMALL SUBUNIT 3B) >gi_68060_pir__RKMUB3 ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain B3 precursor - Arabidopsis thaliana >gi_16195_emb_CAA32702_ (X14564) ribulose bisphosphate carboxylase [Arabidopsis thaliana]

Seq. No.	161833
Seq. ID	LIB3177-024-P1-K1-G3
Method	BLASTX
NCBI GI	g4454036
BLAST score	373
E value	8.0e-36
Match length	122
% identity	60
NCBI Description	(AL035394) putative major latex protein [Arabidopsis thaliana]

Seq. No.	161834
Seq. ID	LIB3177-024-P1-K1-G4
Method	BLASTX
NCBI GI	g119723
BLAST score	287
E value	6.0e-26
Match length	106
% identity	58

NCBI Description	FRUCTOSE-1,6-BISPHOSPHATASE, CHLOROPLAST PRECURSOR (D-FRUCTOSE-1,6-BISPHOSPHATE 1-PHOSPHOHYDROLASE) (FBPASE) >gi_99693_pir__S16582 fructose-bisphosphatase (EC 3.1.3.11) precursor, chloroplast - Arabidopsis thaliana >gi_11242_emb_CAA41154_ (X58148) fructose-bisphosphatase [Arabidopsis thaliana]
Seq. No.	161835
Seq. ID	LIB3177-024-P1-K1-G8
Method	BLASTX
NCBI GI	g4741954
BLAST score	231
E value	3.0e-19
Match length	66
% identity	70
NCBI Description	(AF134127) Lhcb4.2 protein [Arabidopsis thaliana]
Seq. No.	161836
Seq. ID	LIB3177-024-P1-K1-H11
Method	BLASTX
NCBI GI	g117238
BLAST score	227
E value	7.0e-19
Match length	79
% identity	61
NCBI Description	MAGNESIUM-CHELATASE SUBUNIT CHLI PRECURSOR (PROTEIN CS/CH-42) (MG-PROTOPORPHYRIN IX CHELATASE) >gi_81656_pir__S12785 protein ch-42 precursor, chloroplast - Arabidopsis thaliana >gi_1020100_emb_CAA62754_ (X91411) protoporphyrin-IX Mg-chetalase [Arabidopsis thaliana] >gi_2832653_emb_CAA16728_ (AL021710) protein ch-42 precursor, chloroplast [Arabidopsis thaliana] >gi_4490290_emb_CAB38561.1_ (X51799) chloroplast protein [Arabidopsis thaliana] >gi_228771_prf__1811226A ccsA gene [Euglena gracilis]
Seq. No.	161837
Seq. ID	LIB3177-024-P1-K1-H2
Method	BLASTX
NCBI GI	g2511580
BLAST score	240
E value	3.0e-20
Match length	105
% identity	50
NCBI Description	(Y13179) multicatalytic endopeptidase [Arabidopsis thaliana] >gi_2511582_emb_CAA73623.1_ (Y13180) multicatalytic endopeptidase [Arabidopsis thaliana]
Seq. No.	161838
Seq. ID	LIB3177-024-P1-K1-H4
Method	BLASTX
NCBI GI	g85000
BLAST score	204
E value	4.0e-16
Match length	66
% identity	64
NCBI Description	histone H3 - fruit fly (Drosophila melanogaster)

(fragments)

Seq. No.	161839
Seq. ID	LIB3177-024-P1-K1-H5
Method	BLASTX
NCBI GI	g2654208
BLAST score	173
E value	1.0e-12
Match length	82
% identity	48
NCBI Description	(AF035456) heat shock 70 protein [Spinacia oleracea] >gi_2773050 (AF039083) heat shock 70 protein [Spinacia oleracea]

Seq. No.	161840
Seq. ID	LIB3177-024-P1-K1-H7
Method	BLASTN
NCBI GI	g3641835
BLAST score	65
E value	5.0e-28
Match length	235
% identity	90
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone T4L20 (ESSAII project)

Seq. No.	161841
Seq. ID	LIB3177-024-P1-K1-H8
Method	BLASTX
NCBI GI	g132074
BLAST score	361
E value	2.0e-34
Match length	107
% identity	69
NCBI Description	RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN 1A PRECURSOR (RUBISCO SMALL SUBUNIT 1A) >gi_68063_pir__RKMUA1 ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain A1 precursor - Arabidopsis thaliana

Seq. No.	161842
Seq. ID	LIB3177-024-P1-K1-H9
Method	BLASTX
NCBI GI	g4567319
BLAST score	349
E value	5.0e-33
Match length	108
% identity	66
NCBI Description	(AC005956) putative copper amine oxidase [Arabidopsis thaliana]

Seq. No.	161843
Seq. ID	LIB3177-024-P1-K2-A1
Method	BLASTX
NCBI GI	g1350930
BLAST score	525
E value	1.0e-53
Match length	105
% identity	98

NCBI Description	40S RIBOSOMAL PROTEIN S13

Seq. No.	161844
Seq. ID	LIB3177-024-P1-K2-A11
Method	BLASTX
NCBI GI	g4512671
BLAST score	160
E value	2.0e-11
Match length	66
% identity	53
NCBI Description	(AC006931) unknown protein [Arabidopsis thaliana]

Seq. No.	161845
Seq. ID	LIB3177-024-P1-K2-A12
Method	BLASTX
NCBI GI	g4741960
BLAST score	572
E value	4.0e-59
Match length	127
% identity	86
NCBI Description	(AF134130) Lhcb6 protein [Arabidopsis thaliana]

Seq. No.	161846
Seq. ID	LIB3177-024-P1-K2-A2
Method	BLASTX
NCBI GI	g132074
BLAST score	601
E value	1.0e-62
Match length	112
% identity	96
NCBI Description	RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN 1A PRECURSOR (RUBISCO SMALL SUBUNIT 1A) >gi_68063_pir__RKMUA1 ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain A1 precursor - Arabidopsis thaliana

Seq. No.	161847
Seq. ID	LIB3177-024-P1-K2-A3
Method	BLASTX
NCBI GI	g266936
BLAST score	246
E value	3.0e-21
Match length	78
% identity	67
NCBI Description	50S RIBOSOMAL PROTEIN L27, CHLOROPLAST PRECURSOR (CL27) >gi_282960_pir__A42840 ribosomal protein L27 - common tobacco >gi_170306 (M98473) ribosomal protein L27 [Nicotiana tabacum] >gi_170326 (M75731) ribosomal protein L27 [Nicotiana tabacum]

Seq. No.	161848
Seq. ID	LIB3177-024-P1-K2-A4
Method	BLASTX
NCBI GI	g1363489
BLAST score	725
E value	5.0e-77
Match length	134
% identity	99

NCBI Description	thioglucosidase (EC 3.2.3.1) 3D precursor - Arabidopsis thaliana >gi_984052_emb_CAA61592_ (X89413) thioglucoside glucohydrolase [Arabidopsis thaliana]
Seq. No.	161849
Seq. ID	LIB3177-024-P1-K2-A5
Method	BLASTX
NCBI GI	g1352460
BLAST score	184
E value	2.0e-13
Match length	51
% identity	65
NCBI Description	IN2-1 PROTEIN >gi_100896_pir__S17743 In2-1 protein - maize >gi_22347_emb_CAA41447_ (X58573) In2-1 [Zea mays]
Seq. No.	161850
Seq. ID	LIB3177-024-P1-K2-A6
Method	BLASTX
NCBI GI	g120667
BLAST score	759
E value	5.0e-81
Match length	151
% identity	99
NCBI Description	GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE, CYTOSOLIC >gi_81622_pir__JQ1287 glyceraldehyde-3-phosphate dehydrogenase (EC 1.2.1.12), cytosolic - Arabidopsis thaliana >gi_166706 (M64116) cystolic glyceraldehyde-3-phosphate dehydrogenase [Arabidopsis thaliana] >gi_166710 (M64119) glyceraldehyde-3-phosphate dehydrogenase [Arabidopsis thaliana]
Seq. No.	161851
Seq. ID	LIB3177-024-P1-K2-A9
Method	BLASTX
NCBI GI	g266936
BLAST score	202
E value	5.0e-16
Match length	84
% identity	55
NCBI Description	50S RIBOSOMAL PROTEIN L27, CHLOROPLAST PRECURSOR (CL27) >gi_282960_pir__A42840 ribosomal protein L27 - common tobacco >gi_170306 (M98473) ribosomal protein L27 [Nicotiana tabacum] >gi_170326 (M75731) ribosomal protein L27 [Nicotiana tabacum]
Seq. No.	161852
Seq. ID	LIB3177-024-P1-K2-B1
Method	BLASTX
NCBI GI	g115783
BLAST score	577
E value	8.0e-60
Match length	118
% identity	99
NCBI Description	CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR (CAB-140) (LHCP) >gi_16376_emb_CAA27543_ (X03909) chlorophyll a/b binding protein (LHCP AB 140) [Arabidopsis thaliana]

Seq. No.	161853
Seq. ID	LIB3177-024-P1-K2-B2
Method	BLASTX
NCBI GI	g3122673
BLAST score	647
E value	7.0e-68
Match length	149
% identity	85
NCBI Description	60S RIBOSOMAL PROTEIN L15 >gi_2245027_emb_CAB10447_ (Z97341) ribosomal protein [Arabidopsis thaliana]

Seq. No.	161854
Seq. ID	LIB3177-024-P1-K2-B3
Method	BLASTX
NCBI GI	g115767
BLAST score	574
E value	3.0e-59
Match length	118
% identity	99
NCBI Description	CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR (CAB-165/180) (LHCP) >gi_81603_pir__A29280 chlorophyll a/b-binding protein ab165 - Arabidopsis thaliana >gi_16368_emb_CAA27540_ (X03907) chlorophyll a/b binding protein (LHCP AB 65) [Arabidopsis thaliana] >gi_16372_emb_CAA27541_ (X03908) chlorophyll a/b binding protein (LHCP AB 180) [Arabidopsis thaliana]

Seq. No.	161855
Seq. ID	LIB3177-024-P1-K2-B4
Method	BLASTX
NCBI GI	g1169585
BLAST score	711
E value	2.0e-75
Match length	149
% identity	93
NCBI Description	FRUCTOSE-1,6-BISPHOSPHATASE, CYTOSOLIC (D-FRUCTOSE-1,6-BISPHOSPHATE 1-PHOSPHOHYDROLASE) (FBPASE) >gi_885894 (U20179) fructose 1,6-bisphosphatase [Brassica napus]

Seq. No.	161856
Seq. ID	LIB3177-024-P1-K2-B5
Method	BLASTX
NCBI GI	g3983125
BLAST score	616
E value	3.0e-64
Match length	143
% identity	83
NCBI Description	(AF097648) phosphate/triose-phosphate translocator precursor [Arabidopsis thaliana]

Seq. No.	161857
Seq. ID	LIB3177-024-P1-K2-B6
Method	BLASTX
NCBI GI	g130261
BLAST score	564

E value	4.0e-58
Match length	144
% identity	81
NCBI Description	PLASTOCYANIN PRECURSOR >gi_65841_pir__CUMUM plastocyanin precursor - Arabidopsis thaliana >gi_166790 (M20937) plastocyanin [Arabidopsis thaliana]

Seq. No.	161858
Seq. ID	LIB3177-024-P1-K2-B7
Method	BLASTN
NCBI GI	g4521999
BLAST score	278
E value	1.0e-155
Match length	366
% identity	93
NCBI Description	Arabidopsis thaliana chromosome II BAC F2G1 genomic sequence, complete sequence

Seq. No.	161859
Seq. ID	LIB3177-024-P1-K2-B8
Method	BLASTX
NCBI GI	g1172969
BLAST score	545
E value	4.0e-56
Match length	112
% identity	97
NCBI Description	60S RIBOSOMAL PROTEIN L11 (L16) >gi_629552_pir__S49033 ribosomal protein L11.e - Arabidopsis thaliana >gi_550544_emb_CAA57394_ (X81798) ribosomal protein L16 [Arabidopsis thaliana]

Seq. No.	161860
Seq. ID	LIB3177-024-P1-K2-C1
Method	BLASTX
NCBI GI	g4539376
BLAST score	177
E value	8.0e-13
Match length	84
% identity	56
NCBI Description	(AL049525) hypothetical protein [Arabidopsis thaliana]

Seq. No.	161861
Seq. ID	LIB3177-024-P1-K2-C12
Method	BLASTX
NCBI GI	g3421123
BLAST score	567
E value	1.0e-58
Match length	112
% identity	98
NCBI Description	(AF043538) 20S proteasome beta subunit PBG1 [Arabidopsis thaliana]

Seq. No.	161862
Seq. ID	LIB3177-024-P1-K2-C2
Method	BLASTX
NCBI GI	g3043536
BLAST score	384

E value	5.0e-37
Match length	89
% identity	88
NCBI Description	(AB000708) SAUR [Raphanus sativus]

Seq. No.	161863
Seq. ID	LIB3177-024-P1-K2-C3
Method	BLASTX
NCBI GI	g2924520
BLAST score	753
E value	3.0e-80
Match length	144
% identity	99
NCBI Description	(AL022023) plasma membrane intrinsic protein (SIMIP) [Arabidopsis thaliana]

Seq. No.	161864
Seq. ID	LIB3177-024-P1-K2-C4
Method	BLASTX
NCBI GI	g1938424
BLAST score	244
E value	5.0e-31
Match length	135
% identity	54
NCBI Description	(U97002) similar to acyl-CoA dehydrogenases and epoxide hydrolases [Caenorhabditis elegans]

Seq. No.	161865
Seq. ID	LIB3177-024-P1-K2-C5
Method	BLASTX
NCBI GI	g132110
BLAST score	526
E value	1.0e-55
Match length	114
% identity	93
NCBI Description	RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN 3B PRECURSOR (RUBISCO SMALL SUBUNIT 3B) >gi_68060_pir__RKMUB3 ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain B3 precursor - Arabidopsis thaliana >gi_16195_emb_CAA32702_ (X14564) ribulose bisphosphate carboxylase [Arabidopsis thaliana]

Seq. No.	161866
Seq. ID	LIB3177-024-P1-K2-C6
Method	BLASTX
NCBI GI	g3980386
BLAST score	431
E value	1.0e-42
Match length	99
% identity	85
NCBI Description	(AC004561) putative glutathione S-transferase [Arabidopsis thaliana]

Seq. No.	161867
Seq. ID	LIB3177-024-P1-K2-C8
Method	BLASTX
NCBI GI	g3913640

BLAST score	229
E value	2.0e-19
Match length	98
% identity	52
NCBI Description	FRUCTOSE-1,6-BISPHOSPHATASE, CYTOSOLIC (D-FRUCTOSE-1,6-BISPHOSPHATE 1-PHOSPHOHYDROLASE) (FBPASE) >gi_3041775_dbj_BAA25422_ (AB007193) fructose-1,6-bisphosphatase [Oryza sativa]

Seq. No.	161868
Seq. ID	LIB3177-024-P1-K2-D1
Method	BLASTX
NCBI GI	g3157947
BLAST score	721
E value	1.0e-76
Match length	137
% identity	54
NCBI Description	(AC002131) Similar to protein gb_Z74962 from Brassica oleracea which is similar to bacterial YRN1 and HEAHIO proteins. ESTs gb_T21954, gb_T04283, gb_Z37609, gb_N37366, gb_R90704, gb_F15500 and gb_F14353 come from this gene. [Arabidopsis tha

Seq. No.	161869
Seq. ID	LIB3177-024-P1-K2-D2
Method	BLASTN
NCBI GI	g3985952
BLAST score	270
E value	1.0e-150
Match length	411
% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MRC8, complete sequence [Arabidopsis thaliana]

Seq. No.	161870
Seq. ID	LIB3177-024-P1-K2-D3
Method	BLASTX
NCBI GI	g3858935
BLAST score	496
E value	3.0e-50
Match length	129
% identity	71
NCBI Description	(AL021636) synaptobrevin-like protein [Arabidopsis thaliana] >gi_4103357 (AF025332) vesicle-associated membrane protein 7C; synaptobrevin 7C [Arabidopsis thaliana]

Seq. No.	161871
Seq. ID	LIB3177-024-P1-K2-D4
Method	BLASTX
NCBI GI	g1170503
BLAST score	623
E value	3.0e-65
Match length	129
% identity	95
NCBI Description	EUKARYOTIC INITIATION FACTOR 4A-1 (EIF-4A-1) >gi_322503_pir__JC1452 translation initiation factor

eIF-4A1 - Arabidopsis thaliana >gi_16554_emb_CAA46188_ (X65052) eukaryotic translation initiation factor 4A-1 [Arabidopsis thaliana]

Seq. No.	161872
Seq. ID	LIB3177-024-P1-K2-D6
Method	BLASTX
NCBI GI	g4585935
BLAST score	714
E value	8.0e-76
Match length	136
% identity	99
NCBI Description	(AC007211) putative chlorophyll A/B binding protein [Arabidopsis thaliana] >gi_4741946_gb_AAD28770.1_AF134123_1 (AF134123) Lhcb2 protein [Arabidopsis thaliana]

Seq. No.	161873
Seq. ID	LIB3177-024-P1-K2-D7
Method	BLASTX
NCBI GI	g2119848
BLAST score	200
E value	4.0e-16
Match length	46
% identity	85
NCBI Description	chlorophyll a/b-binding protein type I precursor Lhb1B1 - Arabidopsis thaliana >gi_16366_emb_CAA45789_ (X64459) photosystem II type I chlorophyll a /b binding protein [Arabidopsis thaliana] >gi_3128229 (AC004077) putative photosystem II type I chlorophyll a/b binding protein [Arabidopsis thaliana] >gi_3337372 (AC004481) putative photosystem II type I chlorophyll a/b binding protein [Arabidopsis thaliana]

Seq. No.	161874
Seq. ID	LIB3177-024-P1-K2-D9
Method	BLASTN
NCBI GI	g3241917
BLAST score	69
E value	1.0e-30
Match length	113
% identity	90
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K19B1, complete sequence [Arabidopsis thaliana]

Seq. No.	161875
Seq. ID	LIB3177-024-P1-K2-E1
Method	BLASTX
NCBI GI	g2642648
BLAST score	572
E value	4.0e-59
Match length	141
% identity	80
NCBI Description	(AF033852) cytosolic heat shock 70 protein; HSC70-3 [Spinacia oleracea] >gi_2660768 (AF034616) cytosolic heat shock 70 protein [Spinacia oleracea] >gi_2660770 (AF034617) cytosolic heat shock 70 protein [Spinacia oleracea]

Seq. No.	161876
Seq. ID	LIB3177-024-P1-K2-E2
Method	BLASTX
NCBI GI	g3335378
BLAST score	292
E value	3.0e-26
Match length	66
% identity	82
NCBI Description	(AC003028) Myb-related transcription activator [Arabidopsis thaliana]

Seq. No.	161877
Seq. ID	LIB3177-024-P1-K2-E3
Method	BLASTX
NCBI GI	g267082
BLAST score	482
E value	1.0e-48
Match length	93
% identity	99
NCBI Description	TUBULIN BETA-8 CHAIN >gi_320189_pir__JQ1592 tubulin beta-8 chain - Arabidopsis thaliana >gi_166908 (M84705) beta-8 tubulin [Arabidopsis thaliana]

Seq. No.	161878
Seq. ID	LIB3177-024-P1-K2-E4
Method	BLASTX
NCBI GI	g2586127
BLAST score	383
E value	6.0e-37
Match length	142
% identity	52
NCBI Description	(U89510) b-keto acyl reductase [Hordeum vulgare]

Seq. No.	161879
Seq. ID	LIB3177-024-P1-K2-E5
Method	BLASTX
NCBI GI	g4539308
BLAST score	671
E value	1.0e-70
Match length	129
% identity	98
NCBI Description	(AL049480) possible apospory-associated like protein [Arabidopsis thaliana]

Seq. No.	161880
Seq. ID	LIB3177-024-P1-K2-E8
Method	BLASTX
NCBI GI	g115767
BLAST score	697
E value	8.0e-74
Match length	136
% identity	95
NCBI Description	CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR (CAB-165/180) (LHCP) >gi_81603_pir__A29280 chlorophyll a/b-binding protein ab165 - Arabidopsis thaliana >gi_16368_emb_CAA27540_ (X03907) chlorophyll a/b binding protein (LHCP AB 65) [Arabidopsis thaliana]

	>gi_16372_emb_CAA27541_ (X03908) chlorophyll a/b binding protein (LHCP AB 180) [Arabidopsis thaliana]
Seq. No.	161881
Seq. ID	LIB3177-024-P1-K2-F4
Method	BLASTN
NCBI GI	g3449314
BLAST score	428
E value	0.0e+00
Match length	438
% identity	99
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K22F20, complete sequence [Arabidopsis thaliana]
Seq. No.	161882
Seq. ID	LIB3177-024-P1-K2-F5
Method	BLASTN
NCBI GI	g2828266
BLAST score	51
E value	9.0e-20
Match length	278
% identity	81
NCBI Description	Arabidopsis thaliana mRNA for geranylgeranyl reductase
Seq. No.	161883
Seq. ID	LIB3177-024-P1-K2-F6
Method	BLASTN
NCBI GI	g4589434
BLAST score	98
E value	1.0e-47
Match length	418
% identity	98
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MNJ7, complete sequence
Seq. No.	161884
Seq. ID	LIB3177-024-P1-K2-F8
Method	BLASTX
NCBI GI	g4335755
BLAST score	138
E value	1.0e-08
Match length	54
% identity	59
NCBI Description	(AC006284) putative hydroxyproline-rich glycoprotein [Arabidopsis thaliana]
Seq. No.	161885
Seq. ID	LIB3177-024-P1-K2-G10
Method	BLASTX
NCBI GI	g1710581
BLAST score	567
E value	1.0e-58
Match length	128
% identity	88
NCBI Description	60S RIBOSOMAL PROTEIN L9 >gi_2129720_pir__S71255 ribosomal protein L9 - Arabidopsis thaliana >gi_1107489_emb_CAA63024_ (X91958) 60S ribosomal protein L9 [Arabidopsis thaliana]

Seq. No.	161886
Seq. ID	LIB3177-024-P1-K2-G12
Method	BLASTX
NCBI GI	g132110
BLAST score	502
E value	2.0e-58
Match length	123
% identity	94
NCBI Description	RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN 3B PRECURSOR (RUBISCO SMALL SUBUNIT 3B) >gi_68060_pir__RKMUB3 ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain B3 precursor - Arabidopsis thaliana >gi_16195_emb_CAA32702_ (X14564) ribulose bisphosphate carboxylase [Arabidopsis thaliana]

Seq. No.	161887
Seq. ID	LIB3177-024-P1-K2-G2
Method	BLASTX
NCBI GI	g4741954
BLAST score	390
E value	6.0e-38
Match length	75
% identity	100
NCBI Description	(AF134127) Lhcb4.2 protein [Arabidopsis thaliana]

Seq. No.	161888
Seq. ID	LIB3177-024-P1-K2-G3
Method	BLASTX
NCBI GI	g4457221
BLAST score	302
E value	2.0e-27
Match length	125
% identity	50
NCBI Description	(AF127797) putative bZIP DNA-binding protein [Capsicum chinense]

Seq. No.	161889
Seq. ID	LIB3177-024-P1-K2-G4
Method	BLASTX
NCBI GI	g119723
BLAST score	684
E value	3.0e-72
Match length	139
% identity	96
NCBI Description	FRUCTOSE-1,6-BISPHOSPHATASE, CHLOROPLAST PRECURSOR (D-FRUCTOSE-1,6-BISPHOSPHATE 1-PHOSPHOHYDROLASE) (FBPASE) >gi_99693_pir__S16582 fructose-bisphosphatase (EC 3.1.3.11) precursor, chloroplast - Arabidopsis thaliana >gi_11242_emb_CAA41154_ (X58148) fructose-bisphosphatase [Arabidopsis thaliana]

Seq. No.	161890
Seq. ID	LIB3177-024-P1-K2-G5
Method	BLASTX
NCBI GI	g4218951
BLAST score	182

E value	1.0e-13
Match length	69
% identity	52
NCBI Description	(AF081796) fructose-1,6-bisphosphatase precursor [Brassica napus]

Seq. No.	161891
Seq. ID	LIB3177-024-P1-K2-G8
Method	BLASTX
NCBI GI	g4454036
BLAST score	422
E value	1.0e-41
Match length	100
% identity	80
NCBI Description	(AL035394) putative major latex protein [Arabidopsis thaliana]

Seq. No.	161892
Seq. ID	LIB3177-024-P1-K2-H1
Method	BLASTN
NCBI GI	g3641835
BLAST score	364
E value	0.0e+00
Match length	424
% identity	96
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone T4L20 (ESSAII project)

Seq. No.	161893
Seq. ID	LIB3177-024-P1-K2-H11
Method	BLASTX
NCBI GI	g117238
BLAST score	489
E value	2.0e-49
Match length	109
% identity	90
NCBI Description	MAGNESIUM-CHELATASE SUBUNIT CHLI PRECURSOR (PROTEIN CS/CH-42) (MG-PROTOPORPHYRIN IX CHELATASE) >gi_81656_pir__S12785 protein ch-42 precursor, chloroplast - Arabidopsis thaliana >gi_1020100_emb_CAA62754_ (X91411) protoporphyrin-IX Mg-chetalase [Arabidopsis thaliana] >gi_2832653_emb_CAA16728_ (AL021710) protein ch-42 precursor, chloroplast [Arabidopsis thaliana] >gi_4490290_emb_CAB38561.1_ (X51799) chloroplast protein [Arabidopsis thaliana] >gi_228771_prf__1811226A ccsA gene [Euglena gracilis]

Seq. No.	161894
Seq. ID	LIB3177-024-P1-K2-H2
Method	BLASTX
NCBI GI	g132074
BLAST score	695
E value	1.0e-73
Match length	135
% identity	96
NCBI Description	RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN 1A PRECURSOR (RUBISCO SMALL SUBUNIT 1A) >gi_68063_pir__RKMUA1

ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain A1 precursor - Arabidopsis thaliana

Seq. No.	161895
Seq. ID	LIB3177-024-P1-K2-H4
Method	BLASTX
NCBI GI	g417103
BLAST score	534
E value	1.0e-54
Match length	108
% identity	99
NCBI Description	HISTONE H3.2, MINOR >gi_282871_pir__S24346 histone H3.3-like protein - Arabidopsis thaliana >gi_16324_emb_CAA42957_ (X60429) histone H3.3 like protein [Arabidopsis thaliana] >gi_404825_emb_CAA42958_ (X60429) histone H3.3 like protein [Arabidopsis thaliana] >gi_488563 (U09458) histone H3.2 [Medicago sativa] >gi_488567 (U09460) histone H3.2 [Medicago sativa] >gi_488569 (U09461) histone H3.2 [Medicago sativa] >gi_488575 (U09464) histone H3.2 [Medicago sativa] >gi_488577 (U09465) histone H3.2 [Medicago sativa] >gi_510911_emb_CAA56153_ (X79714) histone H3 [Lolium temulentum] >gi_1435157_emb_CAA58445_ (X83422) histone H3 variant H3.3 [Lycopersicon esculentum] >gi_2558944 (AF024716) histone 3 [Gossypium hirsutum] >gi_3273350_dbj_BAA31218_ (AB015760) histone H3 [Nicotiana tabacum] >gi_3885890 (AF093633) histone H3 [Oryza sativa] >gi_4038469_gb_AAC97380_ (AF109910) histone H3 [Porteresia coarctata] >gi_4490754_emb_CAB38916.1_ (AL035708) histone H3.3 [Arabidopsis thaliana] >gi_4490755_emb_CAB38917.1_ (AL035708) Histon H3 [Arabidopsis thaliana]

Seq. No.	161896
Seq. ID	LIB3177-024-P1-K2-H5
Method	BLASTX
NCBI GI	g3114753
BLAST score	156
E value	9.0e-11
Match length	79
% identity	44
NCBI Description	(Y17165) heat shock protein DnaK [Campylobacter jejuni]

Seq. No.	161897
Seq. ID	LIB3177-024-P1-K2-H7
Method	BLASTX
NCBI GI	g2511580
BLAST score	570
E value	7.0e-59
Match length	127
% identity	91
NCBI Description	(Y13179) multicatalytic endopeptidase [Arabidopsis thaliana] >gi_2511582_emb_CAA73623.1_ (Y13180) multicatalytic endopeptidase [Arabidopsis thaliana]

Seq. No.	161898
Seq. ID	LIB3177-025-P1-K2-A1
Method	BLASTX
NCBI GI	g4091806

BLAST score	340
E value	5.0e-32
Match length	86
% identity	70
NCBI Description	(AF052585) CONSTANS-like protein 2 [Malus domestica]

Seq. No.	161899
Seq. ID	LIB3177-025-P1-K2-A10
Method	BLASTX
NCBI GI	g4510345
BLAST score	197
E value	3.0e-15
Match length	46
% identity	76
NCBI Description	(AC006921) unknown protein [Arabidopsis thaliana]

Seq. No.	161900
Seq. ID	LIB3177-025-P1-K2-A11
Method	BLASTX
NCBI GI	g4204793
BLAST score	182
E value	2.0e-13
Match length	149
% identity	14
NCBI Description	(U52079) P-glycoprotein [Solanum tuberosum].

Seq. No.	161901
Seq. ID	LIB3177-025-P1-K2-A2
Method	BLASTN
NCBI GI	g2854069
BLAST score	131
E value	2.0e-67
Match length	187
% identity	93
NCBI Description	Arabidopsis thaliana putative histone deacetylase (HD2) mRNA, complete cds

Seq. No.	161902
Seq. ID	LIB3177-025-P1-K2-A3
Method	BLASTX
NCBI GI	g1518540
BLAST score	604
E value	7.0e-63
Match length	130
% identity	91
NCBI Description	(U53418) UDP-glucose dehydrogenase [Glycine max]

Seq. No.	161903
Seq. ID	LIB3177-025-P1-K2-A7
Method	BLASTX
NCBI GI	g4666287
BLAST score	278
E value	1.0e-24
Match length	122
% identity	39
NCBI Description	(D85764) cytosolic monodehydroascorbate reductase [Oryza sativa]

Seq. No.	161904
Seq. ID	LIB3177-025-P1-K2-A8
Method	BLASTN
NCBI GI	g4584531
BLAST score	67
E value	1.0e-29
Match length	112
% identity	94
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone T9E8 (ESSA project)

Seq. No.	161905
Seq. ID	LIB3177-025-P1-K2-A9
Method	BLASTN
NCBI GI	g4584531
BLAST score	79
E value	2.0e-36
Match length	199
% identity	93
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone T9E8 (ESSA project)

Seq. No.	161906
Seq. ID	LIB3177-025-P1-K2-B10
Method	BLASTX
NCBI GI	g4468979
BLAST score	544
E value	8.0e-56
Match length	113
% identity	86
NCBI Description	(AL035605) putative protein [Arabidopsis thaliana]

Seq. No.	161907
Seq. ID	LIB3177-025-P1-K2-B12
Method	BLASTX
NCBI GI	g4585882
BLAST score	596
E value	6.0e-62
Match length	121
% identity	98
NCBI Description	(AC005850) PSI type III chlorophyll a/b-binding protein [Arabidopsis thaliana]

Seq. No.	161908
Seq. ID	LIB3177-025-P1-K2-B2
Method	BLASTN
NCBI GI	g4586241
BLAST score	54
E value	4.0e-22
Match length	66
% identity	95
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone T20K18 (ESSA project)

Seq. No.	161909
Seq. ID	LIB3177-025-P1-K2-B5

Method	BLASTN
NCBI GI	g4468801
BLAST score	325
E value	0.0e+00
Match length	463
% identity	100
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F6G17 (ESSA project)

Seq. No.	161910
Seq. ID	LIB3177-025-P1-K2-B7
Method	BLASTX
NCBI GI	g548655
BLAST score	434
E value	4.0e-43
Match length	96
% identity	95
NCBI Description	50S RIBOSOMAL PROTEIN L12-C, CHLOROPLAST PRECURSOR (CL12-C) >gi_541897_pir__C53394 ribosomal protein L12.C, chloroplast - Arabidopsis thaliana >gi_468773_emb_CAA48183_ (X68046) ribosomal protein L12 [Arabidopsis thaliana]

Seq. No.	161911
Seq. ID	LIB3177-025-P1-K2-C10
Method	BLASTX
NCBI GI	g1168728
BLAST score	775
E value	7.0e-83
Match length	140
% identity	99
NCBI Description	CINNAMYL-ALCOHOL DEHYDROGENASE 1 (CAD) >gi_598071 (L37883) cinnamyl-alcohol dehydrogenase [Arabidopsis thaliana]

Seq. No.	161912
Seq. ID	LIB3177-025-P1-K2-C11
Method	BLASTX
NCBI GI	g1168728
BLAST score	207
E value	2.0e-16
Match length	110
% identity	46
NCBI Description	CINNAMYL-ALCOHOL DEHYDROGENASE 1 (CAD) >gi_598071 (L37883) cinnamyl-alcohol dehydrogenase [Arabidopsis thaliana]

Seq. No.	161913
Seq. ID	LIB3177-025-P1-K2-C12
Method	BLASTX
NCBI GI	g115767
BLAST score	438
E value	1.0e-43
Match length	95
% identity	92
NCBI Description	CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR (CAB-165/180) (LHCP) >gi_81603_pir__A29280 chlorophyll a/b-binding protein ab165 - Arabidopsis thaliana >gi_16368_emb_CAA27540_ (X03907) chlorophyll a/b binding protein (LHCP AB 65) [Arabidopsis thaliana]

>gi_16372_emb_CAA27541_ (X03908) chlorophyll a/b binding protein (LHCP AB 180) [Arabidopsis thaliana]

Seq. No.	161914
Seq. ID	LIB3177-025-P1-K2-C3
Method	BLASTX
NCBI GI	g2829904
BLAST score	583
E value	2.0e-60
Match length	134
% identity	87
NCBI Description	(AC002311) Hypothetical protein [Arabidopsis thaliana]

Seq. No.	161915
Seq. ID	LIB3177-025-P1-K2-C7
Method	BLASTX
NCBI GI	g100490
BLAST score	583
E value	2.0e-60
Match length	127
% identity	26
NCBI Description	polyubiquitin - garden snapdragon (fragment) >gi_16071_emb_CAA48140_ (X67957) ubiquitin [Antirrhinum majus]

Seq. No.	161916
Seq. ID	LIB3177-025-P1-K2-D10
Method	BLASTX
NCBI GI	g132863
BLAST score	714
E value	9.0e-76
Match length	141
% identity	95
NCBI Description	CHLOROPLAST 50S RIBOSOMAL PROTEIN L2 >gi_12214_emb_CAA46568_ (X65615) ribosomal protein L2 [Sinapis alba]

Seq. No.	161917
Seq. ID	LIB3177-025-P1-K2-D12
Method	BLASTX
NCBI GI	g2499476
BLAST score	166
E value	7.0e-12
Match length	81
% identity	48
NCBI Description	2-CYS PEROXIREDOXIN BAS1 PRECURSOR >gi_1498198_emb_CAA63909_ (X94218) 2-Cys peroxiredoxin bas1 [Arabidopsis thaliana] >gi_1783308_emb_CAA71503_ (Y10478) 2-Cys peroxiredoxin [Arabidopsis thaliana]

Seq. No.	161918
Seq. ID	LIB3177-025-P1-K2-D2
Method	BLASTX
NCBI GI	g1708313
BLAST score	579
E value	6.0e-60
Match length	118

% identity	100
NCBI Description	HEAT SHOCK PROTEIN 81-3 (HSP81-3) >gi_999396_bbs_163637 (S77849) heat-shock Protein=HSP81-3 [Arabidopsis thaliana=thale-cress, Peptide, 699 aa] [Arabidopsis thaliana]

Seq. No.	161919
Seq. ID	LIB3177-025-P1-K2-D3
Method	BLASTX
NCBI GI	g1389699
BLAST score	427
E value	5.0e-42
Match length	90
% identity	93
NCBI Description	(U38845) nitrilase 1 [Arabidopsis thaliana]

Seq. No.	161920
Seq. ID	LIB3177-025-P1-K2-D4
Method	BLASTX
NCBI GI	g3421123
BLAST score	648
E value	5.0e-68
Match length	126
% identity	98
NCBI Description	(AF043538) 20S proteasome beta subunit PBG1 [Arabidopsis thaliana]

Seq. No.	161921
Seq. ID	LIB3177-025-P1-K2-D7
Method	BLASTX
NCBI GI	g132090
BLAST score	431
E value	8.0e-43
Match length	92
% identity	93
NCBI Description	RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN 1B PRECURSOR (RUBISCO SMALL SUBUNIT 1B) >gi_68062_pir__RKMUB1 ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain B1 precursor - Arabidopsis thaliana >gi_16193_emb_CAA32700_ (X14564) ribulose bisphosphate carboxylase [Arabidopsis thaliana]

Seq. No.	161922
Seq. ID	LIB3177-025-P1-K2-E10
Method	BLASTN
NCBI GI	g2245031
BLAST score	184
E value	5.0e-99
Match length	268
% identity	91
NCBI Description	Arabidopsis thaliana DNA chromosome 4, ESSA I contig fragment No

Seq. No.	161923
Seq. ID	LIB3177-025-P1-K2-E11
Method	BLASTX
NCBI GI	g4371297

BLAST score	758
E value	7.0e-81
Match length	154
% identity	95
NCBI Description	(AC006260) phenylalanine ammonia-lyase 1, 3' partial [Arabidopsis thaliana]

Seq. No.	161924
Seq. ID	LIB3177-025-P1-K2-E12
Method	BLASTN
NCBI GI	g3702734
BLAST score	338
E value	0.0e+00
Match length	438
% identity	94
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MNB8, complete sequence [Arabidopsis thaliana]

Seq. No.	161925
Seq. ID	LIB3177-025-P1-K2-E2
Method	BLASTX
NCBI GI	g4741948
BLAST score	639
E value	6.0e-67
Match length	126
% identity	95
NCBI Description	(AF134124) Lhcb2 protein [Arabidopsis thaliana]

Seq. No.	161926
Seq. ID	LIB3177-025-P1-K2-E3
Method	BLASTN
NCBI GI	g4220468
BLAST score	283
E value	1.0e-158
Match length	447
% identity	96
NCBI Description	Arabidopsis thaliana chromosome II BAC T8O11 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	161927
Seq. ID	LIB3177-025-P1-K2-E5
Method	BLASTX
NCBI GI	g2829899
BLAST score	243
E value	9.0e-31
Match length	114
% identity	61
NCBI Description	(AC002311) similar to ripening-induced protein, gp_AJ001449_2465015 and major#latex protein, gp_X91961_1107495 [Arabidopsis thaliana]

Seq. No.	161928
Seq. ID	LIB3177-025-P1-K2-E7
Method	BLASTN
NCBI GI	g16367
BLAST score	46
E value	9.0e-17

Match length	164
% identity	91
NCBI Description	A.thaliana gene (LHCP AB 165) for chlorophyll a/b binding protein

Seq. No.	161929
Seq. ID	LIB3177-025-P1-K2-E8
Method	BLASTX
NCBI GI	g416681
BLAST score	343
E value	3.0e-32
Match length	115
% identity	57
NCBI Description	ATP SYNTHASE DELTA CHAIN, CHLOROPLAST PRECURSOR >gi_280404_pir__S26198 H+-transporting ATP synthase (EC 3.6.1.34) delta chain precursor, chloroplast - common tobacco >gi_19787_emb_CAA45153_ (X63607) chloroplast ATP synthase (delta subunit) [Nicotiana tabacum]

Seq. No.	161930
Seq. ID	LIB3177-025-P1-K2-F1
Method	BLASTX
NCBI GI	g4587525
BLAST score	193
E value	1.0e-14
Match length	153
% identity	34
NCBI Description	(AC007060) Contains the PF_00650 CRAL/TRIO phosphatidyl-inositol-transfer protein domain. ESTs gb_T76582, gb_N06574 and gb_Z25700 come from this gene. [Arabidopsis thaliana]

Seq. No.	161931
Seq. ID	LIB3177-025-P1-K2-F10
Method	BLASTX
NCBI GI	g3983125
BLAST score	628
E value	1.0e-65
Match length	149
% identity	82
NCBI Description	(AF097648) phosphate/triose-phosphate translocator precursor [Arabidopsis thaliana]

Seq. No.	161932
Seq. ID	LIB3177-025-P1-K2-F12
Method	BLASTX
NCBI GI	g99696
BLAST score	856
E value	2.0e-92
Match length	153
% identity	99
NCBI Description	glutamate--ammonia ligase (EC 6.3.1.2) precursor, chloroplast (clone lambdaAtgsl1) - Arabidopsis thaliana >gi_240070_bbs_69728 (S69727) light-regulated glutamine synthetase isoenzyme [Arabidopsis thaliana, Peptide, 430 aa] [Arabidopsis thaliana] >gi_228453_prf__1804333A Gln synthetase [Arabidopsis thaliana]

Seq. No.	161933
Seq. ID	LIB3177-025-P1-K2-F2
Method	BLASTX
NCBI GI	g3273743
BLAST score	620
E value	1.0e-64
Match length	118
% identity	100
NCBI Description	(AF057357) lipid transfer protein 2 precursor [Arabidopsis thaliana] >gi_3786019 (AC005499) unknown protein [Arabidopsis thaliana]

Seq. No.	161934
Seq. ID	LIB3177-025-P1-K2-F3
Method	BLASTX
NCBI GI	g132863
BLAST score	728
E value	2.0e-77
Match length	140
% identity	97
NCBI Description	CHLOROPLAST 50S RIBOSOMAL PROTEIN L2 >gi_12214_emb_CAA46568_ (X65615) ribosomal protein L2 [Sinapis alba]

Seq. No.	161935
Seq. ID	LIB3177-025-P1-K2-F5
Method	BLASTX
NCBI GI	g1769905
BLAST score	484
E value	8.0e-49
Match length	137
% identity	69
NCBI Description	(X98108) 23 kDa polypeptide of oxygen-evolving comlex (OEC) [Arabidopsis thaliana]

Seq. No.	161936
Seq. ID	LIB3177-025-P1-K2-F6
Method	BLASTX
NCBI GI	g3915826
BLAST score	180
E value	2.0e-13
Match length	66
% identity	58
NCBI Description	60S RIBOSOMAL PROTEIN L5

Seq. No.	161937
Seq. ID	LIB3177-025-P1-K2-F7
Method	BLASTX
NCBI GI	g1709825
BLAST score	548
E value	2.0e-56
Match length	114
% identity	99
NCBI Description	PHOTOSYSTEM I REACTION CENTRE SUBUNIT PSAN PRECURSOR (PSI-N) >gi_1237124 (U32176) PSI-N [Arabidopsis thaliana]

Seq. No.	161938
Seq. ID	LIB3177-025-P1-K2-F8
Method	BLASTX
NCBI GI	g3149952
BLAST score	342
E value	4.0e-32
Match length	71
% identity	85
NCBI Description	(AB010259) DRH1 [Arabidopsis thaliana]

Seq. No.	161939
Seq. ID	LIB3177-025-P1-K2-G10
Method	BLASTX
NCBI GI	g4103987
BLAST score	565
E value	3.0e-58
Match length	136
% identity	79
NCBI Description	(AF030516) 5,10-methylenetetrahydrofolate dehydrogenase-5,10-methenyltetrahydrofolate cyclohydrolase [Pisum sativum]

Seq. No.	161940
Seq. ID	LIB3177-025-P1-K2-G11
Method	BLASTX
NCBI GI	g131398
BLAST score	386
E value	1.0e-37
Match length	94
% identity	84
NCBI Description	PHOTOSYSTEM II 10 KD POLYPEPTIDE PRECURSOR >gi_72714_pir__F2MU10 photosystem II 10K protein precursor - Arabidopsis thaliana >gi_16447_emb_CAA39441_ (X55970) photosystem II 10 kDa polypeptide [Arabidopsis thaliana] >gi_3152571 (AC002986) Match to photosystem II 10kDa polypeptide gb_X55970. ESTs gb_Z17693, gb_N37616, gb_T41858, gb_T88021, gb_R37531, gb_T04679, gb_N37520, gb_N64965, gb_Z17592 and gb_N65338, gb_N37466 and gb_T45400 come from this gene. [Arabidopsis

Seq. No.	161941
Seq. ID	LIB3177-025-P1-K2-G3
Method	BLASTX
NCBI GI	g2739366
BLAST score	304
E value	1.0e-27
Match length	144
% identity	47
NCBI Description	(AC002505) SF16 like protein [Arabidopsis thaliana]

Seq. No.	161942
Seq. ID	LIB3177-025-P1-K2-G7
Method	BLASTN
NCBI GI	g4580745
BLAST score	153
E value	2.0e-80
Match length	445

% identity	95
NCBI Description	Arabidopsis thaliana chromosome 1 BAC F10O3 sequence, complete sequence

Seq. No.	161943
Seq. ID	LIB3177-025-P1-K2-H1
Method	BLASTX
NCBI GI	g119143
BLAST score	723
E value	8.0e-77
Match length	146
% identity	95
NCBI Description	ELONGATION FACTOR 1-ALPHA (EF-1-ALPHA) >gi_81606_pir__S06724 translation elongation factor eEF-1 alpha chain - Arabidopsis thaliana >gi_295788_emb_CAA34453_ (X16430) elongation factor 1-alpha [Arabidopsis thaliana] >gi_1369927_emb_CAA34454_ (X16431) elongation factor 1-alpha [Arabidopsis thaliana] >gi_1369928_emb_CAA34455_ (X16431) elongation factor 1-alpha [Arabidopsis thaliana] >gi_1532172 (U63815) EF-1alpha-A1 [Arabidopsis thaliana] >gi_1532173 (U63815) EF-1alpha-A2 [Arabidopsis thaliana] >gi_1532174 (U63815) EF-1alpha-A3 [Arabidopsis thaliana]

Seq. No.	161944
Seq. ID	LIB3177-025-P1-K2-H10
Method	BLASTX
NCBI GI	g1944407
BLAST score	598
E value	4.0e-62
Match length	151
% identity	74
NCBI Description	(D86988) KIAA0221 [Homo sapiens]

Seq. No.	161945
Seq. ID	LIB3177-025-P1-K2-H11
Method	BLASTX
NCBI GI	g113024
BLAST score	608
E value	2.0e-63
Match length	149
% identity	84
NCBI Description	ISOCITRATE LYASE (ISOCITRASE) (ISOCITRATASE) (ICL) >gi_553043 (M83534) isocitrate lyase [Arabidopsis thaliana]

Seq. No.	161946
Seq. ID	LIB3177-025-P1-K2-H12
Method	BLASTX
NCBI GI	g461550
BLAST score	469
E value	5.0e-47
Match length	124
% identity	80
NCBI Description	ATP SYNTHASE GAMMA CHAIN 1, CHLOROPLAST PRECURSOR >gi_81635_pir__B39732 H+-transporting ATP synthase (EC 3.6.1.34) gamma-1 chain precursor, chloroplast - Arabidopsis thaliana >gi_166632 (M61741) ATP synthase gamma-subunit [Arabidopsis thaliana]

Seq. No.	161947
Seq. ID	LIB3177-025-P1-K2-H5
Method	BLASTN
NCBI GI	g4662640
BLAST score	48
E value	3.0e-18
Match length	72
% identity	13
NCBI Description	Arabidopsis thaliana chromosome II BAC F15K19 genomic sequence, complete sequence

Seq. No.	161948
Seq. ID	LIB3177-025-P1-K2-H6
Method	BLASTX
NCBI GI	g3123712
BLAST score	167
E value	1.0e-11
Match length	150
% identity	66
NCBI Description	(D89051) ERD6 protein [Arabidopsis thaliana]

Seq. No.	161949
Seq. ID	LIB3177-025-P1-K2-H7
Method	BLASTX
NCBI GI	g2058282
BLAST score	419
E value	3.0e-41
Match length	107
% identity	79
NCBI Description	(X97377) atranbp1a [Arabidopsis thaliana]

Seq. No.	161950
Seq. ID	LIB3177-026-P1-K2-A1
Method	BLASTX
NCBI GI	g3600052
BLAST score	221
E value	4.0e-18
Match length	105
% identity	44
NCBI Description	(AF080120) contains similarity to glycosyl hydrolases family 9 (Pfam: glycosyl_hydro5.hmm, score: 88.03) [Arabidopsis thaliana]

Seq. No.	161951
Seq. ID	LIB3177-026-P1-K2-A11
Method	BLASTX
NCBI GI	g4193388
BLAST score	409
E value	5.0e-40
Match length	120
% identity	66
NCBI Description	(AF091455) translationally controlled tumor protein [Hevea brasiliensis]

Seq. No.	161952
Seq. ID	LIB3177-026-P1-K2-A12

Method	BLASTN
NCBI GI	g3869069
BLAST score	49
E value	1.0e-18
Match length	233
% identity	88
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MEB5, complete sequence [Arabidopsis thaliana]

Seq. No.	161953
Seq. ID	LIB3177-026-P1-K2-A5
Method	BLASTN
NCBI GI	g3449334
BLAST score	78
E value	4.0e-36
Match length	156
% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MYH9, complete sequence [Arabidopsis thaliana]

Seq. No.	161954
Seq. ID	LIB3177-026-P1-K2-A7
Method	BLASTN
NCBI GI	g4490717
BLAST score	192
E value	1.0e-104
Match length	254
% identity	92
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone (ESSA project)

Seq. No.	161955
Seq. ID	LIB3177-026-P1-K2-A9
Method	BLASTX
NCBI GI	g1170040
BLAST score	105
E value	3.0e-04
Match length	155
% identity	87
NCBI Description	GLUTATHIONE REDUCTASE, CHLOROPLAST PRECURSOR (GR) (GRASE) >gi_451198_dbj_BAA03137_ (D14049) glutathione reductase precursor [Arabidopsis thaliana] >gi_1944448_dbj_BAA19653_ (D89620) glutathione reductase precursor [Arabidopsis thaliana] >gi_740576_prf__2005376A glutathione reductase [Arabidopsis thaliana]

Seq. No.	161956
Seq. ID	LIB3177-026-P1-K2-B1
Method	BLASTX
NCBI GI	g3860277
BLAST score	542
E value	1.0e-55
Match length	138
% identity	80
NCBI Description	(AC005824) putative ribosomal protein L10 [Arabidopsis thaliana] >gi_4314394_gb_AAD15604_ (AC006232) putative ribosomal protein L10A [Arabidopsis thaliana]

Seq. No.	161957
Seq. ID	LIB3177-026-P1-K2-B10
Method	BLASTX
NCBI GI	g3549680
BLAST score	154
E value	3.0e-10
Match length	94
% identity	38
NCBI Description	(AL031394) putative protein [Arabidopsis thaliana]

Seq. No.	161958
Seq. ID	LIB3177-026-P1-K2-B11
Method	BLASTX
NCBI GI	g1363487
BLAST score	463
E value	1.0e-46
Match length	96
% identity	95
NCBI Description	IAA7 protein - Arabidopsis thaliana >gi_972917 (U18409) IAA7 [Arabidopsis thaliana]

Seq. No.	161959
Seq. ID	LIB3177-026-P1-K2-B12
Method	BLASTN
NCBI GI	g4581161
BLAST score	97
E value	3.0e-47
Match length	246
% identity	74
NCBI Description	Arabidopsis thaliana chromosome II BAC T20G20 genomic sequence, complete sequence

Seq. No.	161960
Seq. ID	LIB3177-026-P1-K2-B2
Method	BLASTX
NCBI GI	g4220528
BLAST score	254
E value	2.0e-22
Match length	57
% identity	91
NCBI Description	(AL035356) glucose-6-phosphate isomerase [Arabidopsis thaliana]

Seq. No.	161961
Seq. ID	LIB3177-026-P1-K2-B9
Method	BLASTX
NCBI GI	g4165488
BLAST score	697
E value	1.0e-73
Match length	130
% identity	99
NCBI Description	(AJ132399) alpha-tubulin 3 [Hordeum vulgare]

Seq. No.	161962
Seq. ID	LIB3177-026-P1-K2-C10
Method	BLASTX

NCBI GI	g4538963
BLAST score	271
E value	1.0e-47
Match length	132
% identity	61
NCBI Description	(AL049488) chlorophyll a/b-binding protein-like [Arabidopsis thaliana] >gi_4741958_gb_AAD28776.1_AF134129_1 (AF134129) Lhcb5 protein [Arabidopsis thaliana]

Seq. No.	161963
Seq. ID	LIB3177-026-P1-K2-C12
Method	BLASTX
NCBI GI	g4678376
BLAST score	221
E value	4.0e-18
Match length	81
% identity	60
NCBI Description	(AL049656) putative protein [Arabidopsis thaliana]

Seq. No.	161964
Seq. ID	LIB3177-026-P1-K2-C2
Method	BLASTN
NCBI GI	g3046855
BLAST score	211
E value	1.0e-115
Match length	404
% identity	99
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MSL1, complete sequence [Arabidopsis thaliana]

Seq. No.	161965
Seq. ID	LIB3177-026-P1-K2-C3
Method	BLASTX
NCBI GI	g117238
BLAST score	604
E value	7.0e-63
Match length	150
% identity	82
NCBI Description	MAGNESIUM-CHELATASE SUBUNIT CHLI PRECURSOR (PROTEIN CS/CH-42) (MG-PROTOPORPHYRIN IX CHELATASE) >gi_81656_pir__S12785 protein ch-42 precursor, chloroplast - Arabidopsis thaliana >gi_1020100_emb_CAA62754_ (X91411) protoporphyrin-IX Mg-chetalase [Arabidopsis thaliana] >gi_2832653_emb_CAA16728_ (AL021710) protein ch-42 precursor, chloroplast [Arabidopsis thaliana] >gi_4490290_emb_CAB38561.1_ (X51799) chloroplast protein [Arabidopsis thaliana] >gi_228771_prf__1811226A ccsA gene [Euglena gracilis]

Seq. No.	161966
Seq. ID	LIB3177-026-P1-K2-C6
Method	BLASTX
NCBI GI	g135442
BLAST score	88
E value	1.9e-02
Match length	127
% identity	65

NCBI Description	TUBULIN BETA-1 CHAIN >gi_71590_pir__UBMUBM tubulin beta-1 chain - Arabidopsis thaliana >gi_166922 (M20405) beta-1 tubulin [Arabidopsis thaliana]

Seq. No.	161967
Seq. ID	LIB3177-026-P1-K2-C7
Method	BLASTX
NCBI GI	g3212849
BLAST score	154
E value	4.0e-10
Match length	120
% identity	35
NCBI Description	(AC004005) unknown protein [Arabidopsis thaliana]

Seq. No.	161968
Seq. ID	LIB3177-026-P1-K2-C8
Method	BLASTX
NCBI GI	g3176676
BLAST score	590
E value	6.0e-61
Match length	125
% identity	93
NCBI Description	(AC003671) Similar to carbonic anhydrase gb_L19255 from Nicotiana tabacum. ESTs gb_AA597643, gb_T45390, gb_T43963 and gb_AA597734 come from this gene. [Arabidopsis thaliana]

Seq. No.	161969
Seq. ID	LIB3177-026-P1-K2-D10
Method	BLASTX
NCBI GI	g115783
BLAST score	783
E value	7.0e-84
Match length	149
% identity	99
NCBI Description	CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR (CAB-140) (LHCP) >gi_16376_emb_CAA27543_ (X03909) chlorophyll a/b binding protein (LHCP AB 140) [Arabidopsis thaliana]

Seq. No.	161970
Seq. ID	LIB3177-026-P1-K2-D12
Method	BLASTN
NCBI GI	g4757414
BLAST score	56
E value	5.0e-23
Match length	164
% identity	84
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MYF24, complete sequence

Seq. No.	161971
Seq. ID	LIB3177-026-P1-K2-D2
Method	BLASTX
NCBI GI	g115385
BLAST score	315
E value	3.0e-29
Match length	90

% identity	69
NCBI Description	CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR (CAB-4) (LHCP) >gi_166646 (M63931) light-harvesting chlorophyll a/b binding protein [Arabidopsis thaliana]

Seq. No.	161972
Seq. ID	LIB3177-026-P1-K2-D4
Method	BLASTX
NCBI GI	g3915847
BLAST score	420
E value	2.0e-41
Match length	92
% identity	89
NCBI Description	40S RIBOSOMAL PROTEIN S2 >gi_2335095 (AC002339) putative 40S ribosomal protein S2 [Arabidopsis thaliana]

Seq. No.	161973
Seq. ID	LIB3177-026-P1-K2-D5
Method	BLASTX
NCBI GI	g1742961
BLAST score	203
E value	3.0e-16
Match length	54
% identity	83
NCBI Description	(X94756) cystathionine gamma-synthase [Arabidopsis thaliana]

Seq. No.	161974
Seq. ID	LIB3177-026-P1-K2-D6
Method	BLASTX
NCBI GI	g2062167
BLAST score	480
E value	2.0e-48
Match length	95
% identity	94
NCBI Description	(AC001645) Proline-rich protein APG isolog [Arabidopsis thaliana]

Seq. No.	161975
Seq. ID	LIB3177-026-P1-K2-D7
Method	BLASTX
NCBI GI	g4337027
BLAST score	199
E value	1.0e-15
Match length	75
% identity	57
NCBI Description	(AF123254) MFP2 [Arabidopsis thaliana]

Seq. No.	161976
Seq. ID	LIB3177-026-P1-K2-D8
Method	BLASTX
NCBI GI	g4490725
BLAST score	288
E value	5.0e-26
Match length	68
% identity	82
NCBI Description	(AL035709) endo-xyloglucan transferase-like protein

[Arabidopsis thaliana]

Seq. No.	161977
Seq. ID	LIB3177-026-P1-K2-D9
Method	BLASTX
NCBI GI	g3212877
BLAST score	402
E value	9.0e-73
Match length	151
% identity	96
NCBI Description	(AC004005) Lea-like protein [Arabidopsis thaliana]

Seq. No.	161978
Seq. ID	LIB3177-026-P1-K2-E10
Method	BLASTX
NCBI GI	g600178
BLAST score	157
E value	1.0e-69
Match length	136
% identity	96
NCBI Description	(L27074) acetyl-CoA carboxylase [Arabidopsis thaliana] >gi_1090217_prf__2018327A Ac-CoA carboxylase [Arabidopsis thaliana]

Seq. No.	161979
Seq. ID	LIB3177-026-P1-K2-E2
Method	BLASTX
NCBI GI	g4056482
BLAST score	758
E value	6.0e-81
Match length	147
% identity	58
NCBI Description	(AC005896) putative ABC transporter [Arabidopsis thaliana]

Seq. No.	161980
Seq. ID	LIB3177-026-P1-K2-E4
Method	BLASTX
NCBI GI	g1769905
BLAST score	422
E value	1.0e-41
Match length	118
% identity	70
NCBI Description	(X98108) 23 kDa polypeptide of oxygen-evolving comlex (OEC) [Arabidopsis thaliana]

Seq. No.	161981
Seq. ID	LIB3177-026-P1-K2-E5
Method	BLASTX
NCBI GI	g2492514
BLAST score	631
E value	5.0e-66
Match length	146
% identity	87
NCBI Description	CELL DIVISION PROTEIN FTSH HOMOLOG PRECURSOR >gi_1483215_emb_CAA68141_ (X99808) chloroplast FtsH protease [Arabidopsis thaliana]

Seq. No.	161982
Seq. ID	LIB3177-026-P1-K2-E7
Method	BLASTX
NCBI GI	g3158376
BLAST score	565
E value	6.0e-61
Match length	125
% identity	94
NCBI Description	(AF035385) unknown [Arabidopsis thaliana]

Seq. No.	161983
Seq. ID	LIB3177-026-P1-K2-E8
Method	BLASTX
NCBI GI	g417381
BLAST score	637
E value	8.0e-67
Match length	124
% identity	100
NCBI Description	NITRILASE 1 >gi_99738_pir__S22398 nitrilase (EC 3.5.5.1) - Arabidopsis thaliana >gi_16400_emb_CAA45041_ (X63445) nitrilase I [Arabidopsis thaliana]

Seq. No.	161984
Seq. ID	LIB3177-026-P1-K2-F1
Method	BLASTN
NCBI GI	g4159707
BLAST score	149
E value	4.0e-78
Match length	325
% identity	99
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MJK13, complete sequence

Seq. No.	161985
Seq. ID	LIB3177-026-P1-K2-F3
Method	BLASTN
NCBI GI	g3849811
BLAST score	262
E value	1.0e-145
Match length	486
% identity	98
NCBI Description	Arabidopsis thaliana chromosome I BAC T2P11 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	161986
Seq. ID	LIB3177-026-P1-K2-F4
Method	BLASTX
NCBI GI	g1769905
BLAST score	287
E value	5.0e-26
Match length	81
% identity	73
NCBI Description	(X98108) 23 kDa polypeptide of oxygen-evolving comlex (OEC) [Arabidopsis thaliana]

Seq. No.	161987
Seq. ID	LIB3177-026-P1-K2-F5

Method	BLASTX
NCBI GI	g1170936
BLAST score	232
E value	1.0e-19
Match length	44
% identity	98
NCBI Description	S-ADENOSYLMETHIONINE SYNTHETASE 1 (METHIONINE ADENOSYLTRANSFERASE 1) (ADOMET SYNTHETASE 1) >gi_1084406_pir__S46538 methionine adenosyltransferase (EC 2.5.1.6) - tomato >gi_429104_emb_CAA80865_ (Z24741) S-adenosyl-L-methionine synthetase [Lycopersicon esculentum]

Seq. No.	161988
Seq. ID	LIB3177-026-P1-K2-F6
Method	BLASTX
NCBI GI	g4455192
BLAST score	471
E value	2.0e-47
Match length	113
% identity	75
NCBI Description	(AL035440) putative protein [Arabidopsis thaliana]

Seq. No.	161989
Seq. ID	LIB3177-026-P1-K2-F7
Method	BLASTX
NCBI GI	g3877788
BLAST score	202
E value	7.0e-16
Match length	102
% identity	38
NCBI Description	(Z83110) cDNA EST yk472b5.3 comes from this gene; cDNA EST yk474a7.3 comes from this gene; cDNA EST yk472b5.5 comes from this gene; cDNA EST yk468c10.3 comes from this gene; cDNA EST yk468c10.5 comes from this gene; cDNA EST EM

Seq. No.	161990
Seq. ID	LIB3177-026-P1-K2-F8
Method	BLASTX
NCBI GI	g1076626
BLAST score	389
E value	1.0e-39
Match length	82
% identity	99
NCBI Description	glycine rich protein - common tobacco >gi_790473_emb_CAA58702_ (X83731) soluble, glycine rich protein [Nicotiana tabacum]

Seq. No.	161991
Seq. ID	LIB3177-026-P1-K2-F9
Method	BLASTX
NCBI GI	g4512708
BLAST score	657
E value	5.0e-69
Match length	145
% identity	89
NCBI Description	(AC006569) putative glutaredoxin [Arabidopsis thaliana]

Seq. No.	161992
Seq. ID	LIB3177-026-P1-K2-G1
Method	BLASTN
NCBI GI	g4757392
BLAST score	232
E value	1.0e-128
Match length	272
% identity	96
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, TAC clone: K14A17, complete sequence

Seq. No.	161993
Seq. ID	LIB3177-026-P1-K2-G10
Method	BLASTX
NCBI GI	g1705677
BLAST score	437
E value	1.0e-43
Match length	81
% identity	56
NCBI Description	CELL DIVISION CYCLE PROTEIN 48 HOMOLOG >gi_2118115_pir__S60112 cell division control protein CDC48 homolog - Arabidopsis thaliana >gi_1019904 (U37587) cell division cycle protein [Arabidopsis thaliana]

Seq. No.	161994
Seq. ID	LIB3177-026-P1-K2-G11
Method	BLASTX
NCBI GI	g4371284
BLAST score	317
E value	3.0e-29
Match length	64
% identity	92
NCBI Description	(AC006260) putative plasma membrane intrinsic protein 2B [Arabidopsis thaliana]

Seq. No.	161995
Seq. ID	LIB3177-026-P1-K2-G2
Method	BLASTX
NCBI GI	g2791423
BLAST score	198
E value	3.0e-15
Match length	68
% identity	54
NCBI Description	(AL021185) bcp [Mycobacterium tuberculosis]

Seq. No.	161996
Seq. ID	LIB3177-026-P1-K2-G3
Method	BLASTX
NCBI GI	g2829792
BLAST score	552
E value	7.0e-57
Match length	128
% identity	76
NCBI Description	SOLUBLE GLYCOGEN (STARCH) SYNTHASE PRECURSOR (SS I) >gi_1781353_emb_CAA71442_ (Y10416) soluble starch (bacterial glycogen) synthase [Solanum tuberosum]

Seq. No.	161997
Seq. ID	LIB3177-026-P1-K2-G5
Method	BLASTX
NCBI GI	g3334128
BLAST score	232
E value	8.0e-20
Match length	73
% identity	67
NCBI Description	BIOTIN CARBOXYL CARRIER PROTEIN OF ACETYL-COA CARBOXYLASE PRECURSOR (BCCP) >gi_1066348 (U23155) acetyl-CoA carboxylase biotin-containing subunit [Arabidopsis thaliana]

Seq. No.	161998
Seq. ID	LIB3177-026-P1-K2-G8
Method	BLASTX
NCBI GI	g3319350
BLAST score	483
E value	2.0e-82
Match length	159
% identity	95
NCBI Description	(AF077407) No definition line found [Arabidopsis thaliana]

Seq. No.	161999
Seq. ID	LIB3177-026-P1-K2-H1
Method	BLASTN
NCBI GI	g2454181
BLAST score	322
E value	0.0e+00
Match length	406
% identity	97
NCBI Description	Arabidopsis thaliana pyruvate dehydrogenase E1 alpha subunit mRNA, nuclear gene encoding plastid protein, complete cds

Seq. No.	162000
Seq. ID	LIB3177-026-P1-K2-H11
Method	BLASTX
NCBI GI	g399013
BLAST score	447
E value	1.0e-44
Match length	89
% identity	97
NCBI Description	ADP,ATP CARRIER PROTEIN 1 PRECURSOR (ADP/ATP TRANSLOCASE 1) (ADENINE NUCLEOTIDE TRANSLOCATOR 1) (ANT 1) >gi_99658_pir__S21313 ADP,ATP carrier protein - Arabidopsis thaliana (fragment) >gi_16175_emb_CAA46518_ (X65549) adenylate translocator [Arabidopsis thaliana] >gi_445607_prf__1909354A adenylate translocator [Arabidopsis thaliana]

Seq. No.	162001
Seq. ID	LIB3177-026-P1-K2-H12
Method	BLASTX
NCBI GI	g3377797
BLAST score	502

E value	5.0e-51
Match length	107
% identity	92
NCBI Description	(AF075597) Similar to 60S ribosome protein L19; coded for by A. thaliana cDNA T04719; coded for by A. thaliana cDNA H36046; coded for by A. thaliana cDNA T44067; coded for by A. thaliana cDNA T14056; coded for by A. thaliana cDNA R90691 [Ara

Seq. No.	162002
Seq. ID	LIB3177-026-P1-K2-H2
Method	BLASTX
NCBI GI	g1363489
BLAST score	543
E value	3.0e-61
Match length	124
% identity	91
NCBI Description	thioglucosidase (EC 3.2.3.1) 3D precursor - Arabidopsis thaliana >gi_984052_emb_CAA61592_ (X89413) thioglucoside glucohydrolase [Arabidopsis thaliana]

Seq. No.	162003
Seq. ID	LIB3177-026-P1-K2-H3
Method	BLASTX
NCBI GI	g2829899
BLAST score	228
E value	1.0e-31
Match length	111
% identity	60
NCBI Description	(AC002311) similar to ripening-induced protein, gp_AJ001449_2465015 and major#latex protein, gp_X91961_1107495 [Arabidopsis thaliana]

Seq. No.	162004
Seq. ID	LIB3177-026-P1-K2-H5
Method	BLASTX
NCBI GI	g4538963
BLAST score	352
E value	2.0e-33
Match length	97
% identity	72
NCBI Description	(AL049488) chlorophyll a/b-binding protein-like [Arabidopsis thaliana] >gi_4741958_gb_AAD28776.1_AF134129_1 (AF134129) Lhcb5 protein [Arabidopsis thaliana]

Seq. No.	162005
Seq. ID	LIB3177-026-P1-K2-H6
Method	BLASTX
NCBI GI	g1903021
BLAST score	92
E value	5.0e-56
Match length	114
% identity	97
NCBI Description	(Y10216) hypothetical 3-isopropylmalate dehydrogenase [Arabidopsis thaliana]

Seq. No.	162006

Seq. ID	LIB3177-026-P1-K2-H8
Method	BLASTX
NCBI GI	g4585935
BLAST score	552
E value	7.0e-64
Match length	125
% identity	94
NCBI Description	(AC007211) putative chlorophyll A/B binding protein [Arabidopsis thaliana] >gi_4741946_gb_AAD28770.1_AF134123_1 (AF134123) Lhcb2 protein [Arabidopsis thaliana]

Seq. No.	162007
Seq. ID	LIB3177-026-P1-K2-H9
Method	BLASTX
NCBI GI	g2129672
BLAST score	183
E value	1.0e-13
Match length	63
% identity	62
NCBI Description	photosystem II reaction center protein, 6.1K - Arabidopsis thaliana >gi_950023_emb_CAA62296_ (X90769) component of 6.1 kDa polypeptide of photosystem II reaction center [Arabidopsis thaliana]

Seq. No.	162008
Seq. ID	LIB3177-033-P1-K1-A1
Method	BLASTX
NCBI GI	g1402912
BLAST score	190
E value	2.0e-14
Match length	69
% identity	61
NCBI Description	(X98317) peroxidase [Arabidopsis thaliana]

Seq. No.	162009
Seq. ID	LIB3177-033-P1-K1-A10
Method	BLASTN
NCBI GI	g3449321
BLAST score	93
E value	1.0e-44
Match length	269
% identity	84
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MTG10, complete sequence [Arabidopsis thaliana]

Seq. No.	162010
Seq. ID	LIB3177-033-P1-K1-A2
Method	BLASTX
NCBI GI	g3337361
BLAST score	180
E value	3.0e-13
Match length	97
% identity	49
NCBI Description	(AC004481) ankyrin-like protein [Arabidopsis thaliana]

Seq. No.	162011
Seq. ID	LIB3177-033-P1-K1-A4

Method	BLASTX
NCBI GI	g1076289
BLAST score	369
E value	2.0e-35
Match length	122
% identity	62
NCBI Description	amino acid permease AAP5 - Arabidopsis thaliana >gi_608673_emb_CAA54632_ (X77501) amino acid permease [Arabidopsis thaliana]

Seq. No.	162012
Seq. ID	LIB3177-033-P1-K1-A6
Method	BLASTX
NCBI GI	g113026
BLAST score	212
E value	5.0e-17
Match length	77
% identity	62
NCBI Description	ISOCITRATE LYASE (ISOCITRASE) (ISOCITRATASE) (ICL) >gi_68211_pir__WZRPI isocitrate lyase (EC 4.1.3.1) - rape >gi_255220_bbs_112862 isocitrate lyase, threo-D S-isocitrate glyoxylate-lyase, IL {EC 4.1.3.1} [Brassica napus, seedlings, Peptide, 576 aa] >gi_167144 (L08482) isocitrate lyase [Brassica napus] >gi_447142_prf__1913424A isocitrate lyase [Brassica napus]

Seq. No.	162013
Seq. ID	LIB3177-033-P1-K1-A8
Method	BLASTX
NCBI GI	g1321941
BLAST score	254
E value	7.0e-22
Match length	134
% identity	50
NCBI Description	(Z48564) dihydrolipoamide dehydrogenase [Synechocystis PCC6803]

Seq. No.	162014
Seq. ID	LIB3177-033-P1-K1-B12
Method	BLASTX
NCBI GI	g132074
BLAST score	257
E value	2.0e-22
Match length	77
% identity	66
NCBI Description	RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN 1A PRECURSOR (RUBISCO SMALL SUBUNIT 1A) >gi_68063_pir__RKMUA1 ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain A1 precursor - Arabidopsis thaliana

Seq. No.	162015
Seq. ID	LIB3177-033-P1-K1-B3
Method	BLASTX
NCBI GI	g2119848
BLAST score	440
E value	1.0e-43
Match length	113

% identity	77
NCBI Description	chlorophyll a/b-binding protein type I precursor Lhb1B1 - Arabidopsis thaliana >gi_16366_emb_CAA45789_ (X64459) photosystem II type I chlorophyll a /b binding protein [Arabidopsis thaliana] >gi_3128229 (AC004077) putative photosystem II type I chlorophyll a/b binding protein [Arabidopsis thaliana] >gi_3337372 (AC004481) putative photosystem II type I chlorophyll a/b binding protein [Arabidopsis thaliana]
Seq. No.	162016
Seq. ID	LIB3177-033-P1-K1-B5
Method	BLASTX
NCBI GI	g119975
BLAST score	350
E value	4.0e-33
Match length	124
% identity	62
NCBI Description	FERREDOXIN PRECURSOR >gi_99692_pir__S09979 ferredoxin [2Fe-2S] precursor - Arabidopsis thaliana >gi_16437_emb_CAA35754_ (X51370) ferredoxin precursor [Arabidopsis thaliana] >gi_166698 (M35868) ferrodoxin A [Arabidopsis thaliana]
Seq. No.	162017
Seq. ID	LIB3177-033-P1-K1-C1
Method	BLASTX
NCBI GI	g430947
BLAST score	237
E value	8.0e-20
Match length	118
% identity	51
NCBI Description	(U01103) PSI type III chlorophyll a/b-binding protein [Arabidopsis thaliana]
Seq. No.	162018
Seq. ID	LIB3177-033-P1-K1-C2
Method	BLASTX
NCBI GI	g1906830
BLAST score	422
E value	1.0e-41
Match length	129
% identity	71
NCBI Description	(Y11829) heat shock protein [Arabidopsis thaliana]
Seq. No.	162019
Seq. ID	LIB3177-033-P1-K1-C3
Method	BLASTX
NCBI GI	g2781354
BLAST score	269
E value	1.0e-23
Match length	126
% identity	51
NCBI Description	(AC003113) F24O1.10 [Arabidopsis thaliana]
Seq. No.	162020
Seq. ID	LIB3177-033-P1-K1-C7

Method	BLASTX
NCBI GI	g4586256
BLAST score	142
E value	8.0e-09
Match length	99
% identity	38
NCBI Description	(AL049640) probable photosystem I chain XI precursor [Arabidopsis thaliana]

Seq. No.	162021
Seq. ID	LIB3177-033-P1-K1-C8
Method	BLASTX
NCBI GI	g2119846
BLAST score	193
E value	9.0e-15
Match length	94
% identity	51
NCBI Description	chlorophyll a/b-binding protein type I precursor Lhb1B2 - Arabidopsis thaliana >gi_16364_emb_CAA45790_ (X64460) photosystem II type I chlorophyll a /b binding protein [Arabidopsis thaliana] >gi_3128230 (AC004077) photosystem II type I chlorophyll a/b binding protein [Arabidopsis thaliana] >gi_3337371 (AC004481) photosystem II type I chlorophyll a/b binding protein [Arabidopsis thaliana]

Seq. No.	162022
Seq. ID	LIB3177-033-P1-K1-D1
Method	BLASTX
NCBI GI	g730645
BLAST score	271
E value	7.0e-24
Match length	97
% identity	59
NCBI Description	40S RIBOSOMAL PROTEIN S15 >gi_629556_pir__S43412 ribosomal protein S15 - Arabidopsis thaliana >gi_313152_emb_CAA80679_ (Z23161) ribosomal protein S15 [Arabidopsis thaliana] >gi_313188_emb_CAA80681_ (Z23162) ribosomal protein S15 [Arabidopsis thaliana] >gi_1903366_gb_AAB70449_ (AC000104) Strong similarity to Oryza 40S ribosomal protein S15. ESTs gb_R29788,gb_ATTS0365 come from this gene. [Arabidopsis thaliana]

Seq. No.	162023
Seq. ID	LIB3177-033-P1-K1-D2
Method	BLASTX
NCBI GI	g2827143
BLAST score	146
E value	3.0e-09
Match length	90
% identity	39
NCBI Description	(AF027174) cellulose synthase catalytic subunit [Arabidopsis thaliana]

Seq. No.	162024
Seq. ID	LIB3177-033-P1-K1-D4
Method	BLASTX
NCBI GI	g99688

BLAST score 415
E value 1.0e-40
Match length 132
% identity 61
NCBI Description translation elongation factor eEF-1 alpha chain (gene A4) - Arabidopsis thaliana >gi_295789_emb_CAA34456_ (X16432) elongation factor 1-alpha [Arabidopsis thaliana]

Seq. No. 162025
Seq. ID LIB3177-033-P1-K1-E1
Method BLASTX
NCBI GI g2246621
BLAST score 363
E value 1.0e-34
Match length 110
% identity 64
NCBI Description (AF004393) salt-stress induced tonoplast intrinsic protein [Arabidopsis thaliana]

Seq. No. 162026
Seq. ID LIB3177-033-P1-K1-E10
Method BLASTN
NCBI GI g4757662
BLAST score 76
E value 1.0e-34
Match length 324
% identity 80
NCBI Description Genomic sequence for Arabidopsis thaliana BAC F10B6 from chromosome I, complete sequence

Seq. No. 162027
Seq. ID LIB3177-033-P1-K1-E2
Method BLASTX
NCBI GI g3123264
BLAST score 215
E value 3.0e-17
Match length 122
% identity 44
NCBI Description 60S RIBOSOMAL PROTEIN L27 >gi_2244857_emb_CAB10279_ (Z97337) hypothetical protein [Arabidopsis thaliana]

Seq. No. 162028
Seq. ID LIB3177-033-P1-K1-E3
Method BLASTX
NCBI GI g72178
BLAST score 145
E value 4.0e-09
Match length 76
% identity 43
NCBI Description metallothionein-like protein - Arabidopsis thaliana >gi_1362000_pir__S57897 metallothionein-like protein - Arabidopsis thaliana >gi_16184_emb_CAA44630_ (X62818) Metallothionein-like protein [Arabidopsis thaliana] >gi_217857_dbj_BAA01990_ (D11394) metallothionein-like protein [Arabidopsis thaliana]

Seq. No. 162029

Seq. ID	LIB3177-033-P1-K1-E4
Method	BLASTX
NCBI GI	g4337175
BLAST score	378
E value	2.0e-36
Match length	120
% identity	64
NCBI Description	(AC006416) ESTs gb_T20589, gb_T04648, gb_AA597906, gb_T04111, gb_R84180, gb_R65428, gb_T44439, gb_T76570, gb_R90004, gb_T45020, gb_T42457, gb_T20921, gb_AA042762 and gb_AA720210 come from this gene. [Arabidopsis thaliana]

Seq. No.	162030
Seq. ID	LIB3177-033-P1-K1-E6
Method	BLASTX
NCBI GI	g4586256
BLAST score	290
E value	3.0e-26
Match length	106
% identity	61
NCBI Description	(AL049640) probable photosystem I chain XI precursor [Arabidopsis thaliana]

Seq. No.	162031
Seq. ID	LIB3177-033-P1-K1-E9
Method	BLASTX
NCBI GI	g132110
BLAST score	178
E value	4.0e-13
Match length	94
% identity	46
NCBI Description	RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN 3B PRECURSOR (RUBISCO SMALL SUBUNIT 3B) >gi_68060_pir__RKMUB3 ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain B3 precursor - Arabidopsis thaliana >gi_16195_emb_CAA32702_ (X14564) ribulose bisphosphate carboxylase [Arabidopsis thaliana]

Seq. No.	162032
Seq. ID	LIB3177-033-P1-K1-F2
Method	BLASTX
NCBI GI	g4263525
BLAST score	373
E value	8.0e-36
Match length	127
% identity	63
NCBI Description	(AC004044) putative photosystem I reaction center subunit II precursor [Arabidopsis thaliana]

Seq. No.	162033
Seq. ID	LIB3177-033-P1-K1-F4
Method	BLASTN
NCBI GI	g4558521
BLAST score	44
E value	2.0e-15
Match length	211
% identity	85

NCBI Description	Genomic sequence for Arabidopsis thaliana BAC T10O24, complete sequence
Seq. No.	162034
Seq. ID	LIB3177-033-P1-K1-F5
Method	BLASTX
NCBI GI	g2129640
BLAST score	373
E value	7.0e-36
Match length	117
% identity	71
NCBI Description	magnesium chelatase chain - Arabidopsis thaliana >gi_1154627_emb_CAA92802_ (Z68495) magnesium chelatase subunit [Arabidopsis thaliana]
Seq. No.	162035
Seq. ID	LIB3177-033-P1-K1-G1
Method	BLASTX
NCBI GI	g3273743
BLAST score	256
E value	4.0e-22
Match length	85
% identity	65
NCBI Description	(AF057357) lipid transfer protein 2 precursor [Arabidopsis thaliana] >gi_3786019 (AC005499) unknown protein [Arabidopsis thaliana]
Seq. No.	162036
Seq. ID	LIB3177-033-P1-K1-G2
Method	BLASTX
NCBI GI	g3122753
BLAST score	285
E value	2.0e-25
Match length	102
% identity	53
NCBI Description	60S RIBOSOMAL PROTEIN L44 >gi_2244789_emb_CAB10211.1_ (Z97336) ribosomal protein [Arabidopsis thaliana]
Seq. No.	162037
Seq. ID	LIB3177-033-P1-K1-G3
Method	BLASTX
NCBI GI	g1169839
BLAST score	186
E value	7.0e-14
Match length	77
% identity	57
NCBI Description	GIBBERELLIN-REGULATED PROTEIN 1 PRECURSOR >gi_2129588_pir__S71441 GAST1 protein homolog (clone GASA1) - Arabidopsis thaliana >gi_887939 (U11766) GAST1 protein homolog [Arabidopsis thaliana]
Seq. No.	162038
Seq. ID	LIB3177-033-P1-K1-G4
Method	BLASTX
NCBI GI	g687677
BLAST score	278
E value	8.0e-25

Match length	101
% identity	64
NCBI Description	(U19925) unknown [Arabidopsis thaliana]

Seq. No.	162039
Seq. ID	LIB3177-033-P1-K1-G8
Method	BLASTX
NCBI GI	g1304259
BLAST score	226
E value	1.0e-18
Match length	102
% identity	54
NCBI Description	(AB009948) ribulose-1,5-bisphosphate carboxylase large subunit [Uvularia sessilifolia]

Seq. No.	162040
Seq. ID	LIB3177-033-P1-K1-H1
Method	BLASTX
NCBI GI	g2342727
BLAST score	245
E value	8.0e-21
Match length	111
% identity	50
NCBI Description	(AC002341) hypothetical protein [Arabidopsis thaliana]

Seq. No.	162041
Seq. ID	LIB3177-033-P1-K1-H2
Method	BLASTN
NCBI GI	g4314374
BLAST score	97
E value	4.0e-47
Match length	356
% identity	81
NCBI Description	Arabidopsis thaliana chromosome II BAC F10A12 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	162042
Seq. ID	LIB3177-033-P1-K1-H3
Method	BLASTX
NCBI GI	g4512122
BLAST score	177
E value	7.0e-13
Match length	122
% identity	40
NCBI Description	(AF131219) chorismate mutase 3 [Arabidopsis thaliana]

Seq. No.	162043
Seq. ID	LIB3177-033-P1-K1-H4
Method	BLASTX
NCBI GI	g2911047
BLAST score	297
E value	7.0e-27
Match length	100
% identity	60
NCBI Description	(AL021961) putative protein [Arabidopsis thaliana]

Seq. No.	162044

Seq. ID	LIB3177-033-P1-K2-A1
Method	BLASTX
NCBI GI	g1402912
BLAST score	342
E value	2.0e-32
Match length	78
% identity	83
NCBI Description	(X98317) peroxidase [Arabidopsis thaliana]

Seq. No.	162045
Seq. ID	LIB3177-033-P1-K2-A10
Method	BLASTN
NCBI GI	g3449321
BLAST score	209
E value	1.0e-114
Match length	288
% identity	93
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MTG10, complete sequence [Arabidopsis thaliana]

Seq. No.	162046
Seq. ID	LIB3177-033-P1-K2-A2
Method	BLASTN
NCBI GI	g3337347
BLAST score	44
E value	1.0e-15
Match length	96
% identity	86
NCBI Description	Arabidopsis thaliana chromosome II BAC F13P17 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	162047
Seq. ID	LIB3177-033-P1-K2-A4
Method	BLASTX
NCBI GI	g1076289
BLAST score	512
E value	3.0e-52
Match length	115
% identity	87
NCBI Description	amino acid permease AAP5 - Arabidopsis thaliana >gi_608673_emb_CAA54632_ (X77501) amino acid permease [Arabidopsis thaliana]

Seq. No.	162048
Seq. ID	LIB3177-033-P1-K2-A6
Method	BLASTX
NCBI GI	g113026
BLAST score	552
E value	8.0e-57
Match length	117
% identity	91
NCBI Description	ISOCITRATE LYASE (ISOCITRASE) (ISOCITRATASE) (ICL) >gi_68211_pir__WZRPI isocitrate lyase (EC 4.1.3.1) - rape >gi_255220_bbs_112862 isocitrate lyase, threo-D S-isocitrate glyoxylate-lyase, IL {EC 4.1.3.1} [Brassica napus, seedlings, Peptide, 576 aa] >gi_167144 (L08482) isocitrate lyase [Brassica napus] >gi_447142_prf__1913424A

isocitrate lyase [Brassica napus]

Seq. No.	162049
Seq. ID	LIB3177-033-P1-K2-A8
Method	BLASTX
NCBI GI	g1651828
BLAST score	314
E value	4.0e-36
Match length	144
% identity	62
NCBI Description	(D90900) dihydrolipoamide dehydrogenase [Synechocystis sp.]

Seq. No.	162050
Seq. ID	LIB3177-033-P1-K2-B12
Method	BLASTX
NCBI GI	g132074
BLAST score	243
E value	6.0e-21
Match length	80
% identity	64
NCBI Description	RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN 1A PRECURSOR (RUBISCO SMALL SUBUNIT 1A) >gi_68063_pir__RKMUA1 ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain A1 precursor - Arabidopsis thaliana

Seq. No.	162051
Seq. ID	LIB3177-033-P1-K2-B2
Method	BLASTX
NCBI GI	g2347199
BLAST score	165
E value	8.0e-12
Match length	53
% identity	60
NCBI Description	(AC002338) protein kinase isolog [Arabidopsis thaliana]

Seq. No.	162052
Seq. ID	LIB3177-033-P1-K2-B3
Method	BLASTX
NCBI GI	g115780
BLAST score	82
E value	4.0e-15
Match length	68
% identity	68
NCBI Description	CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR (CAB) (LHCP) >gi_81455_pir__JQ0020 chlorophyll a/b-binding protein precursor - spinach >gi_14240_emb_CAA32526_ (X14341) chlorophyll a/b binding protein precursor [Spinacia oleracea]

Seq. No.	162053
Seq. ID	LIB3177-033-P1-K2-C1
Method	BLASTX
NCBI GI	g4585882
BLAST score	550
E value	1.0e-56
Match length	109
% identity	99

NCBI Description	(AC005850) PSI type III chlorophyll a/b-binding protein [Arabidopsis thaliana]

Seq. No.	162054
Seq. ID	LIB3177-033-P1-K2-C10
Method	BLASTN
NCBI GI	g4580386
BLAST score	39
E value	9.0e-13
Match length	166
% identity	80
NCBI Description	Arabidopsis thaliana chromosome II BAC T8O18 genomic sequence, complete sequence

Seq. No.	162055
Seq. ID	LIB3177-033-P1-K2-C2
Method	BLASTX
NCBI GI	g1906830
BLAST score	42
E value	1.0e-46
Match length	123
% identity	85
NCBI Description	(Y11829) heat shock protein [Arabidopsis thaliana]

Seq. No.	162056
Seq. ID	LIB3177-033-P1-K2-C3
Method	BLASTX
NCBI GI	g2781354
BLAST score	674
E value	4.0e-71
Match length	140
% identity	92
NCBI Description	(AC003113) F24O1.10 [Arabidopsis thaliana]

Seq. No.	162057
Seq. ID	LIB3177-033-P1-K2-C8
Method	BLASTX
NCBI GI	g2119846
BLAST score	303
E value	8.0e-28
Match length	77
% identity	73
NCBI Description	chlorophyll a/b-binding protein type I precursor Lhb1B2 - Arabidopsis thaliana >gi_16364_emb_CAA45790_ (X64460) photosystem II type I chlorophyll a /b binding protein [Arabidopsis thaliana] >gi_3128230 (AC004077) photosystem II type I chlorophyll a/b binding protein [Arabidopsis thaliana] >gi_3337371 (AC004481) photosystem II type I chlorophyll a/b binding protein [Arabidopsis thaliana]

Seq. No.	162058
Seq. ID	LIB3177-033-P1-K2-D1
Method	BLASTX
NCBI GI	g730645
BLAST score	488
E value	3.0e-49
Match length	109

D05640.T25.PCT000

% identity	89
NCBI Description	40S RIBOSOMAL PROTEIN S15 >gi_629556_pir__S43412 ribosomal protein S15 - Arabidopsis thaliana >gi_313152_emb_CAA80679_ (Z23161) ribosomal protein S15 [Arabidopsis thaliana] >gi_313188_emb_CAA80681_ (Z23162) ribosomal protein S15 [Arabidopsis thaliana] >gi_1903366_gb_AAB70449_ (AC000104) Strong similarity to Oryza 40S ribosomal protein S15. ESTs gb_R29788,gb_ATTS0365 come from this gene. [Arabidopsis thaliana]

Seq. No.	162059
Seq. ID	LIB3177-033-P1-K2-D12
Method	BLASTX
NCBI GI	g2199574
BLAST score	126
E value	1.0e-13
Match length	65
% identity	66
NCBI Description	(AF004293) aquaporin [Brassica rapa]

Seq. No.	162060
Seq. ID	LIB3177-033-P1-K2-D2
Method	BLASTX
NCBI GI	g2827143
BLAST score	182
E value	7.0e-14
Match length	58
% identity	64
NCBI Description	(AF027174) cellulose synthase catalytic subunit [Arabidopsis thaliana]

Seq. No.	162061
Seq. ID	LIB3177-033-P1-K2-D9
Method	BLASTX
NCBI GI	g3023217
BLAST score	474
E value	1.0e-47
Match length	139
% identity	74
NCBI Description	14-3-3-LIKE PROTEIN GF14 NU >gi_1531631 (U60445) GF14 nu [Arabidopsis thaliana]

Seq. No.	162062
Seq. ID	LIB3177-033-P1-K2-E1
Method	BLASTX
NCBI GI	g2246621
BLAST score	54
E value	2.0e-36
Match length	111
% identity	73
NCBI Description	(AF004393) salt-stress induced tonoplast intrinsic protein [Arabidopsis thaliana]

Seq. No.	162063
Seq. ID	LIB3177-033-P1-K2-E10
Method	BLASTX
NCBI GI	g4406780

BLAST score	480
E value	3.0e-57
Match length	149
% identity	78
NCBI Description	(AC006532) putative multispanning membrane protein [Arabidopsis thaliana]

Seq. No.	162064
Seq. ID	LIB3177-033-P1-K2-E2
Method	BLASTX
NCBI GI	g3123264
BLAST score	525
E value	1.0e-53
Match length	126
% identity	84
NCBI Description	60S RIBOSOMAL PROTEIN L27 >gi_2244857_emb_CAB10279_ (Z97337) hypothetical protein [Arabidopsis thaliana]

Seq. No.	162065
Seq. ID	LIB3177-033-P1-K2-E3
Method	BLASTX
NCBI GI	g2507587
BLAST score	248
E value	3.0e-21
Match length	55
% identity	82
NCBI Description	METALLOTHIONEIN-LIKE PROTEIN 2A (MT-2A) (MT-K) (MT-1G) >gi_1361998_pir__S57861 metallothionein 2a - Arabidopsis thaliana >gi_555976 (U15108) metallothionein-like protein [Arabidopsis thaliana] >gi_1580892_prf__2116236A metallothionein 1 [Arabidopsis thaliana]

Seq. No.	162066
Seq. ID	LIB3177-033-P1-K2-E4
Method	BLASTX
NCBI GI	g4337175
BLAST score	628
E value	1.0e-65
Match length	131
% identity	94
NCBI Description	(AC006416) ESTs gb_T20589, gb_T04648, gb_AA597906, gb_T04111, gb_R84180, gb_R65428, gb_T44439, gb_T76570, gb_R90004, gb_T45020, gb_T42457, gb_T20921, gb_AA042762 and gb_AA720210 come from this gene. [Arabidopsis thaliana]

Seq. No.	162067
Seq. ID	LIB3177-033-P1-K2-E6
Method	BLASTX
NCBI GI	g4586256
BLAST score	510
E value	6.0e-52
Match length	118
% identity	86
NCBI Description	(AL049640) probable photosystem I chain XI precursor [Arabidopsis thaliana]

Seq. No.	162068

Seq. ID	LIB3177-033-P1-K2-E8
Method	BLASTX
NCBI GI	g126766
BLAST score	442
E value	4.0e-44
Match length	100
% identity	88
NCBI Description	MALATE SYNTHASE, GLYOXYSOMAL >gi_68216_pir__SYRPMA malate synthase (EC 4.1.3.2), glyoxysomal - rape >gi_167150 (J04468) malate synthase (EC 4.1.3.2) [Brassica napus]

Seq. No.	162069
Seq. ID	LIB3177-033-P1-K2-E9
Method	BLASTN
NCBI GI	g16192
BLAST score	56
E value	7.0e-23
Match length	128
% identity	28
NCBI Description	A.thaliana ats1B, ats2B and ats3B gene for ribulose-1,5-biphosphate carboxylase small subunit (rbcS) (EC 4.1.1.39)

Seq. No.	162070
Seq. ID	LIB3177-033-P1-K2-F2
Method	BLASTX
NCBI GI	g4263525
BLAST score	433
E value	6.0e-43
Match length	112
% identity	76
NCBI Description	(AC004044) putative photosystem I reaction center subunit II precursor [Arabidopsis thaliana]

Seq. No.	162071
Seq. ID	LIB3177-033-P1-K2-F3
Method	BLASTN
NCBI GI	g4539448
BLAST score	355
E value	0.0e+00
Match length	419
% identity	96
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone T5C23 (ESSA project)

Seq. No.	162072
Seq. ID	LIB3177-033-P1-K2-F4
Method	BLASTX
NCBI GI	g2129770
BLAST score	215
E value	2.0e-17
Match length	89
% identity	46
NCBI Description	xyloglucan endotransglycosylase-related protein XTR-2 - Arabidopsis thaliana >gi_1244756 (U43487) xyloglucan endotransglycosylase-related protein [Arabidopsis thaliana] >gi_2154611_dbj_BAA20290_ (D63510) endoxyloglucan

transferase related protein [Arabidopsis thaliana]

Seq. No.	162073
Seq. ID	LIB3177-033-P1-K2-F5
Method	BLASTX
NCBI GI	g2129640
BLAST score	578
E value	8.0e-60
Match length	133
% identity	87
NCBI Description	magnesium chelatase chain - Arabidopsis thaliana >gi_1154627_emb_CAA92802_ (Z68495) magnesium chelatase subunit [Arabidopsis thaliana]

Seq. No.	162074
Seq. ID	LIB3177-033-P1-K2-G1
Method	BLASTX
NCBI GI	g3273743
BLAST score	457
E value	1.0e-45
Match length	100
% identity	88
NCBI Description	(AF057357) lipid transfer protein 2 precursor [Arabidopsis thaliana] >gi_3786019 (AC005499) unknown protein [Arabidopsis thaliana]

Seq. No.	162075
Seq. ID	LIB3177-033-P1-K2-G2
Method	BLASTX
NCBI GI	g3122753
BLAST score	370
E value	1.0e-35
Match length	90
% identity	79
NCBI Description	60S RIBOSOMAL PROTEIN L44 >gi_2244789_emb_CAB10211.1_ (Z97336) ribosomal protein [Arabidopsis thaliana]

Seq. No.	162076
Seq. ID	LIB3177-033-P1-K2-G3
Method	BLASTX
NCBI GI	g2146733
BLAST score	341
E value	2.0e-32
Match length	87
% identity	71
NCBI Description	GAST1 protein homolog (clone GASA1) - Arabidopsis thaliana

Seq. No.	162077
Seq. ID	LIB3177-033-P1-K2-G4
Method	BLASTX
NCBI GI	g687677
BLAST score	409
E value	3.0e-40
Match length	103
% identity	84
NCBI Description	(U19925) unknown [Arabidopsis thaliana]

Seq. No.	162078
Seq. ID	LIB3177-033-P1-K2-G8
Method	BLASTX
NCBI GI	g132005
BLAST score	353
E value	8.0e-34
Match length	89
% identity	78
NCBI Description	RIBULOSE BISPHOSPHATE CARBOXYLASE LARGE CHAIN PRECURSOR (RUBISCO LARGE SUBUNIT) >gi_68145_pir__RKRZL ribulose-bisphosphate carboxylase (EC 4.1.1.39) large chain precursor - rice chloroplast >gi_11992_emb_CAA34004_ (X15901) rbcL; RuBisCO large subunit [Oryza sativa] >gi_344017_dbj_BAA00147_ (D00207) ribulose 1,5-bisphosphate carboxylase large subunit [Oryza sativa] >gi_226613_prf__1603356AK ribulose bisphosphate carboxylase oxygenase L [Oryza sativa]

Seq. No.	162079
Seq. ID	LIB3177-033-P1-K2-H1
Method	BLASTX
NCBI GI	g2342727
BLAST score	531
E value	2.0e-54
Match length	123
% identity	81
NCBI Description	(AC002341) hypothetical protein [Arabidopsis thaliana]

Seq. No.	162080
Seq. ID	LIB3177-033-P1-K2-H11
Method	BLASTN
NCBI GI	g3702315
BLAST score	188
E value	1.0e-101
Match length	427
% identity	95
NCBI Description	Arabidopsis thaliana chromosome II BAC T3F17 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	162081
Seq. ID	LIB3177-033-P1-K2-H12
Method	BLASTX
NCBI GI	g2119846
BLAST score	350
E value	2.0e-33
Match length	83
% identity	81
NCBI Description	chlorophyll a/b-binding protein type I precursor Lhb1B2 - Arabidopsis thaliana >gi_16364_emb_CAA45790_ (X64460) photosystem II type I chlorophyll a /b binding protein [Arabidopsis thaliana] >gi_3128230 (AC004077) photosystem II type I chlorophyll a/b binding protein [Arabidopsis thaliana] >gi_3337371 (AC004481) photosystem II type I chlorophyll a/b binding protein [Arabidopsis thaliana]

Seq. No.	162082
Seq. ID	LIB3177-033-P1-K2-H2

Method	BLASTN
NCBI GI	g4314374
BLAST score	302
E value	1.0e-169
Match length	337
% identity	97
NCBI Description	Arabidopsis thaliana chromosome II BAC F10A12 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	162083
Seq. ID	LIB3177-033-P1-K2-H3
Method	BLASTX
NCBI GI	g4512122
BLAST score	516
E value	1.0e-52
Match length	124
% identity	83
NCBI Description	(AF131219) chorismate mutase 3 [Arabidopsis thaliana]

Seq. No.	162084
Seq. ID	LIB3177-033-P1-K2-H4
Method	BLASTN
NCBI GI	g3763944
BLAST score	121
E value	1.0e-61
Match length	300
% identity	96
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F28A23 (ESSAII project)

Seq. No.	162085
Seq. ID	LIB3177-033-P1-K2-H5
Method	BLASTN
NCBI GI	g2564044
BLAST score	136
E value	2.0e-70
Match length	364
% identity	95
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K19P17, complete sequence [Arabidopsis thaliana]

Seq. No.	162086
Seq. ID	LIB3177-033-P1-K2-H8
Method	BLASTN
NCBI GI	g4587641
BLAST score	170
E value	8.0e-91
Match length	262
% identity	91
NCBI Description	Arabidopsis thaliana chromosome I BAC F20D21 genomic sequence, complete sequence

Seq. No.	162087
Seq. ID	LIB3177-035-P1-K2-A2
Method	BLASTX
NCBI GI	g2996158
BLAST score	327

E value	2.0e-30
Match length	61
% identity	84
NCBI Description	(AF051753) GASA5-like protein [Picea mariana] >gi_2996160 (AF051754) GASA5-like protein [Picea mariana]

Seq. No.	162088
Seq. ID	LIB3177-035-P1-K2-A3
Method	BLASTX
NCBI GI	g1169476
BLAST score	654
E value	9.0e-69
Match length	125
% identity	100
NCBI Description	ELONGATION FACTOR 1-ALPHA (EF-1-ALPHA) (VITRONECTIN-LIKE ADHESION PROTEIN 1) (PVN1) >gi_439577 (U04632) vitronectin-like adhesion protein [Nicotiana tabacum]

Seq. No.	162089
Seq. ID	LIB3177-035-P1-K2-A4
Method	BLASTX
NCBI GI	g1170159
BLAST score	343
E value	3.0e-32
Match length	73
% identity	96
NCBI Description	HISTONE H2B

Seq. No.	162090
Seq. ID	LIB3177-035-P1-K2-B1
Method	BLASTX
NCBI GI	g2764941
BLAST score	600
E value	2.0e-62
Match length	106
% identity	98
NCBI Description	(X98255) transcriptionally stimulated by gibberellins; expressed in meristematic region, and style [Arabidopsis thaliana]

Seq. No.	162091
Seq. ID	LIB3177-035-P1-K2-B2
Method	BLASTX
NCBI GI	g2062167
BLAST score	534
E value	1.0e-54
Match length	108
% identity	94
NCBI Description	(AC001645) Proline-rich protein APG isolog [Arabidopsis thaliana]

Seq. No.	162092
Seq. ID	LIB3177-035-P1-K2-B4
Method	BLASTX
NCBI GI	g2062167
BLAST score	493
E value	6.0e-50

Match length	96
% identity	96
NCBI Description	(AC001645) Proline-rich protein APG isolog [Arabidopsis thaliana]

Seq. No.	162093
Seq. ID	LIB3177-035-P1-K2-B6
Method	BLASTX
NCBI GI	g1769905
BLAST score	321
E value	2.0e-35
Match length	128
% identity	63
NCBI Description	(X98108) 23 kDa polypeptide of oxygen-evolving comlex (OEC) [Arabidopsis thaliana]

Seq. No.	162094
Seq. ID	LIB3177-035-P1-K2-C2
Method	BLASTN
NCBI GI	g3738313
BLAST score	145
E value	1.0e-75
Match length	443
% identity	97
NCBI Description	Arabidopsis thaliana chromosome II BAC T29E15 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	162095
Seq. ID	LIB3177-035-P1-K2-C4
Method	BLASTN
NCBI GI	g3763915
BLAST score	24
E value	1.0e-03
Match length	313
% identity	74
NCBI Description	Arabidopsis thaliana chromosome II BAC F14B2 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	162096
Seq. ID	LIB3177-035-P1-K2-D1
Method	BLASTX
NCBI GI	g2500435
BLAST score	266
E value	3.0e-23
Match length	74
% identity	66
NCBI Description	30S RIBOSOMAL PROTEIN S10 >gi_1653406_dbj_BAA18320_ (D90913) 30S ribosomal protein S10 [Synechocystis sp.]

Seq. No.	162097
Seq. ID	LIB3177-035-P1-K2-D4
Method	BLASTX
NCBI GI	g4741940
BLAST score	678
E value	1.0e-71
Match length	145
% identity	86

NCBI Description	(AF134120) Lhca2 protein [Arabidopsis thaliana]

Seq. No.	162098
Seq. ID	LIB3177-035-P1-K2-E1
Method	BLASTX
NCBI GI	g2244837
BLAST score	352
E value	1.0e-33
Match length	82
% identity	85
NCBI Description	(Z97337) proteasome chain protein [Arabidopsis thaliana] >gi_2511572_emb_CAA73618.1_ (Y13175) multicatalytic endopeptidase [Arabidopsis thaliana] >gi_3421114 (AF043535) 20S proteasome beta subunit PBD2 [Arabidopsis thaliana]

Seq. No.	162099
Seq. ID	LIB3177-035-P1-K2-E4
Method	BLASTN
NCBI GI	g3399678
BLAST score	331
E value	0.0e+00
Match length	399
% identity	96
NCBI Description	Arabidopsis thaliana chromosome 1 BAC F13M7 sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	162100
Seq. ID	LIB3177-035-P1-K2-F1
Method	BLASTN
NCBI GI	g4544461
BLAST score	315
E value	1.0e-177
Match length	438
% identity	98
NCBI Description	Arabidopsis thaliana chromosome II BAC F23E6 genomic sequence, complete sequence

Seq. No.	162101
Seq. ID	LIB3177-035-P1-K2-F11
Method	BLASTN
NCBI GI	g472876
BLAST score	36
E value	5.0e-11
Match length	60
% identity	90
NCBI Description	A.thaliana mRNA for plasma membrane intrinsic protein 2a

Seq. No.	162102
Seq. ID	LIB3177-035-P1-K2-F3
Method	BLASTX
NCBI GI	g282865
BLAST score	526
E value	1.0e-53
Match length	123
% identity	83
NCBI Description	chlorophyll a/b-binding protein - Arabidopsis thaliana >gi_16207_emb_CAA39534_ (X56062) chlorophyll A/B-binding

protein [Arabidopsis thaliana] >gi_166644 (M85150) chlorophyll a/b-binding protein [Arabidopsis thaliana] >gi_4678304_emb_CAB41095.1_ (AL049655) chlorophyll a/b-binding protein [Arabidopsis thaliana]

Seq. No.	162103
Seq. ID	LIB3177-035-P1-K2-F4
Method	BLASTX
NCBI GI	g120667
BLAST score	654
E value	1.0e-68
Match length	142
% identity	89
NCBI Description	GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE, CYTOSOLIC >gi_81622_pir__JQ1287 glyceraldehyde-3-phosphate dehydrogenase (EC 1.2.1.12), cytosolic - Arabidopsis thaliana >gi_166706 (M64116) cystolic glyceraldehyde-3-phosphate dehydrogenase [Arabidopsis thaliana] >gi_166710 (M64119) glyceraldehyde-3-phosphate dehydrogenase [Arabidopsis thaliana]

Seq. No.	162104
Seq. ID	LIB3177-035-P1-K2-F9
Method	BLASTX
NCBI GI	g1370092
BLAST score	218
E value	1.0e-17
Match length	97
% identity	24
NCBI Description	(X96669) kinase [Gallus gallus]

Seq. No.	162105
Seq. ID	LIB3177-035-P1-K2-G12
Method	BLASTX
NCBI GI	g2119846
BLAST score	168
E value	3.0e-12
Match length	58
% identity	66
NCBI Description	chlorophyll a/b-binding protein type I precursor Lhb1B2 - Arabidopsis thaliana >gi_16364_emb_CAA45790_ (X64460) photosystem II type I chlorophyll a /b binding protein [Arabidopsis thaliana] >gi_3128230 (AC004077) photosystem II type I chlorophyll a/b binding protein [Arabidopsis thaliana] >gi_3337371 (AC004481) photosystem II type I chlorophyll a/b binding protein [Arabidopsis thaliana]

Seq. No.	162106
Seq. ID	LIB3177-035-P1-K2-G2
Method	BLASTX
NCBI GI	g3421346
BLAST score	591
E value	2.0e-61
Match length	131
% identity	89
NCBI Description	(AJ007723) ribosomal protein S4 [Orobanche minor]

Seq. No.	162107
Seq. ID	LIB3177-035-P1-K2-H3
Method	BLASTX
NCBI GI	g115783
BLAST score	288
E value	3.0e-26
Match length	84
% identity	65
NCBI Description	CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR (CAB-140) (LHCP) >gi_16376_emb_CAA27543_ (X03909) chlorophyll a/b binding protein (LHCP AB 140) [Arabidopsis thaliana]

Seq. No.	162108
Seq. ID	LIB3177-035-P1-K2-H4
Method	BLASTN
NCBI GI	g2828266
BLAST score	206
E value	1.0e-112
Match length	258
% identity	95
NCBI Description	Arabidopsis thaliana mRNA for geranylgeranyl reductase

Seq. No.	162109
Seq. ID	LIB3177-036-P1-K1-A4
Method	BLASTX
NCBI GI	g2117612
BLAST score	298
E value	5.0e-27
Match length	105
% identity	62
NCBI Description	catalase (EC 1.11.1.6) 3 - Arabidopsis thaliana

Seq. No.	162110
Seq. ID	LIB3177-036-P1-K1-B1
Method	BLASTX
NCBI GI	g99688
BLAST score	257
E value	3.0e-22
Match length	96
% identity	55
NCBI Description	translation elongation factor eEF-1 alpha chain (gene A4) - Arabidopsis thaliana >gi_295789_emb_CAA34456_ (X16432) elongation factor 1-alpha [Arabidopsis thaliana]

Seq. No.	162111
Seq. ID	LIB3177-036-P1-K1-B2
Method	BLASTX
NCBI GI	g2764941
BLAST score	314
E value	7.0e-29
Match length	104
% identity	55
NCBI Description	(X98255) transcriptionally stimulated by gibberellins; expressed in meristematic region, and style [Arabidopsis thaliana]

Seq. No.	162112
Seq. ID	LIB3177-036-P1-K1-B3
Method	BLASTX
NCBI GI	g2119846
BLAST score	441
E value	7.0e-44
Match length	125
% identity	71
NCBI Description	chlorophyll a/b-binding protein type I precursor Lhb1B2 - Arabidopsis thaliana >gi_16364_emb_CAA45790_ (X64460) photosystem II type I chlorophyll a /b binding protein [Arabidopsis thaliana] >gi_3128230 (AC004077) photosystem II type I chlorophyll a/b binding protein [Arabidopsis thaliana] >gi_3337371 (AC004481) photosystem II type I chlorophyll a/b binding protein [Arabidopsis thaliana]

Seq. No.	162113
Seq. ID	LIB3177-036-P1-K1-C12
Method	BLASTX
NCBI GI	g132090
BLAST score	380
E value	1.0e-36
Match length	118
% identity	64
NCBI Description	RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN 1B PRECURSOR (RUBISCO SMALL SUBUNIT 1B) >gi_68062_pir__RKMUB1 ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain B1 precursor - Arabidopsis thaliana >gi_16193_emb_CAA32700_ (X14564) ribulose bisphosphate carboxylase [Arabidopsis thaliana]

Seq. No.	162114
Seq. ID	LIB3177-036-P1-K1-C3
Method	BLASTX
NCBI GI	g4585935
BLAST score	270
E value	6.0e-24
Match length	83
% identity	63
NCBI Description	(AC007211) putative chlorophyll A/B binding protein [Arabidopsis thaliana] >gi_4741946_gb_AAD28770.1_AF134123_1 (AF134123) Lhcb2 protein [Arabidopsis thaliana]

Seq. No.	162115
Seq. ID	LIB3177-036-P1-K1-C5
Method	BLASTN
NCBI GI	g4185120
BLAST score	60
E value	2.0e-25
Match length	164
% identity	84
NCBI Description	Arabidopsis thaliana chromosome 1 BAC F5F19 sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	162116
Seq. ID	LIB3177-036-P1-K1-D1
Method	BLASTX

NCBI GI	g2506443
BLAST score	267
E value	2.0e-23
Match length	93
% identity	59
NCBI Description	GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE A PRECURSOR, CHLOROPLAST >gi_2117520_pir__JQ1285 glyceraldehyde-3-phosphate dehydrogenase (NADP+) (phosphorylating) (EC 1.2.1.13) A precursor, chloroplast - Arabidopsis thaliana >gi_166704 (M64117) glyceraldehyde 3-phosphate dehydrogenase [Arabidopsis thaliana] >gi_1402885_emb_CAA66816_ (X98130) glyceraldehyde-3-phosphate dehydrogenase (NADP+) (phosphorylating) [Arabidopsis thaliana]

Seq. No.	162117
Seq. ID	LIB3177-036-P1-K1-D3
Method	BLASTN
NCBI GI	g4662640
BLAST score	66
E value	1.0e-28
Match length	222
% identity	37
NCBI Description	Arabidopsis thaliana chromosome II BAC F15K19 genomic sequence, complete sequence

Seq. No.	162118
Seq. ID	LIB3177-036-P1-K1-D5
Method	BLASTN
NCBI GI	g2815519
BLAST score	32
E value	1.0e-08
Match length	100
% identity	83
NCBI Description	Arabidopsis thaliana BAC T5J8 from chromosome IV, top arm, complete sequence [Arabidopsis thaliana]

Seq. No.	162119
Seq. ID	LIB3177-036-P1-K1-D6
Method	BLASTX
NCBI GI	g2199574
BLAST score	253
E value	4.0e-22
Match length	70
% identity	69
NCBI Description	(AF004293) aquaporin [Brassica rapa]

Seq. No.	162120
Seq. ID	LIB3177-036-P1-K1-E11
Method	BLASTN
NCBI GI	g2894557
BLAST score	38
E value	3.0e-12
Match length	58
% identity	91
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone T8O5 (ESSAII project)

Seq. No.	162121
Seq. ID	LIB3177-036-P1-K1-E2
Method	BLASTX
NCBI GI	g2244837
BLAST score	258
E value	2.0e-22
Match length	102
% identity	57
NCBI Description	(Z97337) proteasome chain protein [Arabidopsis thaliana] >gi_2511572_emb_CAA73618.1_ (Y13175) multicatalytic endopeptidase [Arabidopsis thaliana] >gi_3421114 (AF043535) 20S proteasome beta subunit PBD2 [Arabidopsis thaliana]

Seq. No.	162122
Seq. ID	LIB3177-036-P1-K1-E3
Method	BLASTX
NCBI GI	g4580527
BLAST score	277
E value	1.0e-24
Match length	99
% identity	62
NCBI Description	(AF036307) scarecrow-like 11 [Arabidopsis thaliana]

Seq. No.	162123
Seq. ID	LIB3177-036-P1-K1-E6
Method	BLASTX
NCBI GI	g3158370
BLAST score	169
E value	2.0e-12
Match length	53
% identity	66
NCBI Description	(AF035382) catalase 3 [Arabidopsis thaliana]

Seq. No.	162124
Seq. ID	LIB3177-036-P1-K1-E9
Method	BLASTX
NCBI GI	g1732570
BLAST score	268
E value	1.0e-23
Match length	113
% identity	56
NCBI Description	(U72153) beta-glucosidase [Arabidopsis thaliana]

Seq. No.	162125
Seq. ID	LIB3177-036-P1-K1-F1
Method	BLASTN
NCBI GI	g2642152
BLAST score	74
E value	2.0e-33
Match length	362
% identity	80
NCBI Description	Arabidopsis thaliana chromosome II BAC T5I7 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	162126
Seq. ID	LIB3177-036-P1-K1-F2

Method	BLASTN
NCBI GI	g4544461
BLAST score	134
E value	3.0e-69
Match length	337
% identity	88
NCBI Description	Arabidopsis thaliana chromosome II BAC F23E6 genomic sequence, complete sequence

Seq. No.	162127
Seq. ID	LIB3177-036-P1-K1-F9
Method	BLASTX
NCBI GI	g4589980
BLAST score	220
E value	6.0e-18
Match length	97
% identity	51
NCBI Description	(AC007195) cyclophilin, 3' partial [Arabidopsis thaliana]

Seq. No.	162128
Seq. ID	LIB3177-036-P1-K1-G4
Method	BLASTX
NCBI GI	g166834
BLAST score	318
E value	3.0e-33
Match length	104
% identity	77
NCBI Description	(M86720) ribulose bisphosphate carboxylase/oxygenase activase [Arabidopsis thaliana] >gi_2642155 (AC003000) Rubisco activase [Arabidopsis thaliana]

Seq. No.	162129
Seq. ID	LIB3177-036-P1-K1-G5
Method	BLASTX
NCBI GI	g166835
BLAST score	305
E value	4.0e-28
Match length	94
% identity	70
NCBI Description	(M86720) ribulose bisphosphate carboxylase/oxygenase activase [Arabidopsis thaliana] >gi_2642170 (AC003000) Rubisco activase [Arabidopsis thaliana]

Seq. No.	162130
Seq. ID	LIB3177-036-P1-K1-H1
Method	BLASTX
NCBI GI	g2388891
BLAST score	292
E value	2.0e-26
Match length	98
% identity	65
NCBI Description	(Y14765) calmodulin [Lycopersicon esculentum]

Seq. No.	162131
Seq. ID	LIB3177-036-P1-K1-H3
Method	BLASTX
NCBI GI	g4049349

BLAST score	213
E value	3.0e-17
Match length	102
% identity	48
NCBI Description	(AL034567) ubiquinol-cytochrome c reductase-like protein [Arabidopsis thaliana]

Seq. No.	162132
Seq. ID	LIB3177-036-P1-K2-A1
Method	BLASTX
NCBI GI	g541858
BLAST score	497
E value	4.0e-60
Match length	121
% identity	96
NCBI Description	endoxyloglucan transferase - Arabidopsis thaliana >gi_469484_dbj_BAA03921_ (D16454) endo-xyloglucan transferase [Arabidopsis thaliana] >gi_4063757 (AC005561) endo-xyloglucan transferase [Arabidopsis thaliana]

Seq. No.	162133
Seq. ID	LIB3177-036-P1-K2-A10
Method	BLASTN
NCBI GI	g166695
BLAST score	108
E value	5.0e-54
Match length	156
% identity	92
NCBI Description	Arabidopsis thaliana recombination and DNA-damage resistance protein (DRT112) mRNA, complete cds

Seq. No.	162134
Seq. ID	LIB3177-036-P1-K2-A11
Method	BLASTN
NCBI GI	g4678291
BLAST score	64
E value	7.0e-28
Match length	132
% identity	89
NCBI Description	Arabidopsis thaliana DNA chromosome 3, BAC clone F28P10 (ESSA project)

Seq. No.	162135
Seq. ID	LIB3177-036-P1-K2-A2
Method	BLASTX
NCBI GI	g4008008
BLAST score	234
E value	6.0e-20
Match length	77
% identity	62
NCBI Description	(AF084035) receptor-like protein kinase [Arabidopsis thaliana]

Seq. No.	162136
Seq. ID	LIB3177-036-P1-K2-A3
Method	BLASTX
NCBI GI	g1703091

BLAST score	473
E value	2.0e-47
Match length	109
% identity	85
NCBI Description	ACYL CARRIER PROTEIN, MITOCHONDRIAL PRECURSOR (ACP) (NADH-UBIQUINONE OXIDOREDUCTASE 9.6 KD SUBUNIT) (MTACP-1) >gi_903689 (L23574) acyl carrier protein precursor [Arabidopsis thaliana] >gi_3341682 (AC003672) acyl carrier protein [Arabidopsis thaliana]

Seq. No.	162137
Seq. ID	LIB3177-036-P1-K2-A4
Method	BLASTX
NCBI GI	g2244780
BLAST score	212
E value	2.0e-17
Match length	49
% identity	88
NCBI Description	(Z97335) hypothetical protein [Arabidopsis thaliana]

Seq. No.	162138
Seq. ID	LIB3177-036-P1-K2-A5
Method	BLASTX
NCBI GI	g132110
BLAST score	228
E value	4.0e-19
Match length	65
% identity	69
NCBI Description	RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN 3B PRECURSOR (RUBISCO SMALL SUBUNIT 3B) >gi_68060_pir__RKMUB3 ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain B3 precursor - Arabidopsis thaliana >gi_16195_emb_CAA32702_ (X14564) ribulose bisphosphate carboxylase [Arabidopsis thaliana]

Seq. No.	162139
Seq. ID	LIB3177-036-P1-K2-A6
Method	BLASTX
NCBI GI	g2462746
BLAST score	378
E value	1.0e-36
Match length	84
% identity	89
NCBI Description	(AC002292) Similar to ATP-citrate-lyase [Arabidopsis thaliana]

Seq. No.	162140
Seq. ID	LIB3177-036-P1-K2-A7
Method	BLASTN
NCBI GI	g4757415
BLAST score	57
E value	1.0e-23
Match length	207
% identity	88
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MYN21, complete sequence

Seq. No.	162141
Seq. ID	LIB3177-036-P1-K2-A9
Method	BLASTX
NCBI GI	g2764941
BLAST score	372
E value	6.0e-38
Match length	102
% identity	82
NCBI Description	(X98255) transcriptionally stimulated by gibberellins; expressed in meristematic region, and style [Arabidopsis thaliana]

Seq. No.	162142
Seq. ID	LIB3177-036-P1-K2-B1
Method	BLASTX
NCBI GI	g2764941
BLAST score	607
E value	3.0e-63
Match length	106
% identity	100
NCBI Description	(X98255) transcriptionally stimulated by gibberellins; expressed in meristematic region, and style [Arabidopsis thaliana]

Seq. No.	162143
Seq. ID	LIB3177-036-P1-K2-B2
Method	BLASTX
NCBI GI	g2119848
BLAST score	731
E value	8.0e-78
Match length	140
% identity	100
NCBI Description	chlorophyll a/b-binding protein type I precursor Lhb1B1 - Arabidopsis thaliana >gi_16366_emb_CAA45789_ (X64459) photosystem II type I chlorophyll a /b binding protein [Arabidopsis thaliana] >gi_3128229 (AC004077) putative photosystem II type I chlorophyll a/b binding protein [Arabidopsis thaliana] >gi_3337372 (AC004481) putative photosystem II type I chlorophyll a/b binding protein [Arabidopsis thaliana]

Seq. No.	162144
Seq. ID	LIB3177-036-P1-K2-B4
Method	BLASTX
NCBI GI	g2062159
BLAST score	400
E value	4.0e-39
Match length	105
% identity	38
NCBI Description	(AC001645) jasmonate inducible protein isolog [Arabidopsis thaliana]

Seq. No.	162145
Seq. ID	LIB3177-036-P1-K2-B8
Method	BLASTN
NCBI GI	g3367500
BLAST score	33

E value	3.0e-09
Match length	107
% identity	87
NCBI Description	REVERSE-COMPLEMENT OF: F23J3.GCG.SEQ CHECK: 2754 FROM: 1 TO: 93489, complete sequence [Arabidopsis thaliana]

Seq. No.	162146
Seq. ID	LIB3177-036-P1-K2-C1
Method	BLASTX
NCBI GI	g2232354
BLAST score	216
E value	2.0e-17
Match length	113
% identity	40
NCBI Description	(AF006081) UDPG glucosyltransferase [Solanum berthaultii]

Seq. No.	162147
Seq. ID	LIB3177-036-P1-K2-C10
Method	BLASTX
NCBI GI	g2119846
BLAST score	170
E value	2.0e-12
Match length	76
% identity	47
NCBI Description	chlorophyll a/b-binding protein type I precursor Lhb1B2 - Arabidopsis thaliana >gi_16364_emb_CAA45790_ (X64460) photosystem II type I chlorophyll a /b binding protein [Arabidopsis thaliana] >gi_3128230 (AC004077) photosystem II type I chlorophyll a/b binding protein [Arabidopsis thaliana] >gi_3337371 (AC004481) photosystem II type I chlorophyll a/b binding protein [Arabidopsis thaliana]

Seq. No.	162148
Seq. ID	LIB3177-036-P1-K2-C11
Method	BLASTX
NCBI GI	g132102
BLAST score	677
E value	2.0e-71
Match length	130
% identity	95
NCBI Description	RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN 2B PRECURSOR (RUBISCO SMALL SUBUNIT 2B) >gi_68061_pir__RKMUB2 ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain B2 precursor - Arabidopsis thaliana >gi_16194_emb_CAA32701_ (X14564) ribulose bisphosphate carboxylase [Arabidopsis thaliana]

Seq. No.	162149
Seq. ID	LIB3177-036-P1-K2-C12
Method	BLASTN
NCBI GI	g14342
BLAST score	132
E value	4.0e-68
Match length	272
% identity	87
NCBI Description	A.thaliana mRNA for carbonic anhydrase

Seq. No.	162150
Seq. ID	LIB3177-036-P1-K2-C2
Method	BLASTX
NCBI GI	g4585935
BLAST score	653
E value	1.0e-68
Match length	125
% identity	98
NCBI Description	(AC007211) putative chlorophyll A/B binding protein [Arabidopsis thaliana] >gi_4741946_gb_AAD28770.1_AF134123_1 (AF134123) Lhcb2 protein [Arabidopsis thaliana]

Seq. No.	162151
Seq. ID	LIB3177-036-P1-K2-C3
Method	BLASTX
NCBI GI	g2506443
BLAST score	314
E value	4.0e-29
Match length	83
% identity	71
NCBI Description	GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE A PRECURSOR, CHLOROPLAST >gi_2117520_pir__JQ1285 glyceraldehyde-3-phosphate dehydrogenase (NADP+) (phosphorylating) (EC 1.2.1.13) A precursor, chloroplast - Arabidopsis thaliana >gi_166704 (M64117) glyceraldehyde 3-phosphate dehydrogenase [Arabidopsis thaliana] >gi_1402885_emb_CAA66816_ (X98130) glyceraldehyde-3-phosphate dehydrogenase (NADP+) (phosphorylating) [Arabidopsis thaliana]

Seq. No.	162152
Seq. ID	LIB3177-036-P1-K2-C4
Method	BLASTX
NCBI GI	g4220457
BLAST score	447
E value	1.0e-44
Match length	119
% identity	32
NCBI Description	(AC006216) Similar to gi_3413714 T19L18.21 putative myrosinase-binding protein from Arabidopsis thaliana BAC gb_AC004747. EST gb_N96478 comes from this gene. [Arabidopsis thaliana]

Seq. No.	162153
Seq. ID	LIB3177-036-P1-K2-C6
Method	BLASTX
NCBI GI	g4585614
BLAST score	167
E value	8.0e-12
Match length	85
% identity	46
NCBI Description	(AL049628) L-aspartate oxidase [Streptomyces coelicolor]

Seq. No.	162154
Seq. ID	LIB3177-036-P1-K2-D1
Method	BLASTX
NCBI GI	g133872

BLAST score	321
E value	9.0e-30
Match length	82
% identity	73
NCBI Description	30S RIBOSOMAL PROTEIN S1, CHLOROPLAST PRECURSOR (CS1) >gi_282838_pir__S26494 ribosomal protein S1, chloroplast - spinach >gi_322404_pir__A44121 small subunit ribosomal protein CS1, CS-S2 - spinach >gi_18060_emb_CAA46927_ (X66135) ribosomal protein S1 [Spinacia oleracea] >gi_170143 (M82923) chloroplast ribosomal protein S1 [Spinacia oleracea]

Seq. No.	162155
Seq. ID	LIB3177-036-P1-K2-D2
Method	BLASTN
NCBI GI	g4662640
BLAST score	113
E value	1.0e-56
Match length	264
% identity	19
NCBI Description	Arabidopsis thaliana chromosome II BAC F15K19 genomic sequence, complete sequence

Seq. No.	162156
Seq. ID	LIB3177-036-P1-K2-D4
Method	BLASTX
NCBI GI	g4587564
BLAST score	235
E value	3.0e-20
Match length	44
% identity	100
NCBI Description	(AC006550) Strong similarity to gb_X14017 photosystem I reaction centre subunit II precursor (psaD) from Spinacia oleracea. ESTs gb_R30423, gb_T42998, gb_Z18178, gb_T14133, gb_N65521, gb_T42498, gb_T41918, gb_N38024

Seq. No.	162157
Seq. ID	LIB3177-036-P1-K2-D5
Method	BLASTX
NCBI GI	g1175011
BLAST score	479
E value	8.0e-53
Match length	107
% identity	99
NCBI Description	PLASMA MEMBRANE INTRINSIC PROTEIN 1B (TRANSMEMBRANE PROTEIN A) (TMP-A) >gi_296085_emb_CAA48356_ (X68293) transmembrane protein [Arabidopsis thaliana] >gi_3386599 (AC004665) plasma membrane intrinsic protein 1B [Arabidopsis thaliana]

Seq. No.	162158
Seq. ID	LIB3177-036-P1-K2-E1
Method	BLASTX
NCBI GI	g2244837
BLAST score	548
E value	2.0e-56
Match length	110
% identity	98

NCBI Description	(Z97337) proteasome chain protein [Arabidopsis thaliana] >gi_2511572_emb_CAA73618.1_ (Y13175) multicatalytic endopeptidase [Arabidopsis thaliana] >gi_3421114 (AF043535) 20S proteasome beta subunit PBD2 [Arabidopsis thaliana]
Seq. No.	162159
Seq. ID	LIB3177-036-P1-K2-E10
Method	BLASTX
NCBI GI	g2894564
BLAST score	220
E value	6.0e-18
Match length	40
% identity	100
NCBI Description	(AL021890) putative protein [Arabidopsis thaliana]
Seq. No.	162160
Seq. ID	LIB3177-036-P1-K2-E11
Method	BLASTN
NCBI GI	g2894557
BLAST score	50
E value	1.0e-19
Match length	94
% identity	88
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone T8O5 (ESSAII project)
Seq. No.	162161
Seq. ID	LIB3177-036-P1-K2-E2
Method	BLASTX
NCBI GI	g4580527
BLAST score	602
E value	1.0e-62
Match length	116
% identity	99
NCBI Description	(AF036307) scarecrow-like 11 [Arabidopsis thaliana]
Seq. No.	162162
Seq. ID	LIB3177-036-P1-K2-E3
Method	BLASTX
NCBI GI	g1346758
BLAST score	279
E value	8.0e-25
Match length	70
% identity	84
NCBI Description	SERINE/THREONINE PROTEIN PHOSPHATASE PP1 ISOZYME 4 >gi_421853_pir__S31088 phosphoprotein phosphatase (EC 3.1.3.16) 1 catalytic chain (clone TOPP4) - Arabidopsis thaliana >gi_166801 (M93411) phosphoprotein phosphatase 1 [Arabidopsis thaliana] >gi_2642169 (AC003000) serine/threonine protein phosphatase PP1 isozyme 4 (TOPP4) [Arabidopsis thaliana]
Seq. No.	162163
Seq. ID	LIB3177-036-P1-K2-E4
Method	BLASTX
NCBI GI	g2507092
BLAST score	230

E value	4.0e-19
Match length	55
% identity	85
NCBI Description	PROTOCHLOROPHYLLIDE REDUCTASE PRECURSOR (PCR) (NADPH-PROTOCHLOROPHYLLIDE OXIDOREDUCTASE) >gi_968977 (U29785) NADPH:protochlorophyllide oxidoreductase B [Arabidopsis thaliana] >gi_1583456_prf__2120441B protochlorophyllide oxidoreductase [Arabidopsis thaliana]

Seq. No.	162164
Seq. ID	LIB3177-036-P1-K2-E5
Method	BLASTX
NCBI GI	g2117612
BLAST score	368
E value	3.0e-44
Match length	98
% identity	95
NCBI Description	catalase (EC 1.11.1.6) 3 - Arabidopsis thaliana

Seq. No.	162165
Seq. ID	LIB3177-036-P1-K2-E9
Method	BLASTN
NCBI GI	g472872
BLAST score	40
E value	2.0e-13
Match length	127
% identity	83
NCBI Description	A.thaliana mRNA for plasma membrane intrinsic protein 1a

Seq. No.	162166
Seq. ID	LIB3177-036-P1-K2-F1
Method	BLASTN
NCBI GI	g4544461
BLAST score	277
E value	1.0e-154
Match length	340
% identity	97
NCBI Description	Arabidopsis thaliana chromosome II BAC F23E6 genomic sequence, complete sequence

Seq. No.	162167
Seq. ID	LIB3177-036-P1-K2-F4
Method	BLASTX
NCBI GI	g4689386
BLAST score	198
E value	2.0e-15
Match length	58
% identity	67
NCBI Description	(AF139468) photosystem I reaction center subunit III [Vigna radiata]

Seq. No.	162168
Seq. ID	LIB3177-036-P1-K2-F6
Method	BLASTX
NCBI GI	g132166
BLAST score	378
E value	4.0e-40

Match length	108
% identity	85
NCBI Description	RIBULOSE BISPHOSPHATE CARBOXYLASE/OXYGENASE ACTIVASE PRECURSOR (RUBISCO ACTIVASE) >gi_81660_pir__S04048 ribulose-bisphosphate carboxylase activase precursor - Arabidopsis thaliana >gi_16471_emb_CAA32429_ (X14212) rubisco activase (AA 1 - 473) [Arabidopsis thaliana]

Seq. No.	162169
Seq. ID	LIB3177-036-P1-K2-F7
Method	BLASTN
NCBI GI	g2246620
BLAST score	32
E value	9.0e-09
Match length	60
% identity	88
NCBI Description	Arabidopsis thaliana salt-stress induced tonoplast intrinsic protein mRNA, complete cds

Seq. No.	162170
Seq. ID	LIB3177-036-P1-K2-F8
Method	BLASTX
NCBI GI	g2129569
BLAST score	363
E value	8.0e-35
Match length	93
% identity	75
NCBI Description	cytosolic cyclophilin ROC3 - Arabidopsis thaliana >gi_1305455 (U40399) cytosolic cyclophilin [Arabidopsis thaliana] >gi_4581104_gb_AAD24594.1_AC005825_1 (AC005825) cytosolic cyclophilin (ROC3) [Arabidopsis thaliana]

Seq. No.	162171
Seq. ID	LIB3177-036-P1-K2-G3
Method	BLASTX
NCBI GI	g1362058
BLAST score	508
E value	1.0e-51
Match length	108
% identity	61
NCBI Description	calmodulin - garden pea

Seq. No.	162172
Seq. ID	LIB3177-036-P1-K2-G4
Method	BLASTX
NCBI GI	g166834
BLAST score	544
E value	6.0e-56
Match length	117
% identity	92
NCBI Description	(M86720) ribulose bisphosphate carboxylase/oxygenase activase [Arabidopsis thaliana] >gi_2642155 (AC003000) Rubisco activase [Arabidopsis thaliana]

Seq. No.	162173
Seq. ID	LIB3177-036-P1-K2-H2
Method	BLASTX

NCBI GI	g4049349
BLAST score	56
E value	2.0e-34
Match length	106
% identity	77
NCBI Description	(AL034567) ubiquinol-cytochrome c reductase-like protein [Arabidopsis thaliana]

Seq. No.	162174
Seq. ID	LIB3177-036-P1-K2-H3
Method	BLASTX
NCBI GI	g3158370
BLAST score	286
E value	4.0e-26
Match length	63
% identity	87
NCBI Description	(AF035382) catalase 3 [Arabidopsis thaliana]

Seq. No.	162175
Seq. ID	LIB3177-038-P1-K1-A11
Method	BLASTN
NCBI GI	g2059328
BLAST score	49
E value	2.0e-18
Match length	109
% identity	86
NCBI Description	A.thaliana gene encoding shaggy-like kinase gamma

Seq. No.	162176
Seq. ID	LIB3177-038-P1-K1-A6
Method	BLASTN
NCBI GI	g2288979
BLAST score	99
E value	2.0e-48
Match length	349
% identity	86
NCBI Description	Arabidopsis thaliana chromosome II BAC T01O24 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	162177
Seq. ID	LIB3177-038-P1-K1-A8
Method	BLASTX
NCBI GI	g2062164
BLAST score	61
E value	6.0e-13
Match length	75
% identity	48
NCBI Description	(AC001645) jasmonate inducible protein isolog [Arabidopsis thaliana]

Seq. No.	162178
Seq. ID	LIB3177-038-P1-K1-A9
Method	BLASTN
NCBI GI	g3169169
BLAST score	50
E value	4.0e-19
Match length	282

% identity	78
NCBI Description	Arabidopsis thaliana chromosome II BAC F21P24 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	162179
Seq. ID	LIB3177-038-P1-K1-B12
Method	BLASTN
NCBI GI	g1020156
BLAST score	86
E value	1.0e-40
Match length	295
% identity	82
NCBI Description	Arabidopsis thaliana clone myb7 DNA-binding protein mRNA, complete cds

Seq. No.	162180
Seq. ID	LIB3177-038-P1-K1-B9
Method	BLASTX
NCBI GI	g2911055
BLAST score	177
E value	5.0e-13
Match length	93
% identity	49
NCBI Description	(AL021961) putative protein [Arabidopsis thaliana]

Seq. No.	162181
Seq. ID	LIB3177-038-P1-K1-C9
Method	BLASTX
NCBI GI	g2583125
BLAST score	344
E value	1.0e-32
Match length	92
% identity	73
NCBI Description	(AC002387) putative transketolase precursor [Arabidopsis thaliana]

Seq. No.	162182
Seq. ID	LIB3177-038-P1-K1-D10
Method	BLASTX
NCBI GI	g2062161
BLAST score	342
E value	3.0e-32
Match length	101
% identity	66
NCBI Description	(AC001645) jasmonate inducible protein isolog [Arabidopsis thaliana]

Seq. No.	162183
Seq. ID	LIB3177-038-P1-K1-D11
Method	BLASTN
NCBI GI	g3702731
BLAST score	103
E value	1.0e-50
Match length	332
% identity	82
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MFC19, complete sequence [Arabidopsis thaliana]

Seq. No.	162184
Seq. ID	LIB3177-038-P1-K1-D12
Method	BLASTN
NCBI GI	g2760168
BLAST score	82
E value	2.0e-38
Match length	234
% identity	83
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MEE6, complete sequence [Arabidopsis thaliana]

Seq. No.	162185
Seq. ID	LIB3177-038-P1-K1-D7
Method	BLASTN
NCBI GI	g2351068
BLAST score	58
E value	5.0e-24
Match length	174
% identity	83
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MRH10, complete sequence [Arabidopsis thaliana]

Seq. No.	162186
Seq. ID	LIB3177-038-P1-K1-E10
Method	BLASTX
NCBI GI	g3228664
BLAST score	159
E value	1.0e-10
Match length	78
% identity	46
NCBI Description	(AF069986) nitrilase and fragile histidine triad fusion protein NitFhit [Caenorhabditis elegans]

Seq. No.	162187
Seq. ID	LIB3177-038-P1-K1-E11
Method	BLASTX
NCBI GI	g3983125
BLAST score	176
E value	3.0e-21
Match length	109
% identity	59
NCBI Description	(AF097648) phosphate/triose-phosphate translocator precursor [Arabidopsis thaliana]

Seq. No.	162188
Seq. ID	LIB3177-038-P1-K1-E12
Method	BLASTN
NCBI GI	g984051
BLAST score	51
E value	8.0e-20
Match length	138
% identity	85
NCBI Description	A.thaliana mRNA for thioglucoside glucohydrolase

Seq. No.	162189
Seq. ID	LIB3177-038-P1-K1-F11

Method	BLASTX
NCBI GI	g3882356
BLAST score	289
E value	5.0e-26
Match length	109
% identity	61
NCBI Description	(U92460) 12-oxophytodienoate reductase OPR2 [Arabidopsis thaliana]

Seq. No.	162190
Seq. ID	LIB3177-038-P1-K1-F12
Method	BLASTN
NCBI GI	g3128137
BLAST score	50
E value	4.0e-19
Match length	286
% identity	86
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K9I9, complete sequence [Arabidopsis thaliana]

Seq. No.	162191
Seq. ID	LIB3177-038-P1-K1-F6
Method	BLASTX
NCBI GI	g132074
BLAST score	250
E value	3.0e-23
Match length	121
% identity	56
NCBI Description	RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN 1A PRECURSOR (RUBISCO SMALL SUBUNIT 1A) >gi_68063_pir__RKMUA1 ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain A1 precursor - Arabidopsis thaliana

Seq. No.	162192
Seq. ID	LIB3177-038-P1-K1-F7
Method	BLASTX
NCBI GI	g2506443
BLAST score	300
E value	3.0e-27
Match length	107
% identity	59
NCBI Description	GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE A PRECURSOR, CHLOROPLAST >gi_2117520_pir__JQ1285 glyceraldehyde-3-phosphate dehydrogenase (NADP+) (phosphorylating) (EC 1.2.1.13) A precursor, chloroplast - Arabidopsis thaliana >gi_166704 (M64117) glyceraldehyde 3-phosphate dehydrogenase [Arabidopsis thaliana] >gi_1402885_emb_CAA66816_ (X98130) glyceraldehyde-3-phosphate dehydrogenase (NADP+) (phosphorylating) [Arabidopsis thaliana]

Seq. No.	162193
Seq. ID	LIB3177-038-P1-K1-F8
Method	BLASTN
NCBI GI	g4589436
BLAST score	139
E value	4.0e-72

Match length	291
% identity	87
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MPA22, complete sequence

Seq. No.	162194
Seq. ID	LIB3177-038-P1-K1-G10
Method	BLASTN
NCBI GI	g4519195
BLAST score	33
E value	5.0e-09
Match length	85
% identity	85
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MQC12, complete sequence

Seq. No.	162195
Seq. ID	LIB3177-038-P1-K1-G11
Method	BLASTX
NCBI GI	g3063442
BLAST score	209
E value	1.0e-16
Match length	102
% identity	49
NCBI Description	(AC003981) F22O13.6 [Arabidopsis thaliana]

Seq. No.	162196
Seq. ID	LIB3177-038-P1-K1-H10
Method	BLASTN
NCBI GI	g2264306
BLAST score	52
E value	3.0e-20
Match length	207
% identity	84
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MBK5, complete sequence [Arabidopsis thaliana]

Seq. No.	162197
Seq. ID	LIB3177-038-P1-K1-H11
Method	BLASTX
NCBI GI	g113024
BLAST score	352
E value	3.0e-33
Match length	139
% identity	55
NCBI Description	ISOCITRATE LYASE (ISOCITRASE) (ISOCITRATASE) (ICL) >gi_553043 (M83534) isocitrate lyase [Arabidopsis thaliana]

Seq. No.	162198
Seq. ID	LIB3177-038-P1-K1-H12
Method	BLASTX
NCBI GI	g2500681
BLAST score	255
E value	4.0e-22
Match length	87
% identity	60
NCBI Description	RIBULOSE BISPHOSPHATE CARBOXYLASE LARGE CHAIN PRECURSOR

(RUBISCO LARGE SUBUNIT) >gi_535102_emb_CAA57012_ (X81106) ribulose bisphosphate carboxylase large subunit [Sherardia arvensis]

Seq. No.	162199
Seq. ID	LIB3177-038-P1-K1-H7
Method	BLASTN
NCBI GI	g3608126
BLAST score	43
E value	5.0e-15
Match length	151
% identity	85
NCBI Description	Arabidopsis thaliana chromosome II BAC T32F12 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	162200
Seq. ID	LIB3177-038-P1-K2-A12
Method	BLASTN
NCBI GI	g2288979
BLAST score	168
E value	1.0e-89
Match length	264
% identity	91
NCBI Description	Arabidopsis thaliana chromosome II BAC T01O24 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	162201
Seq. ID	LIB3177-038-P1-K2-A3
Method	BLASTN
NCBI GI	g2062153
BLAST score	34
E value	6.0e-10
Match length	143
% identity	89
NCBI Description	Arabidopsis thaliana chromosome III BAC T02O04 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	162202
Seq. ID	LIB3177-038-P1-K2-A5
Method	BLASTX
NCBI GI	g3169185
BLAST score	313
E value	6.0e-29
Match length	65
% identity	92
NCBI Description	(AC004401) unknown protein [Arabidopsis thaliana]

Seq. No.	162203
Seq. ID	LIB3177-038-P1-K2-A6
Method	BLASTN
NCBI GI	g456508
BLAST score	117
E value	3.0e-59
Match length	164
% identity	95
NCBI Description	A.thaliana ASK-gamma mRNA

Seq. No.	162204
Seq. ID	LIB3177-038-P1-K2-B1
Method	BLASTN
NCBI GI	g3169169
BLAST score	246
E value	1.0e-136
Match length	250
% identity	71
NCBI Description	Arabidopsis thaliana chromosome II BAC F21P24 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	162205
Seq. ID	LIB3177-038-P1-K2-B11
Method	BLASTN
NCBI GI	g4309683
BLAST score	73
E value	4.0e-33
Match length	157
% identity	87
NCBI Description	Arabidopsis thaliana chromosome 1 BAC T31J12 sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	162206
Seq. ID	LIB3177-038-P1-K2-B12
Method	BLASTN
NCBI GI	g3402671
BLAST score	34
E value	1.0e-09
Match length	158
% identity	88
NCBI Description	Arabidopsis thaliana chromosome II BAC T16B24 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	162207
Seq. ID	LIB3177-038-P1-K2-B2
Method	BLASTX
NCBI GI	g2894378
BLAST score	366
E value	4.0e-35
Match length	119
% identity	61
NCBI Description	(Y14573) putative ribophorin I homologue [Hordeum vulgare]

Seq. No.	162208
Seq. ID	LIB3177-038-P1-K2-B3
Method	BLASTN
NCBI GI	g2245073
BLAST score	62
E value	1.0e-26
Match length	101
% identity	91
NCBI Description	Arabidopsis thaliana DNA chromosome 4, ESSA I contig fragment No

Seq. No.	162209
Seq. ID	LIB3177-038-P1-K2-C1
Method	BLASTX

NCBI GI	g2911055
BLAST score	255
E value	1.0e-22
Match length	71
% identity	73
NCBI Description	(AL021961) putative protein [Arabidopsis thaliana]

Seq. No.	162210
Seq. ID	LIB3177-038-P1-K2-C4
Method	BLASTX
NCBI GI	g2129777
BLAST score	538
E value	3.0e-55
Match length	119
% identity	88
NCBI Description	Y49 protein - Arabidopsis thaliana >gi_928969_emb_CAA62033_ (X90385) Y49 [Arabidopsis thaliana] >gi_1020157 (U26937) DNA-binding protein [Arabidopsis thaliana] >gi_4581115_gb_AAD24605.1_AC005825_12 (AC005825) MYB-like protein;very similar to GB:2129777 [Arabidopsis thaliana]

Seq. No.	162211
Seq. ID	LIB3177-038-P1-K2-D1
Method	BLASTX
NCBI GI	g2583125
BLAST score	530
E value	2.0e-54
Match length	106
% identity	93
NCBI Description	(AC002387) putative transketolase precursor [Arabidopsis thaliana]

Seq. No.	162212
Seq. ID	LIB3177-038-P1-K2-D10
Method	BLASTX
NCBI GI	g421826
BLAST score	309
E value	1.0e-28
Match length	72
% identity	79
NCBI Description	chlorophyll a/b-binding protein CP29 - Arabidopsis thaliana >gi_298036_emb_CAA50712_ (X71878) CP29 [Arabidopsis thaliana]

Seq. No.	162213
Seq. ID	LIB3177-038-P1-K2-D11
Method	BLASTX
NCBI GI	g132677
BLAST score	271
E value	3.0e-24
Match length	87
% identity	63
NCBI Description	50S RIBOSOMAL PROTEIN L15, CHLOROPLAST PRECURSOR (CL15) >gi_71241_pir__R5MUL5 ribosomal protein L15 precursor, chloroplast - Arabidopsis thaliana >gi_16497_emb_CAA77593_ (Z11508) Plastid ribosomal protein CL15 [Arabidopsis thaliana]

Seq. No.	162214
Seq. ID	LIB3177-038-P1-K2-D2
Method	BLASTN
NCBI GI	g2351068
BLAST score	371
E value	0.0e+00
Match length	455
% identity	95
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MRH10, complete sequence [Arabidopsis thaliana]

Seq. No.	162215
Seq. ID	LIB3177-038-P1-K2-D5
Method	BLASTX
NCBI GI	g2062161
BLAST score	487
E value	3.0e-49
Match length	93
% identity	49
NCBI Description	(AC001645) jasmonate inducible protein isolog [Arabidopsis thaliana]

Seq. No.	162216
Seq. ID	LIB3177-038-P1-K2-D9
Method	BLASTX
NCBI GI	g3337361
BLAST score	654
E value	9.0e-69
Match length	144
% identity	82
NCBI Description	(AC004481) ankyrin-like protein [Arabidopsis thaliana]

Seq. No.	162217
Seq. ID	LIB3177-038-P1-K2-E4
Method	BLASTN
NCBI GI	g2760168
BLAST score	177
E value	3.0e-95
Match length	197
% identity	87
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MEE6, complete sequence [Arabidopsis thaliana]

Seq. No.	162218
Seq. ID	LIB3177-038-P1-K2-E5
Method	BLASTX
NCBI GI	g4503719
BLAST score	323
E value	7.0e-30
Match length	122
% identity	50
NCBI Description	fragile histidine triad gene >gi_1706794_sp_P49789_FHIT_HUMAN BIS(5'-ADENOSYL)-TRIPHOSPHATASE (DIADENOSINE 5',5'''-P1,P3-TRIPHOSPHATE HYDROLASE) (DINUCLEOSIDETRIPHOSPHATASE) (AP3A HYDROLASE) (AP3AASE)

(FRAGILE HISTIDINE TRIAD PROTEIN) >gi_3114520_pdb_4FIT_ Fhit-Apo >gi_3114524_pdb_6FIT_ Fhit-Transition State Analog >gi_3318895_pdb_1FHI_ Substrate Analog (Ib2) Complex With The Fragile Histidine Triad Protein, Fhit >gi_1203836 (U46922) member of the histidine triad (HIT) gene family; similar to the S. pombe diadenosine 5',5'''-P1,P4-tetraphosphate asymmetrical hydrolase [Homo sapiens] >gi_1945066 (U76272) diadenosine triphosphate (Ap3A) hydrolase [Homo sapiens]

Seq. No.	162219
Seq. ID	LIB3177-038-P1-K2-E6
Method	BLASTX
NCBI GI	g3983125
BLAST score	340
E value	3.0e-32
Match length	82
% identity	85
NCBI Description	(AF097648) phosphate/triose-phosphate translocator precursor [Arabidopsis thaliana]

Seq. No.	162220
Seq. ID	LIB3177-038-P1-K2-F11
Method	BLASTX
NCBI GI	g3882356
BLAST score	86
E value	1.0e-30
Match length	88
% identity	83
NCBI Description	(U92460) 12-oxophytodienoate reductase OPR2 [Arabidopsis thaliana]

Seq. No.	162221
Seq. ID	LIB3177-038-P1-K2-F2
Method	BLASTX
NCBI GI	g2506443
BLAST score	57
E value	5.0e-65
Match length	130
% identity	94
NCBI Description	GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE A PRECURSOR, CHLOROPLAST >gi_2117520_pir__JQ1285 glyceraldehyde-3-phosphate dehydrogenase (NADP+) (phosphorylating) (EC 1.2.1.13) A precursor, chloroplast - Arabidopsis thaliana >gi_166704 (M64117) glyceraldehyde 3-phosphate dehydrogenase [Arabidopsis thaliana] >gi_1402885_emb_CAA66816_ (X98130) glyceraldehyde-3-phosphate dehydrogenase (NADP+) (phosphorylating) [Arabidopsis thaliana]

Seq. No.	162222
Seq. ID	LIB3177-038-P1-K2-F3
Method	BLASTX
NCBI GI	g3122572
BLAST score	343
E value	2.0e-32
Match length	118

% identity	58
NCBI Description	NADH-UBIQUINONE OXIDOREDUCTASE 75 KD SUBUNIT PRECURSOR (COMPLEX I-75KD) (CI-75KD) (76 KD MITOCHONDRIAL COMPLEX I SUBUNIT) >gi_1084434_pir__S52737 NADH dehydrogenase (ubiquinone) (EC 1.6.5.3) 76K chain precursor - potato >gi_758340_emb_CAA59818_ (X85808) 76 kDa mitochondrial complex I subunit [Solanum tuberosum]

Seq. No.	162223
Seq. ID	LIB3177-038-P1-K2-F6
Method	BLASTX
NCBI GI	g132074
BLAST score	304
E value	2.0e-28
Match length	69
% identity	86
NCBI Description	RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN 1A PRECURSOR (RUBISCO SMALL SUBUNIT 1A) >gi_68063_pir__RKMUA1 ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain A1 precursor - Arabidopsis thaliana

Seq. No.	162224
Seq. ID	LIB3177-038-P1-K2-F7
Method	BLASTN
NCBI GI	g4586241
BLAST score	96
E value	8.0e-47
Match length	199
% identity	87
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone T20K18 (ESSA project)

Seq. No.	162225
Seq. ID	LIB3177-038-P1-K2-G2
Method	BLASTN
NCBI GI	g2351069
BLAST score	60
E value	3.0e-25
Match length	194
% identity	92
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MSH12, complete sequence [Arabidopsis thaliana]

Seq. No.	162226
Seq. ID	LIB3177-038-P1-K2-G6
Method	BLASTN
NCBI GI	g3063438
BLAST score	104
E value	1.0e-51
Match length	201
% identity	94
NCBI Description	Complete sequence of Arabidopsis F22013, complete sequence [Arabidopsis thaliana]

Seq. No.	162227
Seq. ID	LIB3177-038-P1-K2-H1
Method	BLASTN

NCBI GI	g2062153
BLAST score	44
E value	3.0e-16
Match length	64
% identity	32
NCBI Description	Arabidopsis thaliana chromosome III BAC T02O04 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	162228
Seq. ID	LIB3177-038-P1-K2-H11
Method	BLASTX
NCBI GI	g113024
BLAST score	354
E value	3.0e-34
Match length	69
% identity	94
NCBI Description	ISOCITRATE LYASE (ISOCITRASE) (ISOCITRATASE) (ICL) >gi_553043 (M83534) isocitrate lyase [Arabidopsis thaliana]

Seq. No.	162229
Seq. ID	LIB3177-038-P1-K2-H2
Method	BLASTN
NCBI GI	g3608126
BLAST score	163
E value	1.0e-86
Match length	300
% identity	95
NCBI Description	Arabidopsis thaliana chromosome II BAC T32F12 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	162230
Seq. ID	LIB3177-038-P1-K2-H4
Method	BLASTN
NCBI GI	g2264306
BLAST score	154
E value	2.0e-81
Match length	186
% identity	96
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MBK5, complete sequence [Arabidopsis thaliana]

Seq. No.	162231
Seq. ID	LIB3177-038-P1-K2-H5
Method	BLASTX
NCBI GI	g113024
BLAST score	322
E value	2.0e-30
Match length	65
% identity	92
NCBI Description	ISOCITRATE LYASE (ISOCITRASE) (ISOCITRATASE) (ICL) >gi_553043 (M83534) isocitrate lyase [Arabidopsis thaliana]

Seq. No.	162232
Seq. ID	LIB3177-038-P1-K2-H6
Method	BLASTX
NCBI GI	g421969
BLAST score	160

E value	2.0e-11
Match length	37
% identity	81
NCBI Description	ribulose-bisphosphate carboxylase (EC 4.1.1.39) large chain - coffee chloroplast (fragment) >gi_1322147_emb_CAA49827_ (X70364) rbcL [Coffea arabica]

Seq. No.	162233
Seq. ID	LIB3177-039-P1-K1-A1
Method	BLASTX
NCBI GI	g4741960
BLAST score	376
E value	3.0e-36
Match length	113
% identity	64
NCBI Description	(AF134130) Lhcb6 protein [Arabidopsis thaliana]

Seq. No.	162234
Seq. ID	LIB3177-039-P1-K1-A2
Method	BLASTX
NCBI GI	g131398
BLAST score	247
E value	4.0e-21
Match length	90
% identity	57
NCBI Description	PHOTOSYSTEM II 10 KD POLYPEPTIDE PRECURSOR >gi_72714_pir__F2MU10 photosystem II 10K protein precursor - Arabidopsis thaliana >gi_16447_emb_CAA39441_ (X55970) photosystem II 10 kDa polypeptide [Arabidopsis thaliana] >gi_3152571 (AC002986) Match to photosystem II 10kDa polypeptide gb_X55970. ESTs gb_Z17693, gb_N37616, gb_T41858, gb_T88021, gb_R37531, gb_T04679, gb_N37520, gb_N64965, gb_Z17592 and gb_N65338, gb_N37466 and gb_T45400 come from this gene. [Arabidopsis

Seq. No.	162235
Seq. ID	LIB3177-039-P1-K1-A4
Method	BLASTX
NCBI GI	g132110
BLAST score	271
E value	3.0e-24
Match length	79
% identity	68
NCBI Description	RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN 3B PRECURSOR (RUBISCO SMALL SUBUNIT 3B) >gi_68060_pir__RKMUB3 ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain B3 precursor - Arabidopsis thaliana >gi_16195_emb_CAA32702_ (X14564) ribulose bisphosphate carboxylase [Arabidopsis thaliana]

Seq. No.	162236
Seq. ID	LIB3177-039-P1-K1-B1
Method	BLASTX
NCBI GI	g2497733
BLAST score	423
E value	1.0e-41
Match length	116

% identity	74
NCBI Description	NONSPECIFIC LIPID-TRANSFER PROTEIN 1 PRECURSOR (LTP 1) >gi_1177796 (M80567) non-specific lipid transfer protein [Arabidopsis thaliana] >gi_3786018 (AC005499) unknown protein [Arabidopsis thaliana]
Seq. No.	162237
Seq. ID	LIB3177-039-P1-K1-B3
Method	BLASTN
NCBI GI	g3449325
BLAST score	65
E value	3.0e-28
Match length	273
% identity	86
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K16H17, complete sequence [Arabidopsis thaliana]
Seq. No.	162238
Seq. ID	LIB3177-039-P1-K1-C1
Method	BLASTN
NCBI GI	g16371
BLAST score	91
E value	8.0e-44
Match length	183
% identity	87
NCBI Description	A.thaliana gene (LHCP AB 180) for chlorophyll a/b binding protein
Seq. No.	162239
Seq. ID	LIB3177-039-P1-K1-C3
Method	BLASTX
NCBI GI	g132074
BLAST score	366
E value	4.0e-35
Match length	120
% identity	61
NCBI Description	RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN 1A PRECURSOR (RUBISCO SMALL SUBUNIT 1A) >gi_68063_pir__RKMUA1 ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain A1 precursor - Arabidopsis thaliana
Seq. No.	162240
Seq. ID	LIB3177-039-P1-K1-C4
Method	BLASTN
NCBI GI	g3510340
BLAST score	81
E value	2.0e-37
Match length	360
% identity	84
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MDN11, complete sequence [Arabidopsis thaliana]
Seq. No.	162241
Seq. ID	LIB3177-039-P1-K1-D2
Method	BLASTN
NCBI GI	g3128143
BLAST score	34

E value	2.0e-09
Match length	129
% identity	91
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MTI20, complete sequence [Arabidopsis thaliana]

Seq. No.	162242
Seq. ID	LIB3177-039-P1-K1-D3
Method	BLASTX
NCBI GI	g3850914
BLAST score	368
E value	3.0e-35
Match length	119
% identity	66
NCBI Description	(AF060397) ATP synthase beta subunit [Stirlingia latifolia]

Seq. No.	162243
Seq. ID	LIB3177-039-P1-K1-D4
Method	BLASTN
NCBI GI	g259446
BLAST score	53
E value	7.0e-21
Match length	227
% identity	83
NCBI Description	glycine-rich protein {clone atGRP-3} [Arabidopsis thaliana, C24, mRNA, 680 nt]

Seq. No.	162244
Seq. ID	LIB3177-039-P1-K1-E1
Method	BLASTX
NCBI GI	g3286693
BLAST score	280
E value	6.0e-25
Match length	118
% identity	57
NCBI Description	(Y15433) 33 kDa polypeptide of oxygen-evolving complex (OEC) in photosystem II [Arabidopsis thaliana]

Seq. No.	162245
Seq. ID	LIB3177-039-P1-K1-E2
Method	BLASTX
NCBI GI	g2342674
BLAST score	304
E value	9.0e-28
Match length	129
% identity	53
NCBI Description	(AC000106) Similar to ATP-dependent Clp protease (gb_D90915). EST gb_N65461 comes from this gene. [Arabidopsis thaliana]

Seq. No.	162246
Seq. ID	LIB3177-039-P1-K1-E3
Method	BLASTN
NCBI GI	g1495268
BLAST score	46
E value	1.0e-16
Match length	138

% identity	83
NCBI Description	A.thaliana mRNA (orf19) from chromosome III

Seq. No.	162247
Seq. ID	LIB3177-039-P1-K1-E4
Method	BLASTX
NCBI GI	g2119846
BLAST score	334
E value	2.0e-31
Match length	108
% identity	66
NCBI Description	chlorophyll a/b-binding protein type I precursor Lhb1B2 - Arabidopsis thaliana >gi_16364_emb_CAA45790_ (X64460) photosystem II type I chlorophyll a /b binding protein [Arabidopsis thaliana] >gi_3128230 (AC004077) photosystem II type I chlorophyll a/b binding protein [Arabidopsis thaliana] >gi_3337371 (AC004481) photosystem II type I chlorophyll a/b binding protein [Arabidopsis thaliana]

Seq. No.	162248
Seq. ID	LIB3177-039-P1-K1-F3
Method	BLASTN
NCBI GI	g2584827
BLAST score	94
E value	3.0e-45
Match length	186
% identity	88
NCBI Description	Arabidopsis thaliana chromosome 1 BAC F12F1 sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	162249
Seq. ID	LIB3177-039-P1-K1-G2
Method	BLASTX
NCBI GI	g1531762
BLAST score	163
E value	4.0e-11
Match length	51
% identity	69
NCBI Description	(Y07765) S-adenosylmethionine decarboxylase [Arabidopsis thaliana]

Seq. No.	162250
Seq. ID	LIB3177-039-P1-K1-H1
Method	BLASTX
NCBI GI	g2924779
BLAST score	248
E value	3.0e-21
Match length	104
% identity	56
NCBI Description	(AC002334) putative 3-ketoacyl-CoA thiolase [Arabidopsis thaliana] >gi_2981616_dbj_BAA25248_ (AB008854) 3-ketoacyl-CoA thiolase [Arabidopsis thaliana] >gi_2981618_dbj_BAA25249_ (AB008855) 3-ketoacyl-CoA thiolase [Arabidopsis thaliana]

Seq. No.	162251
Seq. ID	LIB3177-039-P1-K2-A1

Method	BLASTX
NCBI GI	g4741960
BLAST score	488
E value	3.0e-49
Match length	115
% identity	83
NCBI Description	(AF134130) Lhcb6 protein [Arabidopsis thaliana]

Seq. No.	162252
Seq. ID	LIB3177-039-P1-K2-A11
Method	BLASTX
NCBI GI	g4741952
BLAST score	496
E value	3.0e-50
Match length	93
% identity	69
NCBI Description	(AF134126) Lhcb3 protein [Arabidopsis thaliana]

Seq. No.	162253
Seq. ID	LIB3177-039-P1-K2-A2
Method	BLASTX
NCBI GI	g131398
BLAST score	438
E value	1.0e-43
Match length	98
% identity	89
NCBI Description	PHOTOSYSTEM II 10 KD POLYPEPTIDE PRECURSOR >gi_72714_pir__F2MU10 photosystem II 10K protein precursor - Arabidopsis thaliana >gi_16447_emb_CAA39441_ (X55970) photosystem II 10 kDa polypeptide [Arabidopsis thaliana] >gi_3152571 (AC002986) Match to photosystem II 10kDa polypeptide gb_X55970. ESTs gb_Z17693, gb_N37616, gb_T41858, gb_T88021, gb_R37531, gb_T04679, gb_N37520, gb_N64965, gb_Z17592 and gb_N65338, gb_N37466 and gb_T45400 come from this gene. [Arabidopsis

Seq. No.	162254
Seq. ID	LIB3177-039-P1-K2-A4
Method	BLASTX
NCBI GI	g132110
BLAST score	207
E value	6.0e-17
Match length	68
% identity	62
NCBI Description	RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN 3B PRECURSOR (RUBISCO SMALL SUBUNIT 3B) >gi_68060_pir__RKMUB3 ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain B3 precursor - Arabidopsis thaliana >gi_16195_emb_CAA32702_ (X14564) ribulose bisphosphate carboxylase [Arabidopsis thaliana]

Seq. No.	162255
Seq. ID	LIB3177-039-P1-K2-B1
Method	BLASTX
NCBI GI	g2497733
BLAST score	563
E value	4.0e-58

Match length	110
% identity	98
NCBI Description	NONSPECIFIC LIPID-TRANSFER PROTEIN 1 PRECURSOR (LTP 1) >gi_1177796 (M80567) non-specific lipid transfer protein [Arabidopsis thaliana] >gi_3786018 (AC005499) unknown protein [Arabidopsis thaliana]

Seq. No.	162256
Seq. ID	LIB3177-039-P1-K2-B3
Method	BLASTN
NCBI GI	g3449325
BLAST score	120
E value	8.0e-61
Match length	417
% identity	95
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K16H17, complete sequence [Arabidopsis thaliana]

Seq. No.	162257
Seq. ID	LIB3177-039-P1-K2-C1
Method	BLASTX
NCBI GI	g115767
BLAST score	521
E value	3.0e-53
Match length	100
% identity	97
NCBI Description	CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR (CAB-165/180) (LHCP) >gi_81603_pir__A29280 chlorophyll a/b-binding protein ab165 - Arabidopsis thaliana >gi_16368_emb_CAA27540_ (X03907) chlorophyll a/b binding protein (LHCP AB 65) [Arabidopsis thaliana] >gi_16372_emb_CAA27541_ (X03908) chlorophyll a/b binding protein (LHCP AB 180) [Arabidopsis thaliana]

Seq. No.	162258
Seq. ID	LIB3177-039-P1-K2-C3
Method	BLASTX
NCBI GI	g132074
BLAST score	681
E value	6.0e-72
Match length	131
% identity	96
NCBI Description	RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN 1A PRECURSOR (RUBISCO SMALL SUBUNIT 1A) >gi_68063_pir__RKMUA1 ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain A1 precursor - Arabidopsis thaliana

Seq. No.	162259
Seq. ID	LIB3177-039-P1-K2-C4
Method	BLASTX
NCBI GI	g2194130
BLAST score	211
E value	9.0e-17
Match length	138
% identity	47
NCBI Description	(AC002062) Similar to Nicotiana 5-epi-aristolochene synthase (gb_L04680). [Arabidopsis thaliana]

Seq. No.	162260
Seq. ID	LIB3177-039-P1-K2-C5
Method	BLASTN
NCBI GI	g3510340
BLAST score	61
E value	4.0e-26
Match length	145
% identity	84
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MDN11, complete sequence [Arabidopsis thaliana]

Seq. No.	162261
Seq. ID	LIB3177-039-P1-K2-D1
Method	BLASTN
NCBI GI	g1871173
BLAST score	269
E value	1.0e-149
Match length	397
% identity	94
NCBI Description	Arabidopsis thaliana chromosome II BAC T06D20 genomic sequence, complete sequence

Seq. No.	162262
Seq. ID	LIB3177-039-P1-K2-D10
Method	BLASTN
NCBI GI	g2642152
BLAST score	51
E value	9.0e-20
Match length	160
% identity	86
NCBI Description	Arabidopsis thaliana chromosome II BAC T5I7 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	162263
Seq. ID	LIB3177-039-P1-K2-D2
Method	BLASTN
NCBI GI	g3128143
BLAST score	123
E value	1.0e-62
Match length	354
% identity	96
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MTI20, complete sequence [Arabidopsis thaliana]

Seq. No.	162264
Seq. ID	LIB3177-039-P1-K2-D3
Method	BLASTX
NCBI GI	g4206564
BLAST score	192
E value	8.0e-15
Match length	76
% identity	57
NCBI Description	(AF066828) ATP synthase beta subunit [Cneorum pulverulentum]

Seq. No.	162265

Seq. ID	LIB3177-039-P1-K2-D4
Method	BLASTX
NCBI GI	g259447
BLAST score	145
E value	3.0e-09
Match length	47
% identity	74
NCBI Description	(S47409) glycine-rich protein, atGRP {clone atGRP-3} [Arabidopsis thaliana, C24, Peptide, 145 aa] [Arabidopsis thaliana]

Seq. No.	162266
Seq. ID	LIB3177-039-P1-K2-E10
Method	BLASTN
NCBI GI	g4519183
BLAST score	83
E value	7.0e-39
Match length	229
% identity	95
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K15C23, complete sequence

Seq. No.	162267
Seq. ID	LIB3177-039-P1-K2-E2
Method	BLASTX
NCBI GI	g2342674
BLAST score	85
E value	1.0e-41
Match length	115
% identity	72
NCBI Description	(AC000106) Similar to ATP-dependent Clp protease (gb_D90915). EST gb_N65461 comes from this gene. [Arabidopsis thaliana]

Seq. No.	162268
Seq. ID	LIB3177-039-P1-K2-E3
Method	BLASTX
NCBI GI	g1495269
BLAST score	528
E value	6.0e-54
Match length	125
% identity	83
NCBI Description	(X97829) product similar to ccr protein, Citrus paradisi; PIR: S52663 [Arabidopsis thaliana] >gi_1550735_emb_CAA66824_ (X98130) unknown [Arabidopsis thaliana]

Seq. No.	162269
Seq. ID	LIB3177-039-P1-K2-E4
Method	BLASTX
NCBI GI	g2119846
BLAST score	654
E value	9.0e-69
Match length	126
% identity	98
NCBI Description	chlorophyll a/b-binding protein type I precursor Lhb1B2 - Arabidopsis thaliana >gi_16364_emb_CAA45790_ (X64460)

	photosystem II type I chlorophyll a /b binding protein [Arabidopsis thaliana] >gi_3128230 (AC004077) photosystem II type I chlorophyll a/b binding protein [Arabidopsis thaliana] >gi_3337371 (AC004481) photosystem II type I chlorophyll a/b binding protein [Arabidopsis thaliana]
Seq. No.	162270
Seq. ID	LIB3177-039-P1-K2-E5
Method	BLASTX
NCBI GI	g2119846
BLAST score	460
E value	4.0e-46
Match length	114
% identity	80
NCBI Description	chlorophyll a/b-binding protein type I precursor Lhb1B2 - Arabidopsis thaliana >gi_16364_emb_CAA45790_ (X64460) photosystem II type I chlorophyll a /b binding protein [Arabidopsis thaliana] >gi_3128230 (AC004077) photosystem II type I chlorophyll a/b binding protein [Arabidopsis thaliana] >gi_3337371 (AC004481) photosystem II type I chlorophyll a/b binding protein [Arabidopsis thaliana]
Seq. No.	162271
Seq. ID	LIB3177-039-P1-K2-F1
Method	BLASTX
NCBI GI	g4651202
BLAST score	321
E value	9.0e-30
Match length	132
% identity	48
NCBI Description	(AB026253) copper amine oxidase [Pisum sativum]
Seq. No.	162272
Seq. ID	LIB3177-039-P1-K2-F3
Method	BLASTN
NCBI GI	g2584827
BLAST score	259
E value	1.0e-144
Match length	279
% identity	98
NCBI Description	Arabidopsis thaliana chromosome 1 BAC F12F1 sequence, complete sequence [Arabidopsis thaliana]
Seq. No.	162273
Seq. ID	LIB3177-039-P1-K2-F4
Method	BLASTN
NCBI GI	g2764517
BLAST score	54
E value	1.0e-21
Match length	170
% identity	84
NCBI Description	Arabidopsis thaliana mRNA for ornithine carbamoyltransferase, complete CDS
Seq. No.	162274
Seq. ID	LIB3177-039-P1-K2-F8
Method	BLASTX

NCBI GI	g3128228
BLAST score	211
E value	2.0e-17
Match length	73
% identity	60
NCBI Description	(AC004077) putative ribosomal protein L18A [Arabidopsis thaliana] >gi_3337376 (AC004481) putative ribosomal protein L18A [Arabidopsis thaliana]

Seq. No.	162275
Seq. ID	LIB3177-039-P1-K2-G1
Method	BLASTN
NCBI GI	g3540210
BLAST score	298
E value	1.0e-167
Match length	338
% identity	96
NCBI Description	Arabidopsis thaliana chromosome I BAC F5A8 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	162276
Seq. ID	LIB3177-039-P1-K2-G3
Method	BLASTX
NCBI GI	g2827551
BLAST score	73
E value	2.0e-16
Match length	110
% identity	42
NCBI Description	(AL021635) predicted protein [Arabidopsis thaliana]

Seq. No.	162277
Seq. ID	LIB3177-039-P1-K2-H1
Method	BLASTX
NCBI GI	g2924779
BLAST score	566
E value	2.0e-58
Match length	116
% identity	97
NCBI Description	(AC002334) putative 3-ketoacyl-CoA thiolase [Arabidopsis thaliana] >gi_2981616_dbj_BAA25248_ (AB008854) 3-ketoacyl-CoA thiolase [Arabidopsis thaliana] >gi_2981618_dbj_BAA25249_ (AB008855) 3-ketoacyl-CoA thiolase [Arabidopsis thaliana]

Seq. No.	162278
Seq. ID	LIB3177-039-P1-K2-H2
Method	BLASTN
NCBI GI	g3763915
BLAST score	21
E value	4.3e-02
Match length	75
% identity	34
NCBI Description	Arabidopsis thaliana chromosome II BAC F14B2 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	162279
Seq. ID	LIB3177-040-P1-K2-A12

Method	BLASTN
NCBI GI	g2924729
BLAST score	47
E value	4.0e-18
Match length	47
% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MNA5, complete sequence [Arabidopsis thaliana]

Seq. No.	162280
Seq. ID	LIB3177-040-P1-K2-D11
Method	BLASTX
NCBI GI	g131381
BLAST score	511
E value	4.0e-52
Match length	106
% identity	99
NCBI Description	OXYGEN-EVOLVING ENHANCER PROTEIN 1 PRECURSOR (OEE1) (33 KD SUBUNIT OF OXYGEN EVOLVING SYSTEM OF PHOTOSYSTEM II) (33 KD THYLAKOID MEMBRANE PROTEIN) >gi_99745_pir__S11852 photosystem II oxygen-evolving complex protein 1 precursor - Arabidopsis thaliana >gi_22571_emb_CAA36675_ (X52428) 33 kDa oxygen-evolving protein [Arabidopsis thaliana]

Seq. No.	162281
Seq. ID	LIB3177-040-P1-K2-E12
Method	BLASTX
NCBI GI	g228403
BLAST score	261
E value	8.0e-23
Match length	90
% identity	59
NCBI Description	glycolate oxidase [Lens culinaris]

Seq. No.	162282
Seq. ID	LIB3177-040-P1-K2-F11
Method	BLASTN
NCBI GI	g2760164
BLAST score	46
E value	1.0e-16
Match length	210
% identity	80
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K18P6, complete sequence [Arabidopsis thaliana]

Seq. No.	162283
Seq. ID	LIB3177-040-P1-K2-F12
Method	BLASTN
NCBI GI	g3327922
BLAST score	43
E value	4.0e-15
Match length	89
% identity	87
NCBI Description	Arabidopsis thaliana chromosome II BAC T31E10 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	162284

Seq. ID	LIB3177-040-P1-K2-G9
Method	BLASTX
NCBI GI	g2062156
BLAST score	292
E value	1.0e-26
Match length	100
% identity	26
NCBI Description	(AC001645) jasmonate inducible protein isolog [Arabidopsis thaliana]

Seq. No.	162285
Seq. ID	LIB3177-041-P1-K2-A1
Method	BLASTN
NCBI GI	g4662640
BLAST score	151
E value	2.0e-79
Match length	356
% identity	35
NCBI Description	Arabidopsis thaliana chromosome II BAC F15K19 genomic sequence, complete sequence

Seq. No.	162286
Seq. ID	LIB3177-041-P1-K2-A10
Method	BLASTN
NCBI GI	g2618603
BLAST score	263
E value	1.0e-146
Match length	395
% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MSL3, complete sequence [Arabidopsis thaliana]

Seq. No.	162287
Seq. ID	LIB3177-041-P1-K2-A11
Method	BLASTX
NCBI GI	g1709825
BLAST score	663
E value	9.0e-70
Match length	134
% identity	100
NCBI Description	PHOTOSYSTEM I REACTION CENTRE SUBUNIT PSAN PRECURSOR (PSI-N) >gi_1237124 (U32176) PSI-N [Arabidopsis thaliana]

Seq. No.	162288
Seq. ID	LIB3177-041-P1-K2-A2
Method	BLASTX
NCBI GI	g4539324
BLAST score	250
E value	2.0e-21
Match length	136
% identity	49
NCBI Description	(AL035679) kinesin like protein [Arabidopsis thaliana]

Seq. No.	162289
Seq. ID	LIB3177-041-P1-K2-A3
Method	BLASTX
NCBI GI	g464986

BLAST score	709
E value	4.0e-75
Match length	133
% identity	98
NCBI Description	UBIQUITIN-CONJUGATING ENZYME E2-17 KD 9 (UBIQUITIN-PROTEIN LIGASE 9) (UBIQUITIN CARRIER PROTEIN 9) (UBCAT4B) >gi_421857_pir__S32674 ubiquitin--protein ligase (EC 6.3.2.19) UBC9 - Arabidopsis thaliana >gi_297884_emb_CAA78714_ (Z14990) ubiquitin conjugating enzyme homolog [Arabidopsis thaliana] >gi_349211 (L00639) ubiquitin conjugating enzyme [Arabidopsis thaliana] >gi_600391_emb_CAA51201_ (X72626) ubiquitin conjugating enzyme E2 [Arabidopsis thaliana] >gi_4455355_emb_CAB36765.1_ (AL035524) ubiquitin-protein ligase UBC9 [Arabidopsis thaliana]

Seq. No.	162290
Seq. ID	LIB3177-041-P1-K2-A4
Method	BLASTX
NCBI GI	g1871503
BLAST score	681
E value	7.0e-72
Match length	141
% identity	92
NCBI Description	(Y11559) beta-fructosidase [Arabidopsis thaliana]

Seq. No.	162291
Seq. ID	LIB3177-041-P1-K2-A5
Method	BLASTX
NCBI GI	g1363489
BLAST score	800
E value	8.0e-86
Match length	151
% identity	99
NCBI Description	thioglucosidase (EC 3.2.3.1) 3D precursor - Arabidopsis thaliana >gi_984052_emb_CAA61592_ (X89413) thioglucoside glucohydrolase [Arabidopsis thaliana]

Seq. No.	162292
Seq. ID	LIB3177-041-P1-K2-A6
Method	BLASTN
NCBI GI	g2584827
BLAST score	406
E value	0.0e+00
Match length	421
% identity	99
NCBI Description	Arabidopsis thaliana chromosome 1 BAC F12F1 sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	162293
Seq. ID	LIB3177-041-P1-K2-A7
Method	BLASTX
NCBI GI	g4580953
BLAST score	256
E value	4.0e-22
Match length	93
% identity	58

NCBI Description	(AF117734) glycerol kinase-like protein 2 [Mus musculus]

Seq. No.	162294
Seq. ID	LIB3177-041-P1-K2-A8
Method	BLASTX
NCBI GI	g4586253
BLAST score	204
E value	8.0e-17
Match length	77
% identity	64
NCBI Description	(AL049640) auxilin-like protein [Arabidopsis thaliana]

Seq. No.	162295
Seq. ID	LIB3177-041-P1-K2-A9
Method	BLASTX
NCBI GI	g115486
BLAST score	578
E value	8.0e-60
Match length	134
% identity	59
NCBI Description	CALMODULIN-2/3/5 >gi_99671_pir__S22503 calmodulin - Arabidopsis thaliana >gi_1076437_pir__S53006 calmodulin - leaf mustard >gi_2146726_pir__S71513 calmodulin - Arabidopsis thaliana >gi_166651 (M38380) calmodulin-2 [Arabidopsis thaliana] >gi_166653 (M73711) calmodulin-3 [Arabidopsis thaliana] >gi_474183_emb_CAA47690_ (X67273) calmodulin [Arabidopsis thaliana] >gi_497992 (U10150) calmodulin [Brassica napus] >gi_899058 (M88307) calmodulin [Brassica juncea] >gi_1183005_dbj_BAA08283_ (D45848) calmodulin [Arabidopsis thaliana] >gi_3402706 (AC004261) unknown protein [Arabidopsis thaliana] >gi_3885333 (AC005623) calmodulin [Arabidopsis thaliana] >gi_228407_prf__1803520A calmodulin 2 [Arabidopsis thaliana]

Seq. No.	162296
Seq. ID	LIB3177-041-P1-K2-B10
Method	BLASTX
NCBI GI	g2586127
BLAST score	322
E value	8.0e-30
Match length	139
% identity	49
NCBI Description	(U89510) b-keto acyl reductase [Hordeum vulgare]

Seq. No.	162297
Seq. ID	LIB3177-041-P1-K2-B11
Method	BLASTX
NCBI GI	g231924
BLAST score	175
E value	1.0e-12
Match length	36
% identity	89
NCBI Description	CYTOCHROME C1, HEME PROTEIN PRECURSOR (CLONE PC18I)

Seq. No.	162298
Seq. ID	LIB3177-041-P1-K2-B7

Method	BLASTX
NCBI GI	g2062161
BLAST score	634
E value	2.0e-66
Match length	130
% identity	47
NCBI Description	(AC001645) jasmonate inducible protein isolog [Arabidopsis thaliana]

Seq. No.	162299
Seq. ID	LIB3177-041-P1-K2-C11
Method	BLASTX
NCBI GI	g477280
BLAST score	178
E value	4.0e-13
Match length	59
% identity	59
NCBI Description	mitochondrial processing peptidase (EC 3.4.99.41) 55K protein precursor - potato >gi_410633_bbs_136740 cytochrome c reductase-processing peptidase subunit I, MPP subunit I, P55 [potatoes, var. Marfona, tuber, Peptide Mitochondrial, 534 aa]

Seq. No.	162300
Seq. ID	LIB3177-041-P1-K2-C12
Method	BLASTX
NCBI GI	g120667
BLAST score	518
E value	7.0e-53
Match length	104
% identity	96
NCBI Description	GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE, CYTOSOLIC >gi_81622_pir__JQ1287 glyceraldehyde-3-phosphate dehydrogenase (EC 1.2.1.12), cytosolic - Arabidopsis thaliana >gi_166706 (M64116) cystolic glyceraldehyde-3-phosphate dehydrogenase [Arabidopsis thaliana] >gi_166710 (M64119) glyceraldehyde-3-phosphate dehydrogenase [Arabidopsis thaliana]

Seq. No.	162301
Seq. ID	LIB3177-041-P1-K2-C5
Method	BLASTN
NCBI GI	g2997685
BLAST score	280
E value	1.0e-156
Match length	387
% identity	94
NCBI Description	Arabidopsis thaliana putative transcriptional co-activator (KELP) mRNA, complete cds

Seq. No.	162302
Seq. ID	LIB3177-041-P1-K2-C7
Method	BLASTX
NCBI GI	g2738248
BLAST score	663
E value	1.0e-69
Match length	153

% identity	86
NCBI Description	(U97200) cobalamin-independent methionine synthase [Arabidopsis thaliana]

Seq. No.	162303
Seq. ID	LIB3177-041-P1-K2-C8
Method	BLASTX
NCBI GI	g4538897
BLAST score	271
E value	3.0e-24
Match length	83
% identity	77
NCBI Description	(AL049482) AX110P-like protein [Arabidopsis thaliana]

Seq. No.	162304
Seq. ID	LIB3177-041-P1-K2-C9
Method	BLASTX
NCBI GI	g2995990
BLAST score	260
E value	1.0e-22
Match length	52
% identity	96
NCBI Description	(AF053746) dormancy-associated protein [Arabidopsis thaliana] >gi_2995992 (AF053747) dormancy-associated protein [Arabidopsis thaliana]

Seq. No.	162305
Seq. ID	LIB3177-041-P1-K2-D10
Method	BLASTX
NCBI GI	g2088654
BLAST score	379
E value	4.0e-37
Match length	120
% identity	73
NCBI Description	(AF002109) 60S acidic ribosomal protein P0 isolog [Arabidopsis thaliana]

Seq. No.	162306
Seq. ID	LIB3177-041-P1-K2-D11
Method	BLASTX
NCBI GI	g132102
BLAST score	728
E value	2.0e-77
Match length	138
% identity	98
NCBI Description	RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN 2B PRECURSOR (RUBISCO SMALL SUBUNIT 2B) >gi_68061_pir__RKMUB2 ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain B2 precursor - Arabidopsis thaliana >gi_16194_emb_CAA32701_ (X14564) ribulose bisphosphate carboxylase [Arabidopsis thaliana]

Seq. No.	162307
Seq. ID	LIB3177-041-P1-K2-D4
Method	BLASTX
NCBI GI	g2493052
BLAST score	347

E value	9.0e-33
Match length	70
% identity	96
NCBI Description	ATP SYNTHASE EPSILON CHAIN, MITOCHONDRIAL >gi_1655486_dbj_BAA13602_ (D88377) epsilon subunit of mitochondrial F1-ATPase [Arabidopsis thaliana]

Seq. No.	162308
Seq. ID	LIB3177-041-P1-K2-D7
Method	BLASTX
NCBI GI	g1172599
BLAST score	741
E value	6.0e-79
Match length	146
% identity	97
NCBI Description	PROTEASOME COMPONENT C5 (MULTICATALYTIC ENDOPEPTIDASE COMPLEX SUBUNIT C5) (TAS-F22/FAFP98) >gi_600387_emb_CAA47753_ (X67338) proteosome subunit [Arabidopsis thaliana]

Seq. No.	162309
Seq. ID	LIB3177-041-P1-K2-D9
Method	BLASTX
NCBI GI	g1621268
BLAST score	334
E value	2.0e-31
Match length	92
% identity	68
NCBI Description	(Z81012) unknown [Ricinus communis]

Seq. No.	162310
Seq. ID	LIB3177-041-P1-K2-E12
Method	BLASTX
NCBI GI	g2760322
BLAST score	528
E value	6.0e-54
Match length	140
% identity	73
NCBI Description	(AC002130) F1N21.7 [Arabidopsis thaliana]

Seq. No.	162311
Seq. ID	LIB3177-041-P1-K2-E5
Method	BLASTN
NCBI GI	g4757414
BLAST score	200
E value	1.0e-109
Match length	232
% identity	97
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MYF24, complete sequence

Seq. No.	162312
Seq. ID	LIB3177-041-P1-K2-F10
Method	BLASTX
NCBI GI	g2275216
BLAST score	244
E value	7.0e-21

Match length	64
% identity	73
NCBI Description	(AC002337) cytochrome c oxidase Vc subunit isolog [Arabidopsis thaliana]

Seq. No.	162313
Seq. ID	LIB3177-041-P1-K2-F11
Method	BLASTX
NCBI GI	g1703723
BLAST score	563
E value	5.0e-58
Match length	130
% identity	86
NCBI Description	ATP SYNTHASE BETA CHAIN >gi_733448 (U23082) CF1 ATP synthase beta subunit [Spinacia oleracea]

Seq. No.	162314
Seq. ID	LIB3177-041-P1-K2-F9
Method	BLASTX
NCBI GI	g4091810
BLAST score	271
E value	4.0e-24
Match length	61
% identity	82
NCBI Description	(AF053345) fatty acid elongase 3-ketoacyl-CoA synthase 1 [Arabidopsis thaliana]

Seq. No.	162315
Seq. ID	LIB3177-041-P1-K2-G10
Method	BLASTX
NCBI GI	g3688799
BLAST score	594
E value	1.0e-61
Match length	124
% identity	96
NCBI Description	(AF057137) gamma tonoplast intrinsic protein 2 [Arabidopsis thaliana]

Seq. No.	162316
Seq. ID	LIB3177-041-P1-K2-G11
Method	BLASTN
NCBI GI	g2827538
BLAST score	264
E value	1.0e-146
Match length	464
% identity	98
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone T12H17 (ESSAII project)

Seq. No.	162317
Seq. ID	LIB3177-041-P1-K2-G8
Method	BLASTX
NCBI GI	g1052960
BLAST score	616
E value	2.0e-64
Match length	122
% identity	93

NCBI Description	(U37437) PNIL34 [Ipomoea nil]

Seq. No.	162318
Seq. ID	LIB3177-041-P1-K2-G9
Method	BLASTX
NCBI GI	g132110
BLAST score	667
E value	3.0e-70
Match length	127
% identity	98
NCBI Description	RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN 3B PRECURSOR (RUBISCO SMALL SUBUNIT 3B) >gi_68060_pir__RKMUB3 ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain B3 precursor - Arabidopsis thaliana >gi_16195_emb_CAA32702_ (X14564) ribulose bisphosphate carboxylase [Arabidopsis thaliana]

Seq. No.	162319
Seq. ID	LIB3177-041-P1-K2-H11
Method	BLASTX
NCBI GI	g282865
BLAST score	694
E value	2.0e-73
Match length	136
% identity	73
NCBI Description	chlorophyll a/b-binding protein - Arabidopsis thaliana >gi_16207_emb_CAA39534_ (X56062) chlorophyll A/B-binding protein [Arabidopsis thaliana] >gi_166644 (M85150) chlorophyll a/b-binding protein [Arabidopsis thaliana] >gi_4678304_emb_CAB41095.1_ (AL049655) chlorophyll a/b-binding protein [Arabidopsis thaliana]

Seq. No.	162320
Seq. ID	LIB3177-041-P1-K2-H12
Method	BLASTN
NCBI GI	g4512690
BLAST score	183
E value	9.0e-99
Match length	207
% identity	97
NCBI Description	Arabidopsis thaliana chromosome II BAC F11A3 genomic sequence, complete sequence

Seq. No.	162321
Seq. ID	LIB3177-041-P1-K2-H7
Method	BLASTX
NCBI GI	g2160175
BLAST score	538
E value	4.0e-55
Match length	104
% identity	99
NCBI Description	(AC000132) Strong similarity to Dianthus cysteine proteinase (gb_U17135). [Arabidopsis thaliana]

Seq. No.	162322
Seq. ID	LIB3177-041-P1-K2-H9
Method	BLASTX

NCBI GI	g1363489
BLAST score	627
E value	1.0e-65
Match length	122
% identity	95
NCBI Description	thioglucosidase (EC 3.2.3.1) 3D precursor - Arabidopsis thaliana >gi_984052_emb_CAA61592_ (X89413) thioglucoside glucohydrolase [Arabidopsis thaliana]

Seq. No.	162323
Seq. ID	LIB3177-042-P1-K2-A10
Method	BLASTX
NCBI GI	g400923
BLAST score	380
E value	9.0e-37
Match length	75
% identity	100
NCBI Description	RAS-RELATED PROTEIN RAB7 >gi_485497_pir__S33531 GTP-binding protein rab - garden pea >gi_20756_emb_CAA46600_ (X65650) RAS-related GTP-binding protein [Pisum sativum]

Seq. No.	162324
Seq. ID	LIB3177-042-P1-K2-A3
Method	BLASTX
NCBI GI	g3128223
BLAST score	243
E value	7.0e-21
Match length	79
% identity	66
NCBI Description	(AC004077) unknown protein [Arabidopsis thaliana] >gi_3337369 (AC004481) unknown protein [Arabidopsis thaliana]

Seq. No.	162325
Seq. ID	LIB3177-042-P1-K2-A5
Method	BLASTX
NCBI GI	g4585935
BLAST score	551
E value	8.0e-57
Match length	120
% identity	88
NCBI Description	(AC007211) putative chlorophyll A/B binding protein [Arabidopsis thaliana] >gi_4741946_gb_AAD28770.1_AF134123_1 (AF134123) Lhcb2 protein [Arabidopsis thaliana]

Seq. No.	162326
Seq. ID	LIB3177-042-P1-K2-A6
Method	BLASTX
NCBI GI	g114532
BLAST score	84
E value	5.0e-56
Match length	146
% identity	82
NCBI Description	ATP SYNTHASE ALPHA CHAIN >gi_67824_pir__PWNTA H+-transporting ATP synthase (EC 3.6.1.34) alpha chain - common tobacco chloroplast >gi_11769_emb_CAA23471_ (V00162) alpha subunit of ATPase [Nicotiana tabacum]

>gi_11811_emb_CAA77341_ (Z00044) ATPase alpha subunit [Nicotiana tabacum] >gi_225270_prf__1211235E ATPase alpha [Nicotiana tabacum]

Seq. No.	162327
Seq. ID	LIB3177-042-P1-K2-A7
Method	BLASTX
NCBI GI	g3834309
BLAST score	291
E value	3.0e-26
Match length	121
% identity	60
NCBI Description	(AC005679) Strong similarity to glycoprotein EP1 gb_L16983 Daucus carota and a member of S locus glycoprotein family PF_00954. ESTs gb_F13813, gb_T21052, gb_R30218 and gb_W43262 come from this gene. [Arabidopsis thaliana]

Seq. No.	162328
Seq. ID	LIB3177-042-P1-K2-A9
Method	BLASTX
NCBI GI	g1514643
BLAST score	122
E value	2.0e-06
Match length	149
% identity	23
NCBI Description	(Z70524) PDR5-like ABC transporter [Spirodela polyrrhiza]

Seq. No.	162329
Seq. ID	LIB3177-042-P1-K2-B10
Method	BLASTN
NCBI GI	g2569935
BLAST score	41
E value	1.0e-13
Match length	84
% identity	94
NCBI Description	Arabidopsis thaliana mRNA for rab GDP dissociation inhibitor, isoform

Seq. No.	162330
Seq. ID	LIB3177-042-P1-K2-B11
Method	BLASTX
NCBI GI	g1709825
BLAST score	635
E value	2.0e-66
Match length	129
% identity	100
NCBI Description	PHOTOSYSTEM I REACTION CENTRE SUBUNIT PSAN PRECURSOR (PSI-N) >gi_1237124 (U32176) PSI-N [Arabidopsis thaliana]

Seq. No.	162331
Seq. ID	LIB3177-042-P1-K2-B7
Method	BLASTX
NCBI GI	g3980403
BLAST score	258
E value	1.0e-22
Match length	89
% identity	64

NCBI Description	(AC004561) putative tropinone reductase [Arabidopsis thaliana]

Seq. No.	162332
Seq. ID	LIB3177-042-P1-K2-B9
Method	BLASTX
NCBI GI	g120667
BLAST score	466
E value	9.0e-47
Match length	112
% identity	80
NCBI Description	GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE, CYTOSOLIC >gi_81622_pir__JQ1287 glyceraldehyde-3-phosphate dehydrogenase (EC 1.2.1.12), cytosolic - Arabidopsis thaliana >gi_166706 (M64116) cystolic glyceraldehyde-3-phosphate dehydrogenase [Arabidopsis thaliana] >gi_166710 (M64119) glyceraldehyde-3-phosphate dehydrogenase [Arabidopsis thaliana]

Seq. No.	162333
Seq. ID	LIB3177-042-P1-K2-C12
Method	BLASTX
NCBI GI	g4538963
BLAST score	95
E value	1.0e-26
Match length	69
% identity	85
NCBI Description	(AL049488) chlorophyll a/b-binding protein-like [Arabidopsis thaliana] >gi_4741958_gb_AAD28776.1_AF134129_1 (AF134129) Lhcb5 protein [Arabidopsis thaliana]

Seq. No.	162334
Seq. ID	LIB3177-042-P1-K2-C3
Method	BLASTX
NCBI GI	g4586256
BLAST score	197
E value	2.0e-18
Match length	101
% identity	56
NCBI Description	(AL049640) probable photosystem I chain XI precursor [Arabidopsis thaliana]

Seq. No.	162335
Seq. ID	LIB3177-042-P1-K2-C6
Method	BLASTX
NCBI GI	g132074
BLAST score	725
E value	5.0e-77
Match length	134
% identity	99
NCBI Description	RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN 1A PRECURSOR (RUBISCO SMALL SUBUNIT 1A) >gi_68063_pir__RKMUA1 ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain A1 precursor - Arabidopsis thaliana

Seq. No.	162336
Seq. ID	LIB3177-042-P1-K2-C7

Method	BLASTN
NCBI GI	g2618720
BLAST score	86
E value	1.0e-40
Match length	202
% identity	86
NCBI Description	Arabidopsis thaliana early auxin-induced (IAA16) mRNA, complete cds

Seq. No.	162337
Seq. ID	LIB3177-042-P1-K2-C8
Method	BLASTX
NCBI GI	g466160
BLAST score	357
E value	6.0e-34
Match length	83
% identity	81
NCBI Description	HYPOTHETICAL 9.8 KD PROTEIN ZK652.3 IN CHROMOSOME III >gi_630771_pir__S44903 ZK652.3 protein - Caenorhabditis elegans >gi_289769 (L14429) putative [Caenorhabditis elegans]

Seq. No.	162338
Seq. ID	LIB3177-042-P1-K2-C9
Method	BLASTN
NCBI GI	g4584351
BLAST score	432
E value	0.0e+00
Match length	452
% identity	99
NCBI Description	Arabidopsis thaliana chromosome II BAC T12H3 genomic sequence, complete sequence

Seq. No.	162339
Seq. ID	LIB3177-042-P1-K2-D10
Method	BLASTN
NCBI GI	g3242700
BLAST score	92
E value	4.0e-44
Match length	458
% identity	97
NCBI Description	Arabidopsis thaliana chromosome II BAC F26B6 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	162340
Seq. ID	LIB3177-042-P1-K2-D11
Method	BLASTX
NCBI GI	g2801536
BLAST score	312
E value	1.0e-28
Match length	121
% identity	51
NCBI Description	(AF039531) lysophospholipase homolog [Oryza sativa]

Seq. No.	162341
Seq. ID	LIB3177-042-P1-K2-D12
Method	BLASTX

NCBI GI	g4204274
BLAST score	800
E value	8.0e-86
Match length	150
% identity	97
NCBI Description	(AC004146) ribulose bisphosphate carboxylase, small subunit [Arabidopsis thaliana]

Seq. No.	162342
Seq. ID	LIB3177-042-P1-K2-D4
Method	BLASTN
NCBI GI	g2864607
BLAST score	165
E value	1.0e-87
Match length	425
% identity	92
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F10M6 (ESSAII project)

Seq. No.	162343
Seq. ID	LIB3177-042-P1-K2-D5
Method	BLASTN
NCBI GI	g3688798
BLAST score	197
E value	1.0e-107
Match length	261
% identity	94
NCBI Description	Arabidopsis thaliana gamma tonoplast intrinsic protein 2 (TIP2) mRNA, complete cds

Seq. No.	162344
Seq. ID	LIB3177-042-P1-K2-D8
Method	BLASTX
NCBI GI	g515377
BLAST score	296
E value	6.0e-27
Match length	67
% identity	93
NCBI Description	(X79715) histone H4 [Lolium temulentum]

Seq. No.	162345
Seq. ID	LIB3177-042-P1-K2-D9
Method	BLASTX
NCBI GI	g4544419
BLAST score	410
E value	4.0e-40
Match length	116
% identity	72
NCBI Description	(AC006955) unknown protein [Arabidopsis thaliana]

Seq. No.	162346
Seq. ID	LIB3177-042-P1-K2-E1
Method	BLASTN
NCBI GI	g4741945
BLAST score	46
E value	7.0e-17
Match length	206

% identity	90
NCBI Description	Arabidopsis thaliana Lhcb2 protein (Lhcb2.2) mRNA, complete cds

Seq. No.	162347
Seq. ID	LIB3177-042-P1-K2-E10
Method	BLASTX
NCBI GI	g4490332
BLAST score	318
E value	1.0e-41
Match length	110
% identity	88
NCBI Description	(AL035656) putative protein [Arabidopsis thaliana]

Seq. No.	162348
Seq. ID	LIB3177-042-P1-K2-E11
Method	BLASTX
NCBI GI	g4263525
BLAST score	594
E value	1.0e-61
Match length	142
% identity	83
NCBI Description	(AC004044) putative photosystem I reaction center subunit II precursor [Arabidopsis thaliana]

Seq. No.	162349
Seq. ID	LIB3177-042-P1-K2-E9
Method	BLASTX
NCBI GI	g2244749
BLAST score	595
E value	8.0e-62
Match length	138
% identity	87
NCBI Description	(Z97335) hydroxymethyltransferase [Arabidopsis thaliana]

Seq. No.	162350
Seq. ID	LIB3177-042-P1-K2-F1
Method	BLASTX
NCBI GI	g124224
BLAST score	350
E value	3.0e-33
Match length	78
% identity	85
NCBI Description	INITIATION FACTOR 5A-1 (EIF-5A) (EIF-4D) >gi_100345_pir__S21060 translation initiation factor eIF-5A - common tobacco >gi_19887_emb_CAA45105_ (X63543) eukaryotic initiatin factor 5A (3) [Nicotiana tabacum]

Seq. No.	162351
Seq. ID	LIB3177-042-P1-K2-F10
Method	BLASTX
NCBI GI	g3916020
BLAST score	205
E value	4.0e-16
Match length	94
% identity	41
NCBI Description	HYPOTHETICAL 15.7 KD HIT-LIKE PROTEIN

	>gi_3261595_emb_CAB00913_ (Z77137) hypothetical protein Rv1262c [Mycobacterium tuberculosis]
Seq. No.	162352
Seq. ID	LIB3177-042-P1-K2-F11
Method	BLASTN
NCBI GI	g3869075
BLAST score	105
E value	4.0e-52
Match length	277
% identity	95
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MXK3, complete sequence [Arabidopsis thaliana]
Seq. No.	162353
Seq. ID	LIB3177-042-P1-K2-F9
Method	BLASTX
NCBI GI	g119975
BLAST score	181
E value	2.0e-15
Match length	61
% identity	79
NCBI Description	FERREDOXIN PRECURSOR >gi_99692_pir__S09979 ferredoxin [2Fe-2S] precursor - Arabidopsis thaliana >gi_16437_emb_CAA35754_ (X51370) ferredoxin precursor [Arabidopsis thaliana] >gi_166698 (M35868) ferrodoxin A [Arabidopsis thaliana]
Seq. No.	162354
Seq. ID	LIB3177-042-P1-K2-G1
Method	BLASTX
NCBI GI	g4734009
BLAST score	178
E value	3.0e-13
Match length	89
% identity	40
NCBI Description	(AC007178) hypothetical protein [Arabidopsis thaliana]
Seq. No.	162355
Seq. ID	LIB3177-042-P1-K2-G11
Method	BLASTX
NCBI GI	g2499535
BLAST score	319
E value	4.0e-49
Match length	118
% identity	85
NCBI Description	2-OXOGLUTARATE/MALATE TRANSLOCATOR PRECURSOR >gi_595681 (U13238) 2-oxoglutarate/malate translocator [Spinacia oleracea]
Seq. No.	162356
Seq. ID	LIB3177-042-P1-K2-G12
Method	BLASTN
NCBI GI	g4539290
BLAST score	108
E value	1.0e-53
Match length	433

% identity	94
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F14M19 (ESSA project)

Seq. No.	162357
Seq. ID	LIB3177-042-P1-K2-G6
Method	BLASTX
NCBI GI	g132074
BLAST score	639
E value	4.0e-67
Match length	123
% identity	98
NCBI Description	RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN 1A PRECURSOR (RUBISCO SMALL SUBUNIT 1A) >gi_68063_pir__RKMUA1 ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain A1 precursor - Arabidopsis thaliana

Seq. No.	162358
Seq. ID	LIB3177-042-P1-K2-G8
Method	BLASTN
NCBI GI	g3046856
BLAST score	131
E value	2.0e-67
Match length	373
% identity	98
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MXI22, complete sequence [Arabidopsis thaliana]

Seq. No.	162359
Seq. ID	LIB3177-042-P1-K2-H10
Method	BLASTN
NCBI GI	g2656028
BLAST score	23
E value	6.0e-03
Match length	433
% identity	99
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MNF13

Seq. No.	162360
Seq. ID	LIB3177-042-P1-K2-H11
Method	BLASTX
NCBI GI	g4587552
BLAST score	204
E value	3.0e-16
Match length	39
% identity	97
NCBI Description	(AC006577) Strong similarity to gb_S77096 aldehyde dehydrogenase homolog from Brassica napus and is a member of PF_00171 Aldehyde dehydrogenase family. ESTs gb_T46213, gb_T42164, gb_T43682, gb_N96380, gb_T42973, gb

Seq. No.	162361
Seq. ID	LIB3177-042-P1-K2-H12
Method	BLASTX
NCBI GI	g267073
BLAST score	599

E value	2.0e-62
Match length	110
% identity	99
NCBI Description	TUBULIN BETA-2/BETA-3 CHAIN >gi_320184_pir__JQ1587 tubulin beta chain - Arabidopsis thaliana >gi_166898 (M84700) beta-2 tubulin [Arabidopsis thaliana] >gi_166900 (M84701) beta-3 tubulin [Arabidopsis thaliana]

Seq. No.	162362
Seq. ID	LIB3177-042-P1-K2-H6
Method	BLASTN
NCBI GI	g4249393
BLAST score	85
E value	3.0e-40
Match length	97
% identity	97
NCBI Description	Arabidopsis thaliana chromosome II BAC T9J23 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	162363
Seq. ID	LIB3177-042-P1-K2-H7
Method	BLASTN
NCBI GI	g4753195
BLAST score	129
E value	3.0e-66
Match length	323
% identity	93
NCBI Description	Arabidopsis thaliana BAC F15A18 from chromosome V near 68.5 cM, complete sequence

Seq. No.	162364
Seq. ID	LIB3177-042-P1-K2-H9
Method	BLASTX
NCBI GI	g515692
BLAST score	475
E value	8.0e-48
Match length	96
% identity	96
NCBI Description	(U12286) beta-tubulin [Glycine max]

Seq. No.	162365
Seq. ID	LIB3177-043-P1-K2-A3
Method	BLASTX
NCBI GI	g2160158
BLAST score	176
E value	2.0e-13
Match length	47
% identity	72
NCBI Description	(AC000132) Similar to elongation factor 1-gamma (gb_EF1G_XENLA). ESTs gb_T20564,gb_T45940,gb_T04527 come from this gene. [Arabidopsis thaliana]

Seq. No.	162366
Seq. ID	LIB3177-043-P1-K2-A4
Method	BLASTX
NCBI GI	g1732570
BLAST score	585

E value	8.0e-61
Match length	115
% identity	97
NCBI Description	(U72153) beta-glucosidase [Arabidopsis thaliana]

Seq. No.	162367
Seq. ID	LIB3177-043-P1-K2-A5
Method	BLASTX
NCBI GI	g3868758
BLAST score	207
E value	1.0e-24
Match length	101
% identity	55
NCBI Description	(D89802) elongation factor 1B gamma [Oryza sativa]

Seq. No.	162368
Seq. ID	LIB3177-043-P1-K2-A6
Method	BLASTX
NCBI GI	g1208794
BLAST score	168
E value	6.0e-12
Match length	88
% identity	45
NCBI Description	(U48376) alcohol dehydrogenase [Pinus banksiana]

Seq. No.	162369
Seq. ID	LIB3177-043-P1-K2-B2
Method	BLASTX
NCBI GI	g4585935
BLAST score	714
E value	9.0e-76
Match length	134
% identity	100
NCBI Description	(AC007211) putative chlorophyll A/B binding protein [Arabidopsis thaliana] >gi_4741946_gb_AAD28770.1_AF134123_1 (AF134123) Lhcb2 protein [Arabidopsis thaliana]

Seq. No.	162370
Seq. ID	LIB3177-043-P1-K2-B3
Method	BLASTX
NCBI GI	g3641252
BLAST score	244
E value	3.0e-21
Match length	74
% identity	64
NCBI Description	(AF053127) leucine-rich receptor-like protein kinase [Malus domestica]

Seq. No.	162371
Seq. ID	LIB3177-043-P1-K2-B4
Method	BLASTX
NCBI GI	g4454037
BLAST score	685
E value	2.0e-72
Match length	127
% identity	99
NCBI Description	(AL035394) putative major latex protein [Arabidopsis

thaliana]

Seq. No.	162372
Seq. ID	LIB3177-043-P1-K2-B8
Method	BLASTX
NCBI GI	g2924772
BLAST score	582
E value	2.0e-60
Match length	126
% identity	90
NCBI Description	(AC002334) unknown protein [Arabidopsis thaliana]

Seq. No.	162373
Seq. ID	LIB3177-043-P1-K2-B9
Method	BLASTX
NCBI GI	g119975
BLAST score	438
E value	2.0e-43
Match length	127
% identity	72
NCBI Description	FERREDOXIN PRECURSOR >gi_99692_pir__S09979 ferredoxin [2Fe-2S] precursor - Arabidopsis thaliana >gi_16437_emb_CAA35754_ (X51370) ferredoxin precursor [Arabidopsis thaliana] >gi_166698 (M35868) ferrodoxin A [Arabidopsis thaliana]

Seq. No.	162374
Seq. ID	LIB3177-043-P1-K2-C1
Method	BLASTX
NCBI GI	g1170373
BLAST score	259
E value	1.0e-22
Match length	64
% identity	84
NCBI Description	HEAT SHOCK COGNATE 70 KD PROTEIN 1 >gi_1072473_pir__S46302 heat shock cognate protein 70-1 - Arabidopsis thaliana >gi_397482_emb_CAA52684_ (X74604) heat shock protein 70 cognate [Arabidopsis thaliana]

Seq. No.	162375
Seq. ID	LIB3177-043-P1-K2-C10
Method	BLASTN
NCBI GI	g2828182
BLAST score	120
E value	4.0e-61
Match length	203
% identity	93
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MOJ9, complete sequence [Arabidopsis thaliana]

Seq. No.	162376
Seq. ID	LIB3177-043-P1-K2-C2
Method	BLASTX
NCBI GI	g2119848
BLAST score	482
E value	1.0e-48
Match length	128

% identity	73
NCBI Description	chlorophyll a/b-binding protein type I precursor Lhb1B1 - Arabidopsis thaliana >gi_16366_emb_CAA45789_ (X64459) photosystem II type I chlorophyll a /b binding protein [Arabidopsis thaliana] >gi_3128229 (AC004077) putative photosystem II type I chlorophyll a/b binding protein [Arabidopsis thaliana] >gi_3337372 (AC004481) putative photosystem II type I chlorophyll a/b binding protein [Arabidopsis thaliana]

Seq. No.	162377
Seq. ID	LIB3177-043-P1-K2-C3
Method	BLASTX
NCBI GI	g4741952
BLAST score	491
E value	8.0e-50
Match length	110
% identity	64
NCBI Description	(AF134126) Lhcb3 protein [Arabidopsis thaliana]

Seq. No.	162378
Seq. ID	LIB3177-043-P1-K2-C4
Method	BLASTX
NCBI GI	g862650
BLAST score	493
E value	8.0e-50
Match length	96
% identity	100
NCBI Description	(U20193) MADS-box protein AGL12 [Arabidopsis thaliana]

Seq. No.	162379
Seq. ID	LIB3177-043-P1-K2-C6
Method	BLASTX
NCBI GI	g4105782
BLAST score	281
E value	3.0e-25
Match length	61
% identity	90
NCBI Description	(AF049922) PGP169-12 [Petunia x hybrida]

Seq. No.	162380
Seq. ID	LIB3177-043-P1-K2-D1
Method	BLASTN
NCBI GI	g4314374
BLAST score	24
E value	2.0e-03
Match length	416
% identity	94
NCBI Description	Arabidopsis thaliana chromosome II BAC F10A12 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	162381
Seq. ID	LIB3177-043-P1-K2-D10
Method	BLASTX
NCBI GI	g115783
BLAST score	541
E value	2.0e-55

Match length	103
% identity	98
NCBI Description	CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR (CAB-140) (LHCP) >gi_16376_emb_CAA27543_ (X03909) chlorophyll a/b binding protein (LHCP AB 140) [Arabidopsis thaliana]

Seq. No.	162382
Seq. ID	LIB3177-043-P1-K2-D2
Method	BLASTN
NCBI GI	g3283056
BLAST score	310
E value	1.0e-174
Match length	391
% identity	95
NCBI Description	Arabidopsis thaliana one helix protein (OHP) mRNA, complete cds

Seq. No.	162383
Seq. ID	LIB3177-043-P1-K2-D3
Method	BLASTX
NCBI GI	g544425
BLAST score	429
E value	2.0e-42
Match length	83
% identity	100
NCBI Description	GLYCINE-RICH RNA-BINDING PROTEIN 8 (CCR1 PROTEIN) >gi_419756_pir__S30148 glycine-rich protein (clone AtGRP8) - Arabidopsis thaliana >gi_16305_emb_CAA78712_ (Z14988) glycine rich protein [Arabidopsis thaliana] >gi_166658 (L04171) ORF [Arabidopsis thaliana] >gi_166839 (L00649) RNA-binding protein [Arabidopsis thaliana]

Seq. No.	162384
Seq. ID	LIB3177-043-P1-K2-D4
Method	BLASTX
NCBI GI	g1550738
BLAST score	441
E value	1.0e-43
Match length	121
% identity	76
NCBI Description	(Y08061) endomembrane-associated protein [Arabidopsis thaliana] >gi_2982443_emb_CAA18251_ (AL022224) endomembrane-associated protein [Arabidopsis thaliana]

Seq. No.	162385
Seq. ID	LIB3177-043-P1-K2-D5
Method	BLASTX
NCBI GI	g1550738
BLAST score	368
E value	4.0e-35
Match length	120
% identity	64
NCBI Description	(Y08061) endomembrane-associated protein [Arabidopsis thaliana] >gi_2982443_emb_CAA18251_ (AL022224) endomembrane-associated protein [Arabidopsis thaliana]

Seq. No.	162386
Seq. ID	LIB3177-043-P1-K2-E1
Method	BLASTN
NCBI GI	g4455168
BLAST score	199
E value	1.0e-108
Match length	459
% identity	99
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F10M10 (ESSAII project)

Seq. No.	162387
Seq. ID	LIB3177-043-P1-K2-E10
Method	BLASTN
NCBI GI	g3046849
BLAST score	241
E value	1.0e-133
Match length	450
% identity	34
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K18L3, complete sequence [Arabidopsis thaliana]

Seq. No.	162388
Seq. ID	LIB3177-043-P1-K2-E11
Method	BLASTN
NCBI GI	g3046849
BLAST score	143
E value	1.0e-74
Match length	267
% identity	33
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K18L3, complete sequence [Arabidopsis thaliana]

Seq. No.	162389
Seq. ID	LIB3177-043-P1-K2-E2
Method	BLASTX
NCBI GI	g267069
BLAST score	756
E value	1.0e-80
Match length	149
% identity	100
NCBI Description	TUBULIN ALPHA-2/ALPHA-4 CHAIN >gi_320183_pir__JQ1594 tubulin alpha chain - Arabidopsis thaliana >gi_166914 (M84696) apha-2 tubulin [Arabidopsis thaliana] >gi_166916 (M84697) alpha-4 tubulin [Arabidopsis thaliana]

Seq. No.	162390
Seq. ID	LIB3177-043-P1-K2-E3
Method	BLASTN
NCBI GI	g4038029
BLAST score	341
E value	0.0e+00
Match length	373
% identity	98
NCBI Description	Arabidopsis thaliana chromosome II BAC F5O4 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	162391
Seq. ID	LIB3177-043-P1-K2-E4
Method	BLASTX
NCBI GI	g4056456
BLAST score	195
E value	1.0e-36
Match length	110
% identity	87
NCBI Description	(AC005990) Strong similarity to gb_U20808 auxin-induced protein from Vigna radiata and a member of the zinc-binding dehydrogenase family PF_00107. ESTs gb_T43674, gb_H77006 and gb_AA395179 come from this gene. [Arabidopsis thaliana]

Seq. No.	162392
Seq. ID	LIB3177-043-P1-K2-F1
Method	BLASTX
NCBI GI	g3123188
BLAST score	627
E value	1.0e-65
Match length	137
% identity	91
NCBI Description	CATALASE 3 >gi_2347178 (U43147) catalase 3 [Arabidopsis thaliana] >gi_2511726 (AF021937) catalase 3 [Arabidopsis thaliana]

Seq. No.	162393
Seq. ID	LIB3177-043-P1-K2-F4
Method	BLASTX
NCBI GI	g1172977
BLAST score	647
E value	6.0e-68
Match length	137
% identity	96
NCBI Description	60S RIBOSOMAL PROTEIN L18 >gi_606970 (U15741) cytoplasmic ribosomal protein L18 [Arabidopsis thaliana]

Seq. No.	162394
Seq. ID	LIB3177-043-P1-K2-F5
Method	BLASTX
NCBI GI	g3057150
BLAST score	591
E value	2.0e-61
Match length	131
% identity	59
NCBI Description	(AF059037) chaperonin 10 [Arabidopsis thaliana]

Seq. No.	162395
Seq. ID	LIB3177-043-P1-K2-F6
Method	BLASTX
NCBI GI	g115385
BLAST score	674
E value	5.0e-71
Match length	133
% identity	98
NCBI Description	CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR (CAB-4) (LHCP) >gi_166646 (M63931) light-harvesting chlorophyll a/b binding protein [Arabidopsis thaliana]

Seq. No.	162396
Seq. ID	LIB3177-043-P1-K2-F8
Method	BLASTN
NCBI GI	g2191126
BLAST score	232
E value	1.0e-128
Match length	272
% identity	96
NCBI Description	Arabidopsis thaliana BAC IG002N01

Seq. No.	162397
Seq. ID	LIB3177-043-P1-K2-F9
Method	BLASTN
NCBI GI	g3789706
BLAST score	322
E value	0.0e+00
Match length	358
% identity	97
NCBI Description	Arabidopsis thaliana chromosome 1 BAC F15K9 sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	162398
Seq. ID	LIB3177-043-P1-K2-G2
Method	BLASTX
NCBI GI	g4586054
BLAST score	211
E value	9.0e-17
Match length	62
% identity	71
NCBI Description	(AC007020) unknown protein [Arabidopsis thaliana]

Seq. No.	162399
Seq. ID	LIB3177-043-P1-K2-G7
Method	BLASTX
NCBI GI	g3142289
BLAST score	398
E value	7.0e-39
Match length	80
% identity	93
NCBI Description	(AC002411) Strong similarity to beta-keto-Coa synthase gb_U37088 from Simmondsia chinensis. [Arabidopsis thaliana]

Seq. No.	162400
Seq. ID	LIB3177-043-P1-K2-G8
Method	BLASTX
NCBI GI	g4559346
BLAST score	650
E value	3.0e-68
Match length	127
% identity	99
NCBI Description	(AC006585) early nodulin 16 [Arabidopsis thaliana]

Seq. No.	162401
Seq. ID	LIB3177-043-P1-K2-H1
Method	BLASTX
NCBI GI	g4454037

BLAST score	751
E value	4.0e-80
Match length	142
% identity	98
NCBI Description	(AL035394) putative major latex protein [Arabidopsis thaliana]

Seq. No.	162402
Seq. ID	LIB3177-043-P1-K2-H2
Method	BLASTX
NCBI GI	g544134
BLAST score	140
E value	8.0e-60
Match length	139
% identity	88
NCBI Description	DNA-DAMAGE-REPAIR/TOLERATION PROTEIN DRT100 PRECURSOR >gi_99720_pir__S22863 hypothetical protein - Arabidopsis thaliana >gi_421844_pir__A46260 RecA functional analog DRT100 - Arabidopsis thaliana (fragment)

Seq. No.	162403
Seq. ID	LIB3177-043-P1-K2-H3
Method	BLASTX
NCBI GI	g1732570
BLAST score	52
E value	6.0e-52
Match length	111
% identity	95
NCBI Description	(U72153) beta-glucosidase [Arabidopsis thaliana]

Seq. No.	162404
Seq. ID	LIB3177-043-P1-K2-H5
Method	BLASTN
NCBI GI	g798819
BLAST score	43
E value	7.0e-15
Match length	154
% identity	86
NCBI Description	A.thaliana mRNA for squalene synthase

Seq. No.	162405
Seq. ID	LIB3177-043-P1-K2-H6
Method	BLASTX
NCBI GI	g132090
BLAST score	48
E value	7.0e-10
Match length	82
% identity	55
NCBI Description	RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN 1B PRECURSOR (RUBISCO SMALL SUBUNIT 1B) >gi_68062_pir__RKMUB1 ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain B1 precursor - Arabidopsis thaliana >gi_16193_emb_CAA32700_ (X14564) ribulose bisphosphate carboxylase [Arabidopsis thaliana]

Seq. No.	162406
Seq. ID	LIB3177-043-P1-K2-H7

Method	BLASTX
NCBI GI	g1170939
BLAST score	419
E value	5.0e-46
Match length	112
% identity	87
NCBI Description	S-ADENOSYLMETHIONINE SYNTHETASE 3 (METHIONINE ADENOSYLTRANSFERASE 3) (ADOMET SYNTHETASE 3) >gi_1084408_pir__S46540 methionine adenosyltransferase (EC 2.5.1.6) - tomato >gi_429108_emb_CAA80867_ (Z24743) S-adenosyl-L-methionine synthetase [Lycopersicon esculentum]

Seq. No.	162407
Seq. ID	LIB3177-044-P1-K2-A1
Method	BLASTX
NCBI GI	g1652057
BLAST score	492
E value	9.0e-50
Match length	142
% identity	68
NCBI Description	(D90902) hypothetical protein [Synechocystis sp.]

Seq. No.	162408
Seq. ID	LIB3177-044-P1-K2-A10
Method	BLASTX
NCBI GI	g2129784
BLAST score	436
E value	4.0e-43
Match length	129
% identity	74
NCBI Description	biotin carboxyl carrier protein (clone BP1) - rape (fragment) >gi_1070000_emb_CAA62261_ (X90727) biotin carboxyl carrier protein [Brassica napus] >gi_1589040_prf__2210244A Ac-CoA carboxylase:ISOTYPE=bp1 [Brassica napus]

Seq. No.	162409
Seq. ID	LIB3177-044-P1-K2-A2
Method	BLASTX
NCBI GI	g4741942
BLAST score	690
E value	6.0e-73
Match length	136
% identity	98
NCBI Description	(AF134121) Lhca5 protein [Arabidopsis thaliana]

Seq. No.	162410
Seq. ID	LIB3177-044-P1-K2-A3
Method	BLASTN
NCBI GI	g3004543
BLAST score	291
E value	1.0e-163
Match length	365
% identity	94
NCBI Description	Arabidopsis thaliana chromosome II BAC F19F24 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	162411
Seq. ID	LIB3177-044-P1-K2-A5
Method	BLASTX
NCBI GI	g1171978
BLAST score	486
E value	6.0e-49
Match length	137
% identity	77
NCBI Description	POLYADENYLATE-BINDING PROTEIN 2 (POLY(A) BINDING PROTEIN 2) (PABP 2) >gi_304109 (L19418) poly(A)-binding protein [Arabidopsis thaliana] >gi_2911051_emb_CAA17561_ (AL021961) poly(A)-binding protein [Arabidopsis thaliana]

Seq. No.	162412
Seq. ID	LIB3177-044-P1-K2-A6
Method	BLASTX
NCBI GI	g99820
BLAST score	535
E value	1.0e-54
Match length	105
% identity	95
NCBI Description	napin nIb - rape

Seq. No.	162413
Seq. ID	LIB3177-044-P1-K2-A7
Method	BLASTX
NCBI GI	g2435518
BLAST score	189
E value	3.0e-14
Match length	85
% identity	58
NCBI Description	(AF024504) contains similarity to C3HC4-type zinc fingers [Arabidopsis thaliana]

Seq. No.	162414
Seq. ID	LIB3177-044-P1-K2-A8
Method	BLASTX
NCBI GI	g1345840
BLAST score	434
E value	5.0e-43
Match length	84
% identity	99
NCBI Description	CRUCIFERIN BNC1 PRECURSOR (11S GLOBULIN) (12S STORAGE PROTEIN) >gi_762919_emb_CAA41984_ (X59294) cruciferin storage protein [Brassica napus]

Seq. No.	162415
Seq. ID	LIB3177-044-P1-K2-A9
Method	BLASTN
NCBI GI	g1069999
BLAST score	38
E value	9.0e-12
Match length	124
% identity	90
NCBI Description	B.napus mRNA for biotin carboxyl carrier protein (pBP1) >gi_3715063_emb_A59872.1_A59872 Sequence 1 from Patent

Seq. No.	162416
Seq. ID	LIB3177-044-P1-K2-B1
Method	BLASTX
NCBI GI	g115783
BLAST score	629
E value	8.0e-66
Match length	120
% identity	98
NCBI Description	CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR (CAB-140) (LHCP) >gi_16376_emb_CAA27543_ (X03909) chlorophyll a/b binding protein (LHCP AB 140) [Arabidopsis thaliana]

Seq. No.	162417
Seq. ID	LIB3177-044-P1-K2-B10
Method	BLASTX
NCBI GI	g3738285
BLAST score	564
E value	3.0e-58
Match length	119
% identity	89
NCBI Description	(AC005309) unknown protein [Arabidopsis thaliana]

Seq. No.	162418
Seq. ID	LIB3177-044-P1-K2-B11
Method	BLASTX
NCBI GI	g730463
BLAST score	320
E value	1.0e-29
Match length	105
% identity	59
NCBI Description	60S RIBOSOMAL PROTEIN L37B (YL37) (RP47) >gi_630323_pir__S44069 ribosomal protein L35a.e.c15 - yeast (Saccharomyces cerevisiae) >gi_484241 (L23923) ribosomal protein L37 [Saccharomyces cerevisiae] >gi_1420537_emb_CAA99454_ (Z75142) ORF YOR234c [Saccharomyces cerevisiae]

Seq. No.	162419
Seq. ID	LIB3177-044-P1-K2-B12
Method	BLASTX
NCBI GI	g124224
BLAST score	616
E value	3.0e-64
Match length	130
% identity	90
NCBI Description	INITIATION FACTOR 5A-1 (EIF-5A) (EIF-4D) >gi_100345_pir__S21060 translation initiation factor eIF-5A - common tobacco >gi_19887_emb_CAA45105_ (X63543) eukaryotic initiatin factor 5A (3) [Nicotiana tabacum]

Seq. No.	162420
Seq. ID	LIB3177-044-P1-K2-B2
Method	BLASTX
NCBI GI	g1769901

BLAST score	261
E value	1.0e-22
Match length	62
% identity	85
NCBI Description	(X95737) proline transporter 1 [Arabidopsis thaliana] >gi_2088642 (AF002109) proline transporter 1 [Arabidopsis thaliana]

Seq. No.	162421
Seq. ID	LIB3177-044-P1-K2-B3
Method	BLASTN
NCBI GI	g2335089
BLAST score	104
E value	3.0e-51
Match length	132
% identity	95
NCBI Description	Arabidopsis thaliana chromosome II BAC T11A7 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	162422
Seq. ID	LIB3177-044-P1-K2-B4
Method	BLASTX
NCBI GI	g1070654
BLAST score	570
E value	7.0e-59
Match length	129
% identity	87
NCBI Description	cruciferin 4 precursor - rape

Seq. No.	162423
Seq. ID	LIB3177-044-P1-K2-B5
Method	BLASTX
NCBI GI	g1070654
BLAST score	636
E value	1.0e-66
Match length	151
% identity	79
NCBI Description	cruciferin 4 precursor - rape

Seq. No.	162424
Seq. ID	LIB3177-044-P1-K2-B6
Method	BLASTX
NCBI GI	g99820
BLAST score	530
E value	4.0e-54
Match length	106
% identity	93
NCBI Description	napin nIb - rape

Seq. No.	162425
Seq. ID	LIB3177-044-P1-K2-B7
Method	BLASTX
NCBI GI	g2435518
BLAST score	412
E value	3.0e-40
Match length	113
% identity	81

NCBI Description	(AF024504) contains similarity to C3HC4-type zinc fingers [Arabidopsis thaliana]
Seq. No.	162426
Seq. ID	LIB3177-044-P1-K2-B8
Method	BLASTX
NCBI GI	g2651314
BLAST score	458
E value	8.0e-46
Match length	116
% identity	79
NCBI Description	(AC002336) putative ribosomal protein S26 [Arabidopsis thaliana]
Seq. No.	162427
Seq. ID	LIB3177-044-P1-K2-B9
Method	BLASTX
NCBI GI	g3122389
BLAST score	438
E value	2.0e-43
Match length	126
% identity	66
NCBI Description	WD-40 REPEAT PROTEIN MSI3 >gi_2394233 (AF016848) WD-40 repeat protein [Arabidopsis thaliana]
Seq. No.	162428
Seq. ID	LIB3177-044-P1-K2-C1
Method	BLASTX
NCBI GI	g167134
BLAST score	632
E value	4.0e-66
Match length	127
% identity	98
NCBI Description	(M16860) cruciferin precursor [Brassica napus]
Seq. No.	162429
Seq. ID	LIB3177-044-P1-K2-C10
Method	BLASTX
NCBI GI	g1072480
BLAST score	364
E value	9.0e-35
Match length	78
% identity	96
NCBI Description	cruciferin 1 precursor - rape
Seq. No.	162430
Seq. ID	LIB3177-044-P1-K2-C11
Method	BLASTX
NCBI GI	g99820
BLAST score	489
E value	2.0e-49
Match length	103
% identity	90
NCBI Description	napin nIb - rape
Seq. No.	162431
Seq. ID	LIB3177-044-P1-K2-C2

Method	BLASTX
NCBI GI	g1769901
BLAST score	223
E value	4.0e-18
Match length	56
% identity	82
NCBI Description	(X95737) proline transporter 1 [Arabidopsis thaliana] >gi_2088642 (AF002109) proline transporter 1 [Arabidopsis thaliana]

Seq. No.	162432
Seq. ID	LIB3177-044-P1-K2-C3
Method	BLASTN
NCBI GI	g2335089
BLAST score	130
E value	6.0e-67
Match length	158
% identity	96
NCBI Description	Arabidopsis thaliana chromosome II BAC T11A7 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	162433
Seq. ID	LIB3177-044-P1-K2-C4
Method	BLASTN
NCBI GI	g17804
BLAST score	52
E value	3.0e-20
Match length	213
% identity	91
NCBI Description	B.napus cru4 mRNA for cruciferin cru4 subunit

Seq. No.	162434
Seq. ID	LIB3177-044-P1-K2-C5
Method	BLASTX
NCBI GI	g1070654
BLAST score	613
E value	6.0e-64
Match length	115
% identity	97
NCBI Description	cruciferin 4 precursor - rape

Seq. No.	162435
Seq. ID	LIB3177-044-P1-K2-C6
Method	BLASTX
NCBI GI	g99820
BLAST score	519
E value	7.0e-53
Match length	103
% identity	95
NCBI Description	napin nIb - rape

Seq. No.	162436
Seq. ID	LIB3177-044-P1-K2-C8
Method	BLASTX
NCBI GI	g1345841
BLAST score	523
E value	2.0e-53

Match length	105
% identity	98
NCBI Description	CRUCIFERIN BNC2 PRECURSOR (11S GLOBULIN) (12S STORAGE PROTEIN) >gi_762920_emb_CAA41985_ (X59295) cruciferin storage protein [Brassica napus]

Seq. No.	162437
Seq. ID	LIB3177-044-P1-K2-C9
Method	BLASTX
NCBI GI	g1072480
BLAST score	365
E value	8.0e-35
Match length	78
% identity	96
NCBI Description	cruciferin 1 precursor - rape

Seq. No.	162438
Seq. ID	LIB3177-044-P1-K2-D1
Method	BLASTX
NCBI GI	g466160
BLAST score	329
E value	1.0e-30
Match length	81
% identity	78
NCBI Description	HYPOTHETICAL 9.8 KD PROTEIN ZK652.3 IN CHROMOSOME III >gi_630771_pir__S44903 ZK652.3 protein - Caenorhabditis elegans >gi_289769 (L14429) putative [Caenorhabditis elegans]

Seq. No.	162439
Seq. ID	LIB3177-044-P1-K2-D10
Method	BLASTX
NCBI GI	g1070654
BLAST score	685
E value	3.0e-72
Match length	165
% identity	79
NCBI Description	cruciferin 4 precursor - rape

Seq. No.	162440
Seq. ID	LIB3177-044-P1-K2-D12
Method	BLASTX
NCBI GI	g99819
BLAST score	552
E value	1.0e-56
Match length	109
% identity	94
NCBI Description	napin nIa - rape

Seq. No.	162441
Seq. ID	LIB3177-044-P1-K2-D2
Method	BLASTX
NCBI GI	g2129579
BLAST score	664
E value	6.0e-70
Match length	146
% identity	92

NCBI Description	Dwarf1 protein - Arabidopsis thaliana >gi_516043 (U12400) Dwarf1 [Arabidopsis thaliana]
Seq. No.	162442
Seq. ID	LIB3177-044-P1-K2-D3
Method	BLASTX
NCBI GI	g4581146
BLAST score	170
E value	1.0e-12
Match length	41
% identity	85
NCBI Description	(AC006919) putative fructose-bisphosphate aldolase, cytoplasmic [Arabidopsis thaliana]
Seq. No.	162443
Seq. ID	LIB3177-044-P1-K2-D4
Method	BLASTX
NCBI GI	g1070654
BLAST score	613
E value	7.0e-64
Match length	157
% identity	76
NCBI Description	cruciferin 4 precursor - rape
Seq. No.	162444
Seq. ID	LIB3177-044-P1-K2-D5
Method	BLASTX
NCBI GI	g4455256
BLAST score	537
E value	6.0e-55
Match length	125
% identity	74
NCBI Description	(AL035523) protein-methionine-S-oxide reductase [Arabidopsis thaliana]
Seq. No.	162445
Seq. ID	LIB3177-044-P1-K2-D6
Method	BLASTX
NCBI GI	g1072480
BLAST score	524
E value	2.0e-53
Match length	100
% identity	98
NCBI Description	cruciferin 1 precursor - rape
Seq. No.	162446
Seq. ID	LIB3177-044-P1-K2-D8
Method	BLASTX
NCBI GI	g1072480
BLAST score	618
E value	2.0e-64
Match length	123
% identity	94
NCBI Description	cruciferin 1 precursor - rape
Seq. No.	162447
Seq. ID	LIB3177-044-P1-K2-D9

Method	BLASTX
NCBI GI	g1070654
BLAST score	692
E value	4.0e-73
Match length	164
% identity	79
NCBI Description	cruciferin 4 precursor - rape

Seq. No.	162448
Seq. ID	LIB3177-044-P1-K2-E1
Method	BLASTX
NCBI GI	g2997684
BLAST score	462
E value	4.0e-46
Match length	100
% identity	89
NCBI Description	(AF053302) putative transcriptional co-activator [Arabidopsis thaliana]

Seq. No.	162449
Seq. ID	LIB3177-044-P1-K2-E10
Method	BLASTX
NCBI GI	g99820
BLAST score	535
E value	1.0e-54
Match length	105
% identity	95
NCBI Description	napin nIb - rape

Seq. No.	162450
Seq. ID	LIB3177-044-P1-K2-E11
Method	BLASTX
NCBI GI	g82051
BLAST score	302
E value	2.0e-27
Match length	130
% identity	46
NCBI Description	lipid body-associated membrane protein - carrot >gi_259453_bbs_117620 (S47635) lipid body membrane protein=DC 59 [Daucus carota=carrots, var Juwarot, Peptide, 180 aa] [Daucus carota]

Seq. No.	162451
Seq. ID	LIB3177-044-P1-K2-E12
Method	BLASTX
NCBI GI	g2129657
BLAST score	529
E value	5.0e-54
Match length	153
% identity	73
NCBI Description	oleosin isoform - Arabidopsis thaliana >gi_987014_emb_CAA90877_ (Z54164) oleosin [Arabidopsis thaliana] >gi_987016_emb_CAA90878_ (Z54165) oleosin [Arabidopsis thaliana]

Seq. No.	162452
Seq. ID	LIB3177-044-P1-K2-E2

Method	BLASTX
NCBI GI	g2501578
BLAST score	569
E value	8.0e-59
Match length	123
% identity	94
NCBI Description	ETHYLENE-INDUCIBLE PROTEIN HEVER >gi_2129913_pir__S60047 ethylene-responsive protein 1 - Para rubber tree >gi_1209317 (M88254) ethylene-inducible protein [Hevea brasiliensis]

Seq. No.	162453
Seq. ID	LIB3177-044-P1-K2-E3
Method	BLASTX
NCBI GI	g2062164
BLAST score	665
E value	6.0e-70
Match length	143
% identity	91
NCBI Description	(AC001645) jasmonate inducible protein isolog [Arabidopsis thaliana]

Seq. No.	162454
Seq. ID	LIB3177-044-P1-K2-E4
Method	BLASTX
NCBI GI	g99819
BLAST score	576
E value	2.0e-59
Match length	113
% identity	95
NCBI Description	napin nIa - rape

Seq. No.	162455
Seq. ID	LIB3177-044-P1-K2-E5
Method	BLASTX
NCBI GI	g112742
BLAST score	649
E value	4.0e-68
Match length	132
% identity	91
NCBI Description	NAPIN PRECURSOR (1.7S SEED STORAGE PROTEIN) >gi_81687_pir__S10018 napin (clone BngNAP1) - rape >gi_1084352_pir__S52027 napin - rape >gi_17833_emb_CAA35580_ (X17542) napin (AA 1-180) [Brassica napus] >gi_468022 (U04945) napin [Brassica napus]

Seq. No.	162456
Seq. ID	LIB3177-044-P1-K2-E6
Method	BLASTX
NCBI GI	g461840
BLAST score	880
E value	4.0e-95
Match length	167
% identity	99
NCBI Description	CRUCIFERIN CRU1 PRECURSOR (11S GLOBULIN) (12S STORAGE PROTEIN) >gi_17801_emb_CAA44042_ (X62120) cuciferin subunit [Brassica napus]

Seq. No.	162457
Seq. ID	LIB3177-044-P1-K2-E7
Method	BLASTX
NCBI GI	g167136
BLAST score	531
E value	3.0e-54
Match length	124
% identity	85
NCBI Description	(J05233) cruciferin precursor [Brassica napus]

Seq. No.	162458
Seq. ID	LIB3177-044-P1-K2-E8
Method	BLASTX
NCBI GI	g1072480
BLAST score	570
E value	7.0e-59
Match length	118
% identity	93
NCBI Description	cruciferin 1 precursor - rape

Seq. No.	162459
Seq. ID	LIB3177-044-P1-K2-E9
Method	BLASTX
NCBI GI	g99819
BLAST score	563
E value	5.0e-58
Match length	111
% identity	95
NCBI Description	napin nIa - rape

Seq. No.	162460
Seq. ID	LIB3177-044-P1-K2-F1
Method	BLASTN
NCBI GI	g2924651
BLAST score	373
E value	0.0e+00
Match length	419
% identity	99
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K2A18, complete sequence [Arabidopsis thaliana]

Seq. No.	162461
Seq. ID	LIB3177-044-P1-K2-F10
Method	BLASTX
NCBI GI	g112742
BLAST score	588
E value	6.0e-61
Match length	129
% identity	88
NCBI Description	NAPIN PRECURSOR (1.7S SEED STORAGE PROTEIN) >gi_81687_pir__S10018 napin (clone BngNAP1) - rape >gi_1084352_pir__S52027 napin - rape >gi_17833_emb_CAA35580_ (X17542) napin (AA 1-180) [Brassica napus] >gi_468022 (U04945) napin [Brassica napus]

Seq. No.	162462

Seq. ID	LIB3177-044-P1-K2-F12
Method	BLASTX
NCBI GI	g112742
BLAST score	587
E value	7.0e-61
Match length	128
% identity	88
NCBI Description	NAPIN PRECURSOR (1.7S SEED STORAGE PROTEIN) >gi_81687_pir__S10018 napin (clone BngNAP1) - rape >gi_1084352_pir__S52027 napin - rape >gi_17833_emb_CAA35580_ (X17542) napin (AA 1-180) [Brassica napus] >gi_468022 (U04945) napin [Brassica napus]

Seq. No.	162463
Seq. ID	LIB3177-044-P1-K2-F2
Method	BLASTX
NCBI GI	g135406
BLAST score	628
E value	1.0e-65
Match length	118
% identity	99
NCBI Description	TUBULIN ALPHA-3/ALPHA-5 CHAIN >gi_99768_pir__A32712 tubulin alpha-5 chain - Arabidopsis thaliana >gi_166912 (M17189) alpha-tubulin [Arabidopsis thaliana] >gi_166918 (M84698) alpha-5 tubulin [Arabidopsis thaliana]

Seq. No.	162464
Seq. ID	LIB3177-044-P1-K2-F3
Method	BLASTX
NCBI GI	g1172568
BLAST score	240
E value	4.0e-20
Match length	90
% identity	56
NCBI Description	LOW MOLECULAR WEIGHT PHOSPHOTYROSINE PROTEIN PHOSPHATASE (LOW MOLECULAR WEIGHT CYTOSOLIC ACID PHOSPHATASE) (PTPASE) (SMALL TYROSINE PHOSPHATASE) >gi_1076916_pir__A55446 protein-tyrosine-phosphatase (EC 3.1.3.48), low molecular weight - fission yeast (Schizosaccharomyces pombe) >gi_602992 (L33929) low Mr protein tyrosine phosphatase [Schizosaccharomyces pombe]

Seq. No.	162465
Seq. ID	LIB3177-044-P1-K2-F4
Method	BLASTX
NCBI GI	g112742
BLAST score	581
E value	3.0e-60
Match length	124
% identity	86
NCBI Description	NAPIN PRECURSOR (1.7S SEED STORAGE PROTEIN) >gi_81687_pir__S10018 napin (clone BngNAP1) - rape >gi_1084352_pir__S52027 napin - rape >gi_17833_emb_CAA35580_ (X17542) napin (AA 1-180) [Brassica napus] >gi_468022 (U04945) napin [Brassica napus]

Seq. No.	162466

Seq. ID	LIB3177-044-P1-K2-F5
Method	BLASTX
NCBI GI	g112742
BLAST score	644
E value	2.0e-67
Match length	158
% identity	80
NCBI Description	NAPIN PRECURSOR (1.7S SEED STORAGE PROTEIN) >gi_81687_pir__S10018 napin (clone BngNAP1) - rape >gi_1084352_pir__S52027 napin - rape >gi_17833_emb_CAA35580_ (X17542) napin (AA 1-180) [Brassica napus] >gi_468022 (U04945) napin [Brassica napus]

Seq. No.	162467
Seq. ID	LIB3177-044-P1-K2-F6
Method	BLASTX
NCBI GI	g99819
BLAST score	563
E value	5.0e-58
Match length	111
% identity	95
NCBI Description	napin nIa - rape

Seq. No.	162468
Seq. ID	LIB3177-044-P1-K2-F7
Method	BLASTX
NCBI GI	g1345840
BLAST score	506
E value	2.0e-51
Match length	115
% identity	87
NCBI Description	CRUCIFERIN BNC1 PRECURSOR (11S GLOBULIN) (12S STORAGE PROTEIN) >gi_762919_emb_CAA41984_ (X59294) cruciferin storage protein [Brassica napus]

Seq. No.	162469
Seq. ID	LIB3177-044-P1-K2-F8
Method	BLASTN
NCBI GI	g166611
BLAST score	42
E value	1.0e-14
Match length	128
% identity	85
NCBI Description	A.thaliana at2S3 gene encoding albumin 2S subunit 3, complete cds

Seq. No.	162470
Seq. ID	LIB3177-044-P1-K2-F9
Method	BLASTX
NCBI GI	g112742
BLAST score	594
E value	1.0e-61
Match length	129
% identity	88
NCBI Description	NAPIN PRECURSOR (1.7S SEED STORAGE PROTEIN) >gi_81687_pir__S10018 napin (clone BngNAP1) - rape >gi_1084352_pir__S52027 napin - rape

	>gi_17833_emb_CAA35580_ (X17542) napin (AA 1-180) [Brassica napus] >gi_468022 (U04945) napin [Brassica napus]
Seq. No.	162471
Seq. ID	LIB3177-044-P1-K2-G10
Method	BLASTX
NCBI GI	g99819
BLAST score	576
E value	2.0e-59
Match length	113
% identity	95
NCBI Description	napin nIa - rape
Seq. No.	162472
Seq. ID	LIB3177-044-P1-K2-G11
Method	BLASTX
NCBI GI	g1345594
BLAST score	419
E value	4.0e-41
Match length	85
% identity	98
NCBI Description	14-3-3-LIKE PROTEIN GF14 KAPPA >gi_1022780 (U36447) GF14 Kappa isoform [Arabidopsis thaliana]
Seq. No.	162473
Seq. ID	LIB3177-044-P1-K2-G12
Method	BLASTX
NCBI GI	g167136
BLAST score	656
E value	6.0e-69
Match length	136
% identity	92
NCBI Description	(J05233) cruciferin precursor [Brassica napus]
Seq. No.	162474
Seq. ID	LIB3177-044-P1-K2-G2
Method	BLASTX
NCBI GI	g4406820
BLAST score	624
E value	4.0e-65
Match length	164
% identity	79
NCBI Description	(AC006201) putative ras superfamily member [Arabidopsis thaliana]
Seq. No.	162475
Seq. ID	LIB3177-044-P1-K2-G3
Method	BLASTX
NCBI GI	g2623296
BLAST score	381
E value	8.0e-37
Match length	95
% identity	77
NCBI Description	(AC002409) hypothetical protein [Arabidopsis thaliana]
Seq. No.	162476
Seq. ID	LIB3177-044-P1-K2-G4

Method	BLASTX
NCBI GI	g1084351
BLAST score	498
E value	2.0e-50
Match length	105
% identity	88
NCBI Description	napin - rape >gi_468018 (U04943) napin [Brassica napus] >gi_468020 (U04944) napin [Brassica napus]

Seq. No.	162477
Seq. ID	LIB3177-044-P1-K2-G5
Method	BLASTX
NCBI GI	g2129657
BLAST score	441
E value	1.0e-43
Match length	134
% identity	71
NCBI Description	oleosin isoform - Arabidopsis thaliana >gi_987014_emb_CAA90877_ (Z54164) oleosin [Arabidopsis thaliana] >gi_987016_emb_CAA90878_ (Z54165) oleosin [Arabidopsis thaliana]

Seq. No.	162478
Seq. ID	LIB3177-044-P1-K2-G6
Method	BLASTX
NCBI GI	g167134
BLAST score	606
E value	5.0e-63
Match length	124
% identity	98
NCBI Description	(M16860) cruciferin precursor [Brassica napus]

Seq. No.	162479
Seq. ID	LIB3177-044-P1-K2-G7
Method	BLASTN
NCBI GI	g4165340
BLAST score	127
E value	5.0e-65
Match length	362
% identity	86
NCBI Description	Arabidopsis thaliana chromosome I BAC F11M15 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	162480
Seq. ID	LIB3177-044-P1-K2-G8
Method	BLASTX
NCBI GI	g112747
BLAST score	508
E value	2.0e-51
Match length	160
% identity	64
NCBI Description	NAPIN EMBRYO SPECIFIC PRECURSOR (1.7S SEED STORAGE PROTEIN) >gi_81689_pir__A29802 napin precursor (gNa) - rape >gi_167179 (J02782) napin, 1.7S embryo specific [Brassica napus]

Seq. No.	162481

Seq. ID	LIB3177-044-P1-K2-G9
Method	BLASTX
NCBI GI	g99819
BLAST score	576
E value	2.0e-59
Match length	113
% identity	95
NCBI Description	napin nIa - rape

Seq. No.	162482
Seq. ID	LIB3177-044-P1-K2-H10
Method	BLASTX
NCBI GI	g4753655
BLAST score	159
E value	3.0e-20
Match length	60
% identity	85
NCBI Description	(AL049751) pectate lyase like protein [Arabidopsis thaliana]

Seq. No.	162483
Seq. ID	LIB3177-044-P1-K2-H11
Method	BLASTX
NCBI GI	g1172977
BLAST score	201
E value	1.0e-15
Match length	81
% identity	64
NCBI Description	60S RIBOSOMAL PROTEIN L18 >gi_606970 (U15741) cytoplasmic ribosomal protein L18 [Arabidopsis thaliana]

Seq. No.	162484
Seq. ID	LIB3177-044-P1-K2-H2
Method	BLASTX
NCBI GI	g3777600
BLAST score	443
E value	6.0e-44
Match length	145
% identity	61
NCBI Description	(AF095708) 50S ribosomal protein L5 [Oryza sativa]

Seq. No.	162485
Seq. ID	LIB3177-044-P1-K2-H3
Method	BLASTX
NCBI GI	g1072480
BLAST score	685
E value	2.0e-72
Match length	144
% identity	92
NCBI Description	cruciferin 1 precursor - rape

Seq. No.	162486
Seq. ID	LIB3177-044-P1-K2-H4
Method	BLASTX
NCBI GI	g167134
BLAST score	819
E value	5.0e-88

Match length	160
% identity	99
NCBI Description	(M16860) cruciferin precursor [Brassica napus]

Seq. No.	162487
Seq. ID	LIB3177-044-P1-K2-H5
Method	BLASTX
NCBI GI	g1084351
BLAST score	494
E value	5.0e-50
Match length	124
% identity	75
NCBI Description	napin - rape >gi_468018 (U04943) napin [Brassica napus] >gi_468020 (U04944) napin [Brassica napus]

Seq. No.	162488
Seq. ID	LIB3177-044-P1-K2-H6
Method	BLASTX
NCBI GI	g99820
BLAST score	453
E value	4.0e-45
Match length	91
% identity	95
NCBI Description	napin nIb - rape

Seq. No.	162489
Seq. ID	LIB3177-044-P1-K2-H8
Method	BLASTX
NCBI GI	g167136
BLAST score	720
E value	2.0e-76
Match length	147
% identity	93
NCBI Description	(J05233) cruciferin precursor [Brassica napus]

Seq. No.	162490
Seq. ID	LIB3177-044-P1-K2-H9
Method	BLASTX
NCBI GI	g4753655
BLAST score	159
E value	9.0e-23
Match length	60
% identity	88
NCBI Description	(AL049751) pectate lyase like protein [Arabidopsis thaliana]

Seq. No.	162491
Seq. ID	LIB3177-045-P1-K2-A1
Method	BLASTN
NCBI GI	g4559319
BLAST score	74
E value	8.0e-34
Match length	136
% identity	88
NCBI Description	Arabidopsis thaliana chromosome II BAC F14N22 genomic sequence, complete sequence

Seq. No.	162492
Seq. ID	LIB3177-045-P1-K2-A10
Method	BLASTX
NCBI GI	g2829899
BLAST score	92
E value	1.0e-15
Match length	109
% identity	46
NCBI Description	(AC002311) similar to ripening-induced protein, gp_AJ001449_2465015 and major#latex protein, gp_X91961_1107495 [Arabidopsis thaliana]

Seq. No.	162493
Seq. ID	LIB3177-045-P1-K2-A11
Method	BLASTN
NCBI GI	g2264302
BLAST score	59
E value	3.0e-25
Match length	86
% identity	99
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MAC12, complete sequence [Arabidopsis thaliana]

Seq. No.	162494
Seq. ID	LIB3177-045-P1-K2-A12
Method	BLASTX
NCBI GI	g1363489
BLAST score	239
E value	1.0e-20
Match length	47
% identity	91
NCBI Description	thioglucosidase (EC 3.2.3.1) 3D precursor - Arabidopsis thaliana >gi_984052_emb_CAA61592_ (X89413) thioglucoside glucohydrolase [Arabidopsis thaliana]

Seq. No.	162495
Seq. ID	LIB3177-045-P1-K2-A2
Method	BLASTN
NCBI GI	g4559344
BLAST score	401
E value	0.0e+00
Match length	425
% identity	99
NCBI Description	Arabidopsis thaliana chromosome II BAC F27C12 genomic sequence, complete sequence

Seq. No.	162496
Seq. ID	LIB3177-045-P1-K2-A3
Method	BLASTX
NCBI GI	g115767
BLAST score	93
E value	2.0e-73
Match length	144
% identity	98
NCBI Description	CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR (CAB-165/180) (LHCP) >gi_81603_pir__A29280 chlorophyll a/b-binding protein ab165 - Arabidopsis thaliana

>gi_16368_emb_CAA27540_ (X03907) chlorophyll a/b binding protein (LHCP AB 65) [Arabidopsis thaliana]
>gi_16372_emb_CAA27541_ (X03908) chlorophyll a/b binding protein (LHCP AB 180) [Arabidopsis thaliana]

Seq. No.	162497
Seq. ID	LIB3177-045-P1-K2-A4
Method	BLASTN
NCBI GI	g3090402
BLAST score	97
E value	1.0e-47
Match length	132
% identity	95
NCBI Description	Arabidopsis thaliana mRNA for cytochrome b6f complex subunit

Seq. No.	162498
Seq. ID	LIB3177-045-P1-K2-A8
Method	BLASTX
NCBI GI	g2119927
BLAST score	445
E value	2.0e-44
Match length	101
% identity	83
NCBI Description	translation elongation factor G, chloroplast - soybean

Seq. No.	162499
Seq. ID	LIB3177-045-P1-K2-B1
Method	BLASTX
NCBI GI	g1524370
BLAST score	392
E value	5.0e-38
Match length	124
% identity	64
NCBI Description	(X92491) TOM20 [Solanum tuberosum]

Seq. No.	162500
Seq. ID	LIB3177-045-P1-K2-B11
Method	BLASTN
NCBI GI	g2342717
BLAST score	127
E value	2.0e-65
Match length	159
% identity	96
NCBI Description	Arabidopsis thaliana chromosome II BAC T14G11 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	162501
Seq. ID	LIB3177-045-P1-K2-B12
Method	BLASTN
NCBI GI	g2351063
BLAST score	154
E value	2.0e-81
Match length	185
% identity	96
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MCL19, complete sequence [Arabidopsis thaliana]

Seq. No.	162502
Seq. ID	LIB3177-045-P1-K2-B3
Method	BLASTX
NCBI GI	g416681
BLAST score	117
E value	3.0e-20
Match length	145
% identity	47
NCBI Description	ATP SYNTHASE DELTA CHAIN, CHLOROPLAST PRECURSOR >gi_280404_pir__S26198 H+-transporting ATP synthase (EC 3.6.1.34) delta chain precursor, chloroplast - common tobacco >gi_19787_emb_CAA45153_ (X63607) chloroplast ATP synthase (delta subunit) [Nicotiana tabacum]

Seq. No.	162503
Seq. ID	LIB3177-045-P1-K2-B8
Method	BLASTX
NCBI GI	g4741952
BLAST score	238
E value	5.0e-20
Match length	101
% identity	49
NCBI Description	(AF134126) Lhcb3 protein [Arabidopsis thaliana]

Seq. No.	162504
Seq. ID	LIB3177-045-P1-K2-B9
Method	BLASTX
NCBI GI	g3914442
BLAST score	460
E value	5.0e-46
Match length	120
% identity	76
NCBI Description	PHOTOSYSTEM I REACTION CENTRE SUBUNIT VI PRECURSOR (LIGHT-HARVESTING COMPLEX I 11 KD PROTEIN) (PSI-H) >gi_1916350 (U92504) PSI-H subunit [Brassica rapa]

Seq. No.	162505
Seq. ID	LIB3177-045-P1-K2-C1
Method	BLASTX
NCBI GI	g4337175
BLAST score	638
E value	7.0e-67
Match length	142
% identity	89
NCBI Description	(AC006416) ESTs gb_T20589, gb_T04648, gb_AA597906, gb_T04111, gb_R84180, gb_R65428, gb_T44439, gb_T76570, gb_R90004, gb_T45020, gb_T42457, gb_T20921, gb_AA042762 and gb_AA720210 come from this gene. [Arabidopsis thaliana]

Seq. No.	162506
Seq. ID	LIB3177-045-P1-K2-C11
Method	BLASTN
NCBI GI	g166814
BLAST score	237
E value	1.0e-131
Match length	273

% identity	97
NCBI Description	Arabidopsis thaliana pyrroline carboxylate reductase gene, complete cds
Seq. No.	162507
Seq. ID	LIB3177-045-P1-K2-C2
Method	BLASTX
NCBI GI	g4538963
BLAST score	651
E value	2.0e-68
Match length	140
% identity	70
NCBI Description	(AL049488) chlorophyll a/b-binding protein-like [Arabidopsis thaliana] >gi_4741958_gb_AAD28776.1_AF134129_1 (AF134129) Lhcb5 protein [Arabidopsis thaliana]
Seq. No.	162508
Seq. ID	LIB3177-045-P1-K2-C3
Method	BLASTX
NCBI GI	g125576
BLAST score	310
E value	1.0e-28
Match length	109
% identity	61
NCBI Description	PHOSPHORIBULOKINASE PRECURSOR (PHOSPHOPENTOKINASE) (PRKASE) (PRK) >gi_99744_pir__S16583 phosphoribulokinase (EC 2.7.1.19) precursor - Arabidopsis thaliana >gi_16441_emb_CAA41155_ (X58149) Ribulose-5-phosphate kinase [Arabidopsis thaliana]
Seq. No.	162509
Seq. ID	LIB3177-045-P1-K2-C7
Method	BLASTN
NCBI GI	g2696018
BLAST score	105
E value	7.0e-52
Match length	373
% identity	91
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MXC9, complete sequence [Arabidopsis thaliana]
Seq. No.	162510
Seq. ID	LIB3177-045-P1-K2-C9
Method	BLASTX
NCBI GI	g2708741
BLAST score	712
E value	2.0e-75
Match length	150
% identity	93
NCBI Description	(AC003952) hypothetical protein [Arabidopsis thaliana]
Seq. No.	162511
Seq. ID	LIB3177-045-P1-K2-D1
Method	BLASTX
NCBI GI	g627469
BLAST score	206
E value	3.0e-16

Match length	150
% identity	8
NCBI Description	hypothetical protein 2 - human (fragment)

Seq. No.	162512
Seq. ID	LIB3177-045-P1-K2-D11
Method	BLASTX
NCBI GI	g1706130
BLAST score	192
E value	3.0e-15
Match length	52
% identity	71
NCBI Description	CDPK-RELATED PROTEIN KINASE (PK421) >gi_2129917_pir__S60052 calcium-dependent protein kinase homolog - carrot >gi_1103386_emb_CAA58750_ (X83869) CDPK-related protein kinase [Daucus carota]

Seq. No.	162513
Seq. ID	LIB3177-045-P1-K2-D2
Method	BLASTN
NCBI GI	g2264307
BLAST score	151
E value	3.0e-79
Match length	378
% identity	96
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MED24, complete sequence [Arabidopsis thaliana]

Seq. No.	162514
Seq. ID	LIB3177-045-P1-K2-D4
Method	BLASTN
NCBI GI	g3046853
BLAST score	134
E value	1.0e-69
Match length	170
% identity	95
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MRA19, complete sequence [Arabidopsis thaliana]

Seq. No.	162515
Seq. ID	LIB3177-045-P1-K2-D5
Method	BLASTX
NCBI GI	g555576
BLAST score	89
E value	8.0e-17
Match length	89
% identity	50
NCBI Description	(X80036) ascorbate peroxidase [Arabidopsis thaliana] >gi_1523789_emb_CAA66925_ (X98275) L-ascorbate peroxidase [Arabidopsis thaliana]

Seq. No.	162516
Seq. ID	LIB3177-045-P1-K2-D8
Method	BLASTX
NCBI GI	g1669387
BLAST score	189
E value	3.0e-14

Match length	41
% identity	85
NCBI Description	(U41998) actin 2 [Arabidopsis thaliana]

Seq. No.	162517
Seq. ID	LIB3177-045-P1-K2-D9
Method	BLASTX
NCBI GI	g1169201
BLAST score	400
E value	4.0e-39
Match length	106
% identity	79
NCBI Description	DNA-DAMAGE-REPAIR/TOLERATION PROTEIN DRT112 PRECURSOR >gi_421830_pir__S33707 DRT112 protein - Arabidopsis thaliana >gi_166696 (M98456) DRT112 [Arabidopsis thaliana]

Seq. No.	162518
Seq. ID	LIB3177-045-P1-K2-E1
Method	BLASTX
NCBI GI	g2499973
BLAST score	409
E value	5.0e-40
Match length	100
% identity	83
NCBI Description	PHOTOSYSTEM II 5 KD PROTEIN PRECURSOR (PSII-T) >gi_1465366_emb_CAA66701_ (X98078) photosystem II [Arabidopsis thaliana]

Seq. No.	162519
Seq. ID	LIB3177-045-P1-K2-E2
Method	BLASTX
NCBI GI	g3929651
BLAST score	696
E value	1.0e-73
Match length	137
% identity	100
NCBI Description	(AJ131206) microbody NAD-dependent malate dehydrogenase [Arabidopsis thaliana]

Seq. No.	162520
Seq. ID	LIB3177-045-P1-K2-E3
Method	BLASTX
NCBI GI	g3914442
BLAST score	545
E value	6.0e-56
Match length	145
% identity	75
NCBI Description	PHOTOSYSTEM I REACTION CENTRE SUBUNIT VI PRECURSOR (LIGHT-HARVESTING COMPLEX I 11 KD PROTEIN) (PSI-H) >gi_1916350 (U92504) PSI-H subunit [Brassica rapa]

Seq. No.	162521
Seq. ID	LIB3177-045-P1-K2-E4
Method	BLASTN
NCBI GI	g3510343
BLAST score	155
E value	4.0e-82

Match length	163
% identity	99
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MJC20, complete sequence [Arabidopsis thaliana]

Seq. No.	162522
Seq. ID	LIB3177-045-P1-K2-E7
Method	BLASTN
NCBI GI	g469113
BLAST score	223
E value	1.0e-122
Match length	355
% identity	91
NCBI Description	A.thaliana (Columbia) Dr4 mRNA

Seq. No.	162523
Seq. ID	LIB3177-045-P1-K2-F1
Method	BLASTX
NCBI GI	g1363489
BLAST score	672
E value	6.0e-71
Match length	122
% identity	99
NCBI Description	thioglucosidase (EC 3.2.3.1) 3D precursor - Arabidopsis thaliana >gi_984052_emb_CAA61592_ (X89413) thioglucoside glucohydrolase [Arabidopsis thaliana]

Seq. No.	162524
Seq. ID	LIB3177-045-P1-K2-F10
Method	BLASTX
NCBI GI	g3914740
BLAST score	216
E value	5.0e-18
Match length	51
% identity	86
NCBI Description	60S RIBOSOMAL PROTEIN L26 >gi_2160300_dbj_BAA18941_ (D78495) ribosomal protein [Brassica rapa]

Seq. No.	162525
Seq. ID	LIB3177-045-P1-K2-F11
Method	BLASTN
NCBI GI	g4584531
BLAST score	73
E value	2.0e-33
Match length	130
% identity	93
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone T9E8 (ESSA project)

Seq. No.	162526
Seq. ID	LIB3177-045-P1-K2-F2
Method	BLASTX
NCBI GI	g2506443
BLAST score	216
E value	6.0e-18
Match length	72
% identity	71

NCBI Description	GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE A PRECURSOR, CHLOROPLAST >gi_2117520_pir__JQ1285 glyceraldehyde-3-phosphate dehydrogenase (NADP+) (phosphorylating) (EC 1.2.1.13) A precursor, chloroplast - Arabidopsis thaliana >gi_166704 (M64117) glyceraldehyde 3-phosphate dehydrogenase [Arabidopsis thaliana] >gi_1402885_emb_CAA66816_ (X98130) glyceraldehyde-3-phosphate dehydrogenase (NADP+) (phosphorylating) [Arabidopsis thaliana]

Seq. No.	162527
Seq. ID	LIB3177-045-P1-K2-F3
Method	BLASTX
NCBI GI	g4006848
BLAST score	344
E value	2.0e-32
Match length	124
% identity	54
NCBI Description	(AJ131433) selenocysteine methyltransferase [Astragalus bisulcatus]

Seq. No.	162528
Seq. ID	LIB3177-045-P1-K2-F4
Method	BLASTX
NCBI GI	g4741952
BLAST score	229
E value	2.0e-19
Match length	46
% identity	100
NCBI Description	(AF134126) Lhcb3 protein [Arabidopsis thaliana]

Seq. No.	162529
Seq. ID	LIB3177-045-P1-K2-F5
Method	BLASTX
NCBI GI	g2253010
BLAST score	246
E value	2.0e-21
Match length	76
% identity	61
NCBI Description	(Y14199) MAP3K delta-1 protein kinase [Arabidopsis thaliana]

Seq. No.	162530
Seq. ID	LIB3177-045-P1-K2-F6
Method	BLASTN
NCBI GI	g1465365
BLAST score	103
E value	3.0e-51
Match length	115
% identity	98
NCBI Description	A.thaliana mRNA for subunit T of photosystem II

Seq. No.	162531
Seq. ID	LIB3177-045-P1-K2-F7
Method	BLASTN
NCBI GI	g4262276
BLAST score	171

E value	2.0e-91
Match length	233
% identity	91
NCBI Description	Arabidopsis thaliana gamma-glutamylcysteine synthetase gene, complete cds

Seq. No.	162532
Seq. ID	LIB3177-045-P1-K2-G1
Method	BLASTN
NCBI GI	g3451055
BLAST score	207
E value	1.0e-112
Match length	442
% identity	98
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F16G20 (ESSAII project)

Seq. No.	162533
Seq. ID	LIB3177-045-P1-K2-G10
Method	BLASTN
NCBI GI	g3421086
BLAST score	70
E value	2.0e-31
Match length	91
% identity	93
NCBI Description	Arabidopsis thaliana 20S proteasome subunit PAE1 (PAE1) mRNA, complete cds

Seq. No.	162534
Seq. ID	LIB3177-045-P1-K2-G2
Method	BLASTX
NCBI GI	g4455329
BLAST score	670
E value	1.0e-70
Match length	133
% identity	97
NCBI Description	(AL035525) lysine-ketoglutarate reductase/saccharopine [Arabidopsis thaliana]

Seq. No.	162535
Seq. ID	LIB3177-045-P1-K2-G3
Method	BLASTX
NCBI GI	g4759274
BLAST score	172
E value	2.0e-12
Match length	106
% identity	40
NCBI Description	thioredoxin-like, 32kD >gi_2897942 (AF003938) thioredoxin-like protein [Homo sapiens] >gi_2961254 (AF051896) thioredoxin homolog [Homo sapiens] >gi_2970689 (AF052659) thioredoxin-related protein [Homo sapiens]

Seq. No.	162536
Seq. ID	LIB3177-045-P1-K2-G5
Method	BLASTX
NCBI GI	g120662
BLAST score	180

E value	9.0e-14
Match length	37
% identity	95
NCBI Description	GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE B PRECURSOR, CHLOROPLAST >gi_81621_pir__JQ1286 glyceraldehyde-3-phosphate dehydrogenase (NADP+) (phosphorylating) (EC 1.2.1.13) B precursor, chloroplast - Arabidopsis thaliana >gi_336390 (M64115) glyceraldehyde 3-phosphate dehydrogenase B subunit [Arabidopsis thaliana]

Seq. No.	162537
Seq. ID	LIB3177-045-P1-K2-G6
Method	BLASTN
NCBI GI	g2832667
BLAST score	33
E value	2.0e-09
Match length	111
% identity	92
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone T10I14 (ESSAII project)

Seq. No.	162538
Seq. ID	LIB3177-045-P1-K2-G7
Method	BLASTX
NCBI GI	g3885511
BLAST score	425
E value	6.0e-42
Match length	106
% identity	80
NCBI Description	(AF084200) similar to PSI-K subunit of photosystem I from barley [Medicago sativa]

Seq. No.	162539
Seq. ID	LIB3177-045-P1-K2-G8
Method	BLASTX
NCBI GI	g3264757
BLAST score	341
E value	3.0e-32
Match length	100
% identity	69
NCBI Description	(AF071888) zeaxanthin epoxidase [Prunus armeniaca]

Seq. No.	162540
Seq. ID	LIB3177-045-P1-K2-G9
Method	BLASTX
NCBI GI	g124224
BLAST score	435
E value	4.0e-43
Match length	102
% identity	81
NCBI Description	INITIATION FACTOR 5A-1 (EIF-5A) (EIF-4D) >gi_100345_pir__S21060 translation initiation factor eIF-5A - common tobacco >gi_19887_emb_CAA45105_ (X63543) eukaryotic initiatin factor 5A (3) [Nicotiana tabacum]

Seq. No.	162541
Seq. ID	LIB3177-045-P1-K2-H1

Method	BLASTN
NCBI GI	g3608126
BLAST score	212
E value	1.0e-116
Match length	342
% identity	97
NCBI Description	Arabidopsis thaliana chromosome II BAC T32F12 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	162542
Seq. ID	LIB3177-045-P1-K2-H12
Method	BLASTN
NCBI GI	g4539378
BLAST score	128
E value	5.0e-66
Match length	156
% identity	96
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F28A21 (ESSA project)

Seq. No.	162543
Seq. ID	LIB3177-045-P1-K2-H3
Method	BLASTX
NCBI GI	g4580394
BLAST score	395
E value	2.0e-38
Match length	142
% identity	52
NCBI Description	(AC007171) putative fatty acid elongase [Arabidopsis thaliana]

Seq. No.	162544
Seq. ID	LIB3177-045-P1-K2-H4
Method	BLASTX
NCBI GI	g1841462
BLAST score	58
E value	8.0e-17
Match length	56
% identity	82
NCBI Description	(Y10991) Elongation factor 2 [Nicotiana tabacum]

Seq. No.	162545
Seq. ID	LIB3177-045-P1-K2-H5
Method	BLASTX
NCBI GI	g131398
BLAST score	240
E value	8.0e-21
Match length	53
% identity	94
NCBI Description	PHOTOSYSTEM II 10 KD POLYPEPTIDE PRECURSOR >gi_72714_pir__F2MU10 photosystem II 10K protein precursor - Arabidopsis thaliana >gi_16447_emb_CAA39441_ (X55970) photosystem II 10 kDa polypeptide [Arabidopsis thaliana] >gi_3152571 (AC002986) Match to photosystem II 10kDa polypeptide gb_X55970. ESTs gb_Z17693, gb_N37616, gb_T41858, gb_T88021, gb_R37531, gb_T04679, gb_N37520, gb_N64965, gb_Z17592 and gb_N65338, gb_N37466 and gb_T45400

come from this gene. [Arabidopsis

Seq. No.	162546
Seq. ID	LIB3177-045-P1-K2-H7
Method	BLASTX
NCBI GI	g115385
BLAST score	519
E value	6.0e-53
Match length	100
% identity	100
NCBI Description	CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR (CAB-4) (LHCP) >gi_166646 (M63931) light-harvesting chlorophyll a/b binding protein [Arabidopsis thaliana]

Seq. No.	162547
Seq. ID	LIB3177-045-P1-K2-H8
Method	BLASTN
NCBI GI	g531828
BLAST score	36
E value	9.0e-11
Match length	80
% identity	86
NCBI Description	Cloning vector pSport1, complete cds

Seq. No.	162548
Seq. ID	LIB3177-045-P1-K2-H9
Method	BLASTN
NCBI GI	g469113
BLAST score	281
E value	1.0e-157
Match length	349
% identity	95
NCBI Description	A.thaliana (Columbia) Dr4 mRNA

Seq. No.	162549
Seq. ID	LIB3177-046-P1-K2-A1
Method	BLASTX
NCBI GI	g2160158
BLAST score	443
E value	5.0e-44
Match length	137
% identity	66
NCBI Description	(AC000132) Similar to elongation factor 1-gamma (gb_EF1G_XENLA). ESTs gb_T20564,gb_T45940,gb_T04527 come from this gene. [Arabidopsis thaliana]

Seq. No.	162550
Seq. ID	LIB3177-046-P1-K2-A10
Method	BLASTX
NCBI GI	g2829899
BLAST score	315
E value	5.0e-29
Match length	119
% identity	61
NCBI Description	(AC002311) similar to ripening-induced protein, gp_AJ001449_2465015 and major#latex protein, gp_X91961_1107495 [Arabidopsis thaliana]

Seq. No.	162551
Seq. ID	LIB3177-046-P1-K2-A12
Method	BLASTN
NCBI GI	g4468801
BLAST score	339
E value	0.0e+00
Match length	387
% identity	98
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F6G17 (ESSA project)

Seq. No.	162552
Seq. ID	LIB3177-046-P1-K2-A3
Method	BLASTN
NCBI GI	g4757393
BLAST score	151
E value	1.0e-79
Match length	198
% identity	98
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K16E14, complete sequence

Seq. No.	162553
Seq. ID	LIB3177-046-P1-K2-A4
Method	BLASTX
NCBI GI	g459009
BLAST score	387
E value	2.0e-37
Match length	109
% identity	62
NCBI Description	(U00037) similar to multifunctional aminoacyl-tRNA synthetase, especially to the prolyl-tRNA synthetase region [Caenorhabditis elegans]

Seq. No.	162554
Seq. ID	LIB3177-046-P1-K2-A5
Method	BLASTX
NCBI GI	g3785990
BLAST score	391
E value	7.0e-38
Match length	126
% identity	70
NCBI Description	(AC005560) hypothetical protein [Arabidopsis thaliana] >gi_4220487 (AC006069) hypothetical protein [Arabidopsis thaliana]

Seq. No.	162555
Seq. ID	LIB3177-046-P1-K2-A6
Method	BLASTX
NCBI GI	g2119848
BLAST score	671
E value	1.0e-70
Match length	126
% identity	98
NCBI Description	chlorophyll a/b-binding protein type I precursor Lhb1B1 - Arabidopsis thaliana >gi_16366_emb_CAA45789_ (X64459)

photosystem II type I chlorophyll a /b binding protein [Arabidopsis thaliana] >gi_3128229 (AC004077) putative photosystem II type I chlorophyll a/b binding protein [Arabidopsis thaliana] >gi_3337372 (AC004481) putative photosystem II type I chlorophyll a/b binding protein [Arabidopsis thaliana]

Seq. No.	162556
Seq. ID	LIB3177-046-P1-K2-A7
Method	BLASTX
NCBI GI	g4468807
BLAST score	48
E value	4.0e-80
Match length	154
% identity	100
NCBI Description	(AL035601) cytochrome P450 monooxygenase-like protein [Arabidopsis thaliana]

Seq. No.	162557
Seq. ID	LIB3177-046-P1-K2-A9
Method	BLASTN
NCBI GI	g3399678
BLAST score	201
E value	1.0e-109
Match length	472
% identity	96
NCBI Description	Arabidopsis thaliana chromosome 1 BAC F13M7 sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	162558
Seq. ID	LIB3177-046-P1-K2-B1
Method	BLASTX
NCBI GI	g1363489
BLAST score	157
E value	4.0e-11
Match length	32
% identity	94
NCBI Description	thioglucosidase (EC 3.2.3.1) 3D precursor - Arabidopsis thaliana >gi_984052_emb_CAA61592_ (X89413) thioglucoside glucohydrolase [Arabidopsis thaliana]

Seq. No.	162559
Seq. ID	LIB3177-046-P1-K2-B10
Method	BLASTX
NCBI GI	g115530
BLAST score	89
E value	1.7e-02
Match length	132
% identity	23
NCBI Description	CALMODULIN >gi_71679_pir__MCUTG calmodulin - Trypanosoma brucei gambiense >gi_539401_pir__A48111 calmodulin C - Trypanosoma brucei >gi_10386_emb_CAA39861_ (X56511) calmodulin [Trypanosoma brucei]

Seq. No.	162560
Seq. ID	LIB3177-046-P1-K2-B12
Method	BLASTX

NCBI GI	g4646203
BLAST score	354
E value	2.0e-33
Match length	151
% identity	48
NCBI Description	(AC007230) Belongs to PF_00026 Eukaryotic aspartyl protease family. [Arabidopsis thaliana]

Seq. No.	162561
Seq. ID	LIB3177-046-P1-K2-B2
Method	BLASTX
NCBI GI	g1922937
BLAST score	700
E value	4.0e-74
Match length	137
% identity	100
NCBI Description	(AC000106) Similar to Glycine SRC2 (gb_AB000130). ESTs gb_H76869,gb_T21700,gb_ATTS5089 come from this gene. [Arabidopsis thaliana]

Seq. No.	162562
Seq. ID	LIB3177-046-P1-K2-B3
Method	BLASTX
NCBI GI	g3402676
BLAST score	741
E value	7.0e-79
Match length	144
% identity	34
NCBI Description	(AC004697) putative myrosinase-binding protein [Arabidopsis thaliana]

Seq. No.	162563
Seq. ID	LIB3177-046-P1-K2-B4
Method	BLASTN
NCBI GI	g4455229
BLAST score	192
E value	1.0e-104
Match length	453
% identity	100
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F13M23 (ESSAII project)

Seq. No.	162564
Seq. ID	LIB3177-046-P1-K2-B8
Method	BLASTN
NCBI GI	g2062153
BLAST score	29
E value	8.0e-07
Match length	148
% identity	71
NCBI Description	Arabidopsis thaliana chromosome III BAC T02004 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	162565
Seq. ID	LIB3177-046-P1-K2-B9
Method	BLASTX
NCBI GI	g1009234

BLAST score	458
E value	8.0e-46
Match length	117
% identity	79
NCBI Description	(L38829) SUP2 gene product [Nicotiana tabacum]

Seq. No.	162566
Seq. ID	LIB3177-046-P1-K2-C1
Method	BLASTX
NCBI GI	g2306917
BLAST score	151
E value	2.0e-10
Match length	38
% identity	68
NCBI Description	(AF003728) plasma membrane intrinsic protein [Arabidopsis thaliana]

Seq. No.	162567
Seq. ID	LIB3177-046-P1-K2-C10
Method	BLASTX
NCBI GI	g1350680
BLAST score	451
E value	5.0e-45
Match length	120
% identity	77
NCBI Description	60S RIBOSOMAL PROTEIN L1

Seq. No.	162568
Seq. ID	LIB3177-046-P1-K2-C11
Method	BLASTX
NCBI GI	g115767
BLAST score	416
E value	7.0e-41
Match length	79
% identity	100
NCBI Description	CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR (CAB-165/180) (LHCP) >gi_81603_pir__A29280 chlorophyll a/b-binding protein ab165 - Arabidopsis thaliana >gi_16368_emb_CAA27540_ (X03907) chlorophyll a/b binding protein (LHCP AB 65) [Arabidopsis thaliana] >gi_16372_emb_CAA27541_ (X03908) chlorophyll a/b binding protein (LHCP AB 180) [Arabidopsis thaliana]

Seq. No.	162569
Seq. ID	LIB3177-046-P1-K2-C12
Method	BLASTN
NCBI GI	g2462264
BLAST score	33
E value	6.0e-09
Match length	45
% identity	93
NCBI Description	Cucumis sativus mRNA for patatin-like protein, partial

Seq. No.	162570
Seq. ID	LIB3177-046-P1-K2-C2
Method	BLASTN
NCBI GI	g4406805

BLAST score	353
E value	0.0e+00
Match length	464
% identity	100
NCBI Description	Arabidopsis thaliana chromosome II BAC T27K22 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	162571
Seq. ID	LIB3177-046-P1-K2-C3
Method	BLASTX
NCBI GI	g2271477
BLAST score	640
E value	4.0e-67
Match length	144
% identity	88
NCBI Description	(AF009631) AP47/50p [Arabidopsis thaliana]

Seq. No.	162572
Seq. ID	LIB3177-046-P1-K2-C4
Method	BLASTX
NCBI GI	g132074
BLAST score	174
E value	3.0e-75
Match length	137
% identity	98
NCBI Description	RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN 1A PRECURSOR (RUBISCO SMALL SUBUNIT 1A) >gi_68063_pir__RKMUA1 ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain A1 precursor - Arabidopsis thaliana

Seq. No.	162573
Seq. ID	LIB3177-046-P1-K2-C5
Method	BLASTX
NCBI GI	g131398
BLAST score	274
E value	3.0e-24
Match length	137
% identity	67
NCBI Description	PHOTOSYSTEM II 10 KD POLYPEPTIDE PRECURSOR >gi_72714_pir__F2MU10 photosystem II 10K protein precursor - Arabidopsis thaliana >gi_16447_emb_CAA39441_ (X55970) photosystem II 10 kDa polypeptide [Arabidopsis thaliana] >gi_3152571 (AC002986) Match to photosystem II 10kDa polypeptide gb_X55970. ESTs gb_Z17693, gb_N37616, gb_T41858, gb_T88021, gb_R37531, gb_T04679, gb_N37520, gb_N64965, gb_Z17592 and gb_N65338, gb_N37466 and gb_T45400 come from this gene. [Arabidopsis

Seq. No.	162574
Seq. ID	LIB3177-046-P1-K2-C6
Method	BLASTX
NCBI GI	g132110
BLAST score	425
E value	6.0e-42
Match length	100
% identity	84
NCBI Description	RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN 3B PRECURSOR

	(RUBISCO SMALL SUBUNIT 3B) >gi_68060_pir__RKMUB3 ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain B3 precursor - Arabidopsis thaliana >gi_16195_emb_CAA32702_ (X14564) ribulose bisphosphate carboxylase [Arabidopsis thaliana]
Seq. No.	162575
Seq. ID	LIB3177-046-P1-K2-C8
Method	BLASTX
NCBI GI	g4006858
BLAST score	728
E value	2.0e-77
Match length	155
% identity	90
NCBI Description	(Z99707) cold acclimation protein homolog [Arabidopsis thaliana]
Seq. No.	162576
Seq. ID	LIB3177-046-P1-K2-C9
Method	BLASTX
NCBI GI	g2244736
BLAST score	149
E value	1.0e-09
Match length	54
% identity	56
NCBI Description	(D88415) expansin [Gossypium hirsutum]
Seq. No.	162577
Seq. ID	LIB3177-046-P1-K2-D1
Method	BLASTN
NCBI GI	g4159709
BLAST score	330
E value	0.0e+00
Match length	434
% identity	98
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MLN21, complete sequence
Seq. No.	162578
Seq. ID	LIB3177-046-P1-K2-D10
Method	BLASTX
NCBI GI	g1175010
BLAST score	634
E value	2.0e-66
Match length	135
% identity	92
NCBI Description	PLASMA MEMBRANE INTRINSIC PROTEIN 1A >gi_629540_pir__S44082 plasma membrane intrinsic protein 1a - Arabidopsis thaliana >gi_472873_emb_CAA53475_ (X75881) plasma membrane intrinsic protein 1a [Arabidopsis thaliana]
Seq. No.	162579
Seq. ID	LIB3177-046-P1-K2-D12
Method	BLASTX
NCBI GI	g2642445
BLAST score	352
E value	3.0e-33

Match length	152
% identity	97
NCBI Description	(AC002391) putative serine/threonine protein kinase [Arabidopsis thaliana]

Seq. No.	162580
Seq. ID	LIB3177-046-P1-K2-D2
Method	BLASTX
NCBI GI	g3885331
BLAST score	458
E value	7.0e-46
Match length	122
% identity	74
NCBI Description	(AC005623) putative cytochrome p450 protein [Arabidopsis thaliana]

Seq. No.	162581
Seq. ID	LIB3177-046-P1-K2-D3
Method	BLASTX
NCBI GI	g3914425
BLAST score	598
E value	6.0e-65
Match length	129
% identity	100
NCBI Description	PROTEASOME EPSILON CHAIN PRECURSOR (MACROPAIN EPSILON CHAIN) (MULTICATALYTIC ENDOPEPTIDASE COMPLEX EPSILON CHAIN) >gi_2511596_emb_CAA74029.1_ (Y13695) multicatalytic endopeptidase complex, proteasome precursor, beta subunit [Arabidopsis thaliana] >gi_3421117 (AF043536) 20S proteasome beta subunit PBE1 [Arabidopsis thaliana]

Seq. No.	162582
Seq. ID	LIB3177-046-P1-K2-D4
Method	BLASTN
NCBI GI	g2623294
BLAST score	327
E value	0.0e+00
Match length	327
% identity	100
NCBI Description	Arabidopsis thaliana chromosome II BAC T20B5 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	162583
Seq. ID	LIB3177-046-P1-K2-D6
Method	BLASTN
NCBI GI	g4741184
BLAST score	124
E value	3.0e-63
Match length	362
% identity	89
NCBI Description	Arabidopsis thaliana DNA chromosome 3, BAC clone T23J7 (ESSA project)

Seq. No.	162584
Seq. ID	LIB3177-046-P1-K2-D7
Method	BLASTX
NCBI GI	g132110

BLAST score	675
E value	3.0e-71
Match length	126
% identity	98
NCBI Description	RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN 3B PRECURSOR (RUBISCO SMALL SUBUNIT 3B) >gi_68060_pir__RKMUB3 ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain B3 precursor - Arabidopsis thaliana >gi_16195_emb_CAA32702_ (X14564) ribulose bisphosphate carboxylase [Arabidopsis thaliana]

Seq. No.	162585
Seq. ID	LIB3177-046-P1-K2-D8
Method	BLASTX
NCBI GI	g2760832
BLAST score	406
E value	1.0e-39
Match length	129
% identity	64
NCBI Description	(AC003105) similar to barley ids-4 gene product [Arabidopsis thaliana]

Seq. No.	162586
Seq. ID	LIB3177-046-P1-K2-D9
Method	BLASTX
NCBI GI	g4741952
BLAST score	585
E value	1.0e-60
Match length	115
% identity	69
NCBI Description	(AF134126) Lhcb3 protein [Arabidopsis thaliana]

Seq. No.	162587
Seq. ID	LIB3177-046-P1-K2-E11
Method	BLASTX
NCBI GI	g2894445
BLAST score	789
E value	2.0e-84
Match length	151
% identity	100
NCBI Description	(Y14333) transketolase [Arabidopsis thaliana]

Seq. No.	162588
Seq. ID	LIB3177-046-P1-K2-E12
Method	BLASTN
NCBI GI	g4757401
BLAST score	48
E value	5.0e-18
Match length	68
% identity	93
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MGH6, complete sequence

Seq. No.	162589
Seq. ID	LIB3177-046-P1-K2-E3
Method	BLASTN
NCBI GI	g4662640

BLAST score	409
E value	0.0e+00
Match length	436
% identity	99
NCBI Description	Arabidopsis thaliana chromosome II BAC F15K19 genomic sequence, complete sequence

Seq. No.	162590
Seq. ID	LIB3177-046-P1-K2-E4
Method	BLASTN
NCBI GI	g3449331
BLAST score	258
E value	1.0e-143
Match length	258
% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MNC17, complete sequence [Arabidopsis thaliana]

Seq. No.	162591
Seq. ID	LIB3177-046-P1-K2-E5
Method	BLASTN
NCBI GI	g2351063
BLAST score	159
E value	2.0e-84
Match length	179
% identity	97
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MCL19, complete sequence [Arabidopsis thaliana]

Seq. No.	162592
Seq. ID	LIB3177-046-P1-K2-E6
Method	BLASTN
NCBI GI	g2924651
BLAST score	140
E value	5.0e-73
Match length	239
% identity	90
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K2A18, complete sequence [Arabidopsis thaliana]

Seq. No.	162593
Seq. ID	LIB3177-046-P1-K2-E9
Method	BLASTX
NCBI GI	g3128168
BLAST score	240
E value	4.0e-20
Match length	79
% identity	61
NCBI Description	(AC004521) putative carboxyl-terminal peptidase [Arabidopsis thaliana]

Seq. No.	162594
Seq. ID	LIB3177-046-P1-K2-F1
Method	BLASTX
NCBI GI	g2506443
BLAST score	633
E value	3.0e-66

Match length	155
% identity	82
NCBI Description	GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE A PRECURSOR, CHLOROPLAST >gi_2117520_pir__JQ1285 glyceraldehyde-3-phosphate dehydrogenase (NADP+) (phosphorylating) (EC 1.2.1.13) A precursor, chloroplast - Arabidopsis thaliana >gi_166704 (M64117) glyceraldehyde 3-phosphate dehydrogenase [Arabidopsis thaliana] >gi_1402885_emb_CAA66816_ (X98130) glyceraldehyde-3-phosphate dehydrogenase (NADP+) (phosphorylating) [Arabidopsis thaliana]
Seq. No.	162595
Seq. ID	LIB3177-046-P1-K2-F10
Method	BLASTX
NCBI GI	g2506276
BLAST score	618
E value	2.0e-64
Match length	144
% identity	89
NCBI Description	RUBISCO SUBUNIT BINDING-PROTEIN ALPHA SUBUNIT PRECURSOR (60 KD CHAPERONIN ALPHA SUBUNIT) (CPN-60 ALPHA) >gi_2129561_pir__S71235 chaperonin-60 alpha chain - Arabidopsis thaliana >gi_1223910 (U49357) chaperonin-60 alpha subunit [Arabidopsis thaliana] >gi_4510416_gb_AAD21502.1_ (AC006929) putative rubisco binding protein alpha subunit [Arabidopsis thaliana]
Seq. No.	162596
Seq. ID	LIB3177-046-P1-K2-F11
Method	BLASTX
NCBI GI	g4455206
BLAST score	287
E value	1.0e-25
Match length	58
% identity	88
NCBI Description	(AL035440) putative beta-1, 3-glucanase [Arabidopsis thaliana]
Seq. No.	162597
Seq. ID	LIB3177-046-P1-K2-F2
Method	BLASTN
NCBI GI	g2264320
BLAST score	100
E value	2.0e-49
Match length	116
% identity	36
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MXI10, complete sequence [Arabidopsis thaliana]
Seq. No.	162598
Seq. ID	LIB3177-046-P1-K2-F3
Method	BLASTN
NCBI GI	g2924651
BLAST score	329
E value	0.0e+00
Match length	365

% identity	98
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K2A18, complete sequence [Arabidopsis thaliana]

Seq. No.	162599
Seq. ID	LIB3177-046-P1-K2-F4
Method	BLASTX
NCBI GI	g4115377
BLAST score	395
E value	2.0e-38
Match length	121
% identity	73
NCBI Description	(AC005967) unknown protein [Arabidopsis thaliana]

Seq. No.	162600
Seq. ID	LIB3177-046-P1-K2-F5
Method	BLASTX
NCBI GI	g4115377
BLAST score	102
E value	4.0e-26
Match length	91
% identity	70
NCBI Description	(AC005967) unknown protein [Arabidopsis thaliana]

Seq. No.	162601
Seq. ID	LIB3177-046-P1-K2-F7
Method	BLASTX
NCBI GI	g1169278
BLAST score	305
E value	8.0e-28
Match length	75
% identity	84
NCBI Description	DEHYDRIN ERD14 >gi_556474_dbj_BAA04569_ (D17715) ERD14 protein [Arabidopsis thaliana]

Seq. No.	162602
Seq. ID	LIB3177-046-P1-K2-F9
Method	BLASTN
NCBI GI	g527636
BLAST score	71
E value	1.0e-31
Match length	75
% identity	99
NCBI Description	Arabidopsis thaliana clone HAT7 homeobox protein mRNA, complete cds

Seq. No.	162603
Seq. ID	LIB3177-046-P1-K2-G1
Method	BLASTX
NCBI GI	g115385
BLAST score	789
E value	2.0e-84
Match length	153
% identity	98
NCBI Description	CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR (CAB-4) (LHCP) >gi_166646 (M63931) light-harvesting chlorophyll a/b binding protein [Arabidopsis thaliana]

Seq. No.	162604
Seq. ID	LIB3177-046-P1-K2-G10
Method	BLASTN
NCBI GI	g3831448
BLAST score	123
E value	8.0e-63
Match length	267
% identity	94
NCBI Description	Arabidopsis thaliana chromosome II BAC T32F6 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	162605
Seq. ID	LIB3177-046-P1-K2-G11
Method	BLASTN
NCBI GI	g3869065
BLAST score	280
E value	1.0e-156
Match length	458
% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K24M7, complete sequence [Arabidopsis thaliana]

Seq. No.	162606
Seq. ID	LIB3177-046-P1-K2-G12
Method	BLASTX
NCBI GI	g282865
BLAST score	363
E value	8.0e-35
Match length	86
% identity	80
NCBI Description	chlorophyll a/b-binding protein - Arabidopsis thaliana >gi_16207_emb_CAA39534_ (X56062) chlorophyll A/B-binding protein [Arabidopsis thaliana] >gi_166644 (M85150) chlorophyll a/b-binding protein [Arabidopsis thaliana] >gi_4678304_emb_CAB41095.1_ (AL049655) chlorophyll a/b-binding protein [Arabidopsis thaliana]

Seq. No.	162607
Seq. ID	LIB3177-046-P1-K2-G2
Method	BLASTX
NCBI GI	g4056502
BLAST score	492
E value	1.0e-49
Match length	103
% identity	98
NCBI Description	(AC005896) 40S ribosomal protein S5 [Arabidopsis thaliana]

Seq. No.	162608
Seq. ID	LIB3177-046-P1-K2-G3
Method	BLASTX
NCBI GI	g544242
BLAST score	524
E value	2.0e-53
Match length	109
% identity	86
NCBI Description	ENDOPLASMIN HOMOLOG PRECURSOR (GRP94 HOMOLOG)

	>gi_485498_pir__S33533 heat shock protein 90 homolog precursor - barley >gi_22652_emb_CAA48143_ (X67960) GRP94 homologue [Hordeum vulgare]
Seq. No.	162609
Seq. ID	LIB3177-046-P1-K2-G4
Method	BLASTX
NCBI GI	g464987
BLAST score	577
E value	1.0e-59
Match length	117
% identity	98
NCBI Description	UBIQUITIN-CONJUGATING ENZYME E2-17 KD 10 (UBIQUITIN-PROTEIN LIGASE 10) (UBIQUITIN CARRIER PROTEIN 10) >gi_421858_pir__S32672 ubiquitin--protein ligase (EC 6.3.2.19) UBC10 - Arabidopsis thaliana >gi_297878_emb_CAA78715_ (Z14991) ubiquitin conjugating enzyme [Arabidopsis thaliana] >gi_349213 (L00640) ubiquitin conjugating enzyme [Arabidopsis thaliana]
Seq. No.	162610
Seq. ID	LIB3177-046-P1-K2-G7
Method	BLASTX
NCBI GI	g2982454
BLAST score	685
E value	2.0e-72
Match length	145
% identity	96
NCBI Description	(AL022223) fructose-bisphosphate aldolase [Arabidopsis thaliana]
Seq. No.	162611
Seq. ID	LIB3177-046-P1-K2-G8
Method	BLASTX
NCBI GI	g3914442
BLAST score	489
E value	2.0e-49
Match length	119
% identity	82
NCBI Description	PHOTOSYSTEM I REACTION CENTRE SUBUNIT VI PRECURSOR (LIGHT-HARVESTING COMPLEX I 11 KD PROTEIN) (PSI-H) >gi_1916350 (U92504) PSI-H subunit [Brassica rapa]
Seq. No.	162612
Seq. ID	LIB3177-046-P1-K2-G9
Method	BLASTN
NCBI GI	g2618602
BLAST score	72
E value	2.0e-32
Match length	189
% identity	92
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MSJ1, complete sequence [Arabidopsis thaliana]
Seq. No.	162613
Seq. ID	LIB3177-046-P1-K2-H1
Method	BLASTX

NCBI GI	g166708
BLAST score	357
E value	1.0e-34
Match length	67
% identity	100
NCBI Description	(M64118) glyceraldehyde-3-phosphate dehydrogenase [Arabidopsis thaliana]

Seq. No.	162614
Seq. ID	LIB3177-046-P1-K2-H10
Method	BLASTX
NCBI GI	g132110
BLAST score	644
E value	1.0e-67
Match length	120
% identity	97
NCBI Description	RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN 3B PRECURSOR (RUBISCO SMALL SUBUNIT 3B) >gi_68060_pir__RKMUB3 ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain B3 precursor - Arabidopsis thaliana >gi_16195_emb_CAA32702_ (X14564) ribulose bisphosphate carboxylase [Arabidopsis thaliana]

Seq. No.	162615
Seq. ID	LIB3177-046-P1-K2-H11
Method	BLASTN
NCBI GI	g4587641
BLAST score	253
E value	1.0e-140
Match length	364
% identity	98
NCBI Description	Arabidopsis thaliana chromosome I BAC F20D21 genomic sequence, complete sequence

Seq. No.	162616
Seq. ID	LIB3177-046-P1-K2-H12
Method	BLASTX
NCBI GI	g1173221
BLAST score	50
E value	2.0e-31
Match length	93
% identity	80
NCBI Description	40S RIBOSOMAL PROTEIN S11-BETA >gi_166869 (L07877) ribosomal protein S11 [Arabidopsis thaliana]

Seq. No.	162617
Seq. ID	LIB3177-046-P1-K2-H2
Method	BLASTX
NCBI GI	g4490329
BLAST score	435
E value	5.0e-43
Match length	143
% identity	62
NCBI Description	(AL035656) extensin-like protein [Arabidopsis thaliana]

Seq. No.	162618
Seq. ID	LIB3177-046-P1-K2-H3

Method	BLASTX
NCBI GI	g2062164
BLAST score	717
E value	4.0e-76
Match length	138
% identity	99
NCBI Description	(AC001645) jasmonate inducible protein isolog [Arabidopsis thaliana]

Seq. No.	162619
Seq. ID	LIB3177-046-P1-K2-H4
Method	BLASTX
NCBI GI	g166708
BLAST score	728
E value	2.0e-77
Match length	144
% identity	99
NCBI Description	(M64118) glyceraldehyde-3-phosphate dehydrogenase [Arabidopsis thaliana]

Seq. No.	162620
Seq. ID	LIB3177-046-P1-K2-H6
Method	BLASTN
NCBI GI	g4587641
BLAST score	123
E value	7.0e-63
Match length	202
% identity	91
NCBI Description	Arabidopsis thaliana chromosome I BAC F20D21 genomic sequence, complete sequence

Seq. No.	162621
Seq. ID	LIB3177-046-P1-K2-H7
Method	BLASTN
NCBI GI	g3510343
BLAST score	212
E value	1.0e-116
Match length	278
% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MJC20, complete sequence [Arabidopsis thaliana]

Seq. No.	162622
Seq. ID	LIB3177-046-P1-K2-H8
Method	BLASTX
NCBI GI	g541858
BLAST score	767
E value	6.0e-82
Match length	146
% identity	99
NCBI Description	endoxyloglucan transferase - Arabidopsis thaliana >gi_469484_dbj_BAA03921_ (D16454) endo-xyloglucan transferase [Arabidopsis thaliana] >gi_4063757 (AC005561) endo-xyloglucan transferase [Arabidopsis thaliana]

Seq. No.	162623
Seq. ID	LIB3177-046-P1-K2-H9

Method	BLASTX
NCBI GI	g1173218
BLAST score	302
E value	1.0e-27
Match length	84
% identity	77
NCBI Description	40S RIBOSOMAL PROTEIN S15A >gi_440824 (L27461) ribosomal protein S15 [Arabidopsis thaliana] >gi_2150130 (AF001412) cytoplasmic ribosomal protein S15a [Arabidopsis thaliana]

Seq. No.	162624
Seq. ID	LIB3177-047-P1-K1-A1
Method	BLASTX
NCBI GI	g2781354
BLAST score	207
E value	2.0e-16
Match length	109
% identity	45
NCBI Description	(AC003113) F24O1.10 [Arabidopsis thaliana]

Seq. No.	162625
Seq. ID	LIB3177-047-P1-K1-A11
Method	BLASTX
NCBI GI	g4539292
BLAST score	287
E value	1.0e-25
Match length	109
% identity	56
NCBI Description	(AL049480) putative ribosomal protein S10 [Arabidopsis thaliana]

Seq. No.	162626
Seq. ID	LIB3177-047-P1-K1-A2
Method	BLASTN
NCBI GI	g2459406
BLAST score	58
E value	7.0e-24
Match length	300
% identity	86
NCBI Description	Arabidopsis thaliana chromosome II BAC F4P9 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	162627
Seq. ID	LIB3177-047-P1-K1-A3
Method	BLASTX
NCBI GI	g4741948
BLAST score	204
E value	4.0e-16
Match length	74
% identity	58
NCBI Description	(AF134124) Lhcb2 protein [Arabidopsis thaliana]

Seq. No.	162628
Seq. ID	LIB3177-047-P1-K1-A6
Method	BLASTX
NCBI GI	g4741960
BLAST score	327

E value	2.0e-30
Match length	94
% identity	72
NCBI Description	(AF134130) Lhcb6 protein [Arabidopsis thaliana]

Seq. No.	162629
Seq. ID	LIB3177-047-P1-K1-A7
Method	BLASTX
NCBI GI	g2055273
BLAST score	180
E value	4.0e-13
Match length	57
% identity	68
NCBI Description	(D85339) hydroxypyruvate reductase [Arabidopsis thaliana]

Seq. No.	162630
Seq. ID	LIB3177-047-P1-K1-A9
Method	BLASTX
NCBI GI	g4580394
BLAST score	209
E value	2.0e-16
Match length	141
% identity	34
NCBI Description	(AC007171) putative fatty acid elongase [Arabidopsis thaliana]

Seq. No.	162631
Seq. ID	LIB3177-047-P1-K1-B10
Method	BLASTX
NCBI GI	g3915847
BLAST score	223
E value	2.0e-18
Match length	101
% identity	51
NCBI Description	40S RIBOSOMAL PROTEIN S2 >gi_2335095 (AC002339) putative 40S ribosomal protein S2 [Arabidopsis thaliana]

Seq. No.	162632
Seq. ID	LIB3177-047-P1-K1-B11
Method	BLASTN
NCBI GI	g4249393
BLAST score	71
E value	1.0e-31
Match length	360
% identity	82
NCBI Description	Arabidopsis thaliana chromosome II BAC T9J23 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	162633
Seq. ID	LIB3177-047-P1-K1-B12
Method	BLASTX
NCBI GI	g2464852
BLAST score	308
E value	4.0e-28
Match length	121
% identity	55
NCBI Description	(Z99707) putative protein [Arabidopsis thaliana]

Seq. No.	162634
Seq. ID	LIB3177-047-P1-K1-B7
Method	BLASTX
NCBI GI	g4455159
BLAST score	176
E value	1.0e-12
Match length	96
% identity	41
NCBI Description	(AL021687) putative protein [Arabidopsis thaliana]

Seq. No.	162635
Seq. ID	LIB3177-047-P1-K1-B9
Method	BLASTX
NCBI GI	g1652678
BLAST score	149
E value	9.0e-10
Match length	89
% identity	36
NCBI Description	(D90907) amidase [Synechocystis sp.]

Seq. No.	162636
Seq. ID	LIB3177-047-P1-K1-C10
Method	BLASTN
NCBI GI	g3309085
BLAST score	84
E value	2.0e-39
Match length	252
% identity	85
NCBI Description	Arabidopsis thaliana calcineurin B-like protein 3 (CBL3) mRNA, complete cds

Seq. No.	162637
Seq. ID	LIB3177-047-P1-K1-C11
Method	BLASTX
NCBI GI	g2129562
BLAST score	369
E value	2.0e-35
Match length	102
% identity	70
NCBI Description	class III ADH, glutathione-dependent formaldehyde dehydrogenase. - Arabidopsis thaliana >gi_1143388_emb_CAA57973_ (X82647) class III ADH, glutathione-dependent formaldehyde dehydrogenase. [Arabidopsis thaliana]

Seq. No.	162638
Seq. ID	LIB3177-047-P1-K1-C6
Method	BLASTX
NCBI GI	g2956690
BLAST score	343
E value	3.0e-32
Match length	127
% identity	47
NCBI Description	(AJ223306) PSBY [Arabidopsis thaliana] >gi_3414928 (AF079800) PsbY precursor [Arabidopsis thaliana]

Seq. No.	162639
Seq. ID	LIB3177-047-P1-K1-C7
Method	BLASTX
NCBI GI	g2317910
BLAST score	338
E value	1.0e-31
Match length	130
% identity	55
NCBI Description	(U89959) CER1 protein [Arabidopsis thaliana]

Seq. No.	162640
Seq. ID	LIB3177-047-P1-K1-C9
Method	BLASTX
NCBI GI	g2245098
BLAST score	239
E value	4.0e-20
Match length	114
% identity	46
NCBI Description	(Z97343) ribosomal protein [Arabidopsis thaliana]

Seq. No.	162641
Seq. ID	LIB3177-047-P1-K1-D12
Method	BLASTN
NCBI GI	g3450888
BLAST score	56
E value	1.0e-22
Match length	333
% identity	83
NCBI Description	Arabidopsis thaliana 19S proteosome subunit 9 mRNA, complete cds

Seq. No.	162642
Seq. ID	LIB3177-047-P1-K1-D5
Method	BLASTN
NCBI GI	g4467094
BLAST score	34
E value	2.0e-09
Match length	182
% identity	83
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F20D10 (ESSA project)

Seq. No.	162643
Seq. ID	LIB3177-047-P1-K1-E10
Method	BLASTX
NCBI GI	g3334404
BLAST score	437
E value	3.0e-43
Match length	145
% identity	63
NCBI Description	VACUOLAR ATP SYNTHASE CATALYTIC SUBUNIT A (V-ATPASE 69 KD SUBUNIT) >gi_2266990 (U65638) vacuolar type ATPase subunit A [Arabidopsis thaliana] >gi_3834305 (AC005679) Identical to gb_U65638 Arabidopsis thaliana vacuolar type ATPase subunit A mRNA. ESTs gb_N96435, gb_N96106, gb_N96189, gb_N96091, gb_AA042286, gb_F14324, gb_W43643, gb_N96027, gb_N96299, gb_R29943, gb_T43460, gb_T43544, gb_T22472

Seq. No.	162644
Seq. ID	LIB3177-047-P1-K1-E11
Method	BLASTX
NCBI GI	g1170660
BLAST score	231
E value	3.0e-19
Match length	109
% identity	46
NCBI Description	MEVALONATE KINASE (MK) >gi_541880_pir__S42088 mevalonate kinase (EC 2.7.1.36) - Arabidopsis thaliana >gi_456614_emb_CAA54820_ (X77793) mevalonate kinase [Arabidopsis thaliana]

Seq. No.	162645
Seq. ID	LIB3177-047-P1-K1-E12
Method	BLASTX
NCBI GI	g132074
BLAST score	345
E value	2.0e-32
Match length	129
% identity	57
NCBI Description	RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN 1A PRECURSOR (RUBISCO SMALL SUBUNIT 1A) >gi_68063_pir__RKMUA1 ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain A1 precursor - Arabidopsis thaliana

Seq. No.	162646
Seq. ID	LIB3177-047-P1-K1-F11
Method	BLASTX
NCBI GI	g2760832
BLAST score	214
E value	2.0e-17
Match length	79
% identity	57
NCBI Description	(AC003105) similar to barley ids-4 gene product [Arabidopsis thaliana]

Seq. No.	162647
Seq. ID	LIB3177-047-P1-K1-F12
Method	BLASTN
NCBI GI	g4757662
BLAST score	56
E value	1.0e-22
Match length	156
% identity	84
NCBI Description	Genomic sequence for Arabidopsis thaliana BAC F10B6 from chromosome I, complete sequence

Seq. No.	162648
Seq. ID	LIB3177-047-P1-K1-F9
Method	BLASTN
NCBI GI	g4741184
BLAST score	44
E value	2.0e-15
Match length	144
% identity	83

NCBI Description	Arabidopsis thaliana DNA chromosome 3, BAC clone T23J7 (ESSA project)

Seq. No.	162649
Seq. ID	LIB3177-047-P1-K1-G10
Method	BLASTX
NCBI GI	g4587542
BLAST score	211
E value	3.0e-17
Match length	81
% identity	54
NCBI Description	(AC006577) Belongs to the PF_00657 Lipase/Acylhydrolase with GDSL-motif family. ESTs gb_T45815, gb_T45130 and gb_Z38046 come from this gene. [Arabidopsis thaliana]

Seq. No.	162650
Seq. ID	LIB3177-047-P1-K1-G11
Method	BLASTX
NCBI GI	g3281858
BLAST score	355
E value	1.0e-33
Match length	134
% identity	54
NCBI Description	(AL031004) ribosomal protein S6 - like [Arabidopsis thaliana]

Seq. No.	162651
Seq. ID	LIB3177-047-P1-K1-G12
Method	BLASTN
NCBI GI	g4581138
BLAST score	107
E value	5.0e-53
Match length	325
% identity	88
NCBI Description	Arabidopsis thaliana chromosome II BAC F1011 genomic sequence, complete sequence

Seq. No.	162652
Seq. ID	LIB3177-047-P1-K1-G5
Method	BLASTX
NCBI GI	g1752734
BLAST score	154
E value	3.0e-10
Match length	101
% identity	41
NCBI Description	(D78510) beta-glucan-elicitor receptor [Glycine max]

Seq. No.	162653
Seq. ID	LIB3177-047-P1-K1-G7
Method	BLASTX
NCBI GI	g1480078
BLAST score	330
E value	7.0e-31
Match length	110
% identity	59
NCBI Description	(X99696) shaggy-like protein kinase iota [Arabidopsis thaliana] >gi_2444277_gb_AAB71545.1_ (AF019927)

GSK3/shaggy-like protein kinase [Arabidopsis thaliana]

Seq. No.	162654
Seq. ID	LIB3177-047-P1-K1-H12
Method	BLASTN
NCBI GI	g2245031
BLAST score	71
E value	8.0e-32
Match length	164
% identity	91
NCBI Description	Arabidopsis thaliana DNA chromosome 4, ESSA I contig fragment No

Seq. No.	162655
Seq. ID	LIB3177-048-P1-K1-A10
Method	BLASTX
NCBI GI	g2921094
BLAST score	183
E value	1.0e-13
Match length	94
% identity	54
NCBI Description	(AF018174) thioredoxin-f [Brassica napus]

Seq. No.	162656
Seq. ID	LIB3177-048-P1-K1-A11
Method	BLASTX
NCBI GI	g3834309
BLAST score	354
E value	1.0e-33
Match length	141
% identity	57
NCBI Description	(AC005679) Strong similarity to glycoprotein EP1 gb_L16983 Daucus carota and a member of S locus glycoprotein family PF_00954. ESTs gb_F13813, gb_T21052, gb_R30218 and gb_W43262 come from this gene. [Arabidopsis thaliana]

Seq. No.	162657
Seq. ID	LIB3177-048-P1-K1-A4
Method	BLASTN
NCBI GI	g4220510
BLAST score	53
E value	5.0e-21
Match length	148
% identity	92
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F22K18 (ESSAII project)

Seq. No.	162658
Seq. ID	LIB3177-048-P1-K1-A6
Method	BLASTX
NCBI GI	g322571
BLAST score	233
E value	8.0e-20
Match length	66
% identity	74
NCBI Description	proteinase inhibitor II - Arabidopsis thaliana >gi_16427_emb_CAA48892_ (X69139) protease inhibitor II

[Arabidopsis thaliana] >gi_4038041 (AC005936) proteinase inhibitor II [Arabidopsis thaliana]

Seq. No.	162659
Seq. ID	LIB3177-048-P1-K1-A7
Method	BLASTN
NCBI GI	g4538949
BLAST score	44
E value	7.0e-16
Match length	97
% identity	85
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F24G24 (ESSA project)

Seq. No.	162660
Seq. ID	LIB3177-048-P1-K1-A9
Method	BLASTX
NCBI GI	g1732570
BLAST score	317
E value	3.0e-29
Match length	105
% identity	61
NCBI Description	(U72153) beta-glucosidase [Arabidopsis thaliana]

Seq. No.	162661
Seq. ID	LIB3177-048-P1-K1-B12
Method	BLASTX
NCBI GI	g421826
BLAST score	198
E value	3.0e-15
Match length	115
% identity	42
NCBI Description	chlorophyll a/b-binding protein CP29 - Arabidopsis thaliana >gi_298036_emb_CAA50712_ (X71878) CP29 [Arabidopsis thaliana]

Seq. No.	162662
Seq. ID	LIB3177-048-P1-K1-C10
Method	BLASTX
NCBI GI	g4585935
BLAST score	380
E value	1.0e-36
Match length	125
% identity	62
NCBI Description	(AC007211) putative chlorophyll A/B binding protein [Arabidopsis thaliana] >gi_4741946_gb_AAD28770.1_AF134123_1 (AF134123) Lhcb2 protein [Arabidopsis thaliana]

Seq. No.	162663
Seq. ID	LIB3177-048-P1-K1-C12
Method	BLASTX
NCBI GI	g2618721
BLAST score	345
E value	2.0e-32
Match length	130
% identity	58
NCBI Description	(U49072) IAA16 [Arabidopsis thaliana]

Seq. No.	162664
Seq. ID	LIB3177-048-P1-K1-C9
Method	BLASTX
NCBI GI	g2262167
BLAST score	308
E value	2.0e-28
Match length	87
% identity	74
NCBI Description	(AC002329) cytosolic ribosomal protein S4 [Arabidopsis thaliana]

Seq. No.	162665
Seq. ID	LIB3177-048-P1-K1-D10
Method	BLASTX
NCBI GI	g132074
BLAST score	304
E value	8.0e-28
Match length	113
% identity	59
NCBI Description	RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN 1A PRECURSOR (RUBISCO SMALL SUBUNIT 1A) >gi_68063_pir__RKMUA1 ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain A1 precursor - Arabidopsis thaliana

Seq. No.	162666
Seq. ID	LIB3177-048-P1-K1-D11
Method	BLASTX
NCBI GI	g4406816
BLAST score	285
E value	1.0e-25
Match length	103
% identity	58
NCBI Description	(AC006201) 60S ribosomal protein L2 [Arabidopsis thaliana]

Seq. No.	162667
Seq. ID	LIB3177-048-P1-K1-E9
Method	BLASTX
NCBI GI	g1172873
BLAST score	191
E value	1.0e-14
Match length	82
% identity	49
NCBI Description	CYSTEINE PROTEINASE RD21A PRECURSOR >gi_541857_pir__JN0719 drought-inducible cysteine proteinase (EC 3.4.22.-) RD21A precursor - Arabidopsis thaliana >gi_435619_dbj_BAA02374_ (D13043) thiol protease [Arabidopsis thaliana]

Seq. No.	162668
Seq. ID	LIB3177-048-P1-K1-F11
Method	BLASTX
NCBI GI	g2129583
BLAST score	263
E value	6.0e-23
Match length	107
% identity	58
NCBI Description	ferritin - Arabidopsis thaliana >gi_1246401_emb_CAA63932_

(X94248) ferritin [Arabidopsis thaliana]

Seq. No.	162669
Seq. ID	LIB3177-048-P1-K1-F12
Method	BLASTX
NCBI GI	g1351272
BLAST score	286
E value	9.0e-26
Match length	102
% identity	60
NCBI Description	TRIOSEPHOSPHATE ISOMERASE, CYTOSOLIC (TIM) >gi_414550 (U02949) cytosolic triose phosphate isomerase [Arabidopsis thaliana] >gi_742408_prf__2009415A triose phosphate isomerase [Arabidopsis thaliana]

Seq. No.	162670
Seq. ID	LIB3177-048-P1-K1-G10
Method	BLASTX
NCBI GI	g4337175
BLAST score	286
E value	1.0e-25
Match length	106
% identity	56
NCBI Description	(AC006416) ESTs gb_T20589, gb_T04648, gb_AA597906, gb_T04111, gb_R84180, gb_R65428, gb_T44439, gb_T76570, gb_R90004, gb_T45020, gb_T42457, gb_T20921, gb_AA042762 and gb_AA720210 come from this gene. [Arabidopsis thaliana]

Seq. No.	162671
Seq. ID	LIB3177-048-P1-K1-G12
Method	BLASTX
NCBI GI	g132074
BLAST score	349
E value	6.0e-33
Match length	150
% identity	52
NCBI Description	RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN 1A PRECURSOR (RUBISCO SMALL SUBUNIT 1A) >gi_68063_pir__RKMUA1 ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain A1 precursor - Arabidopsis thaliana

Seq. No.	162672
Seq. ID	LIB3177-048-P1-K1-G8
Method	BLASTN
NCBI GI	g22564
BLAST score	60
E value	5.0e-25
Match length	212
% identity	82
NCBI Description	A.thaliana tufA gene for elongation factor Tu

Seq. No.	162673
Seq. ID	LIB3177-048-P1-K1-G9
Method	BLASTX
NCBI GI	g3941289
BLAST score	183
E value	2.0e-13

Match length	96
% identity	45
NCBI Description	(AF018093) similarity to SCAMP37 [Pisum_sativum]

Seq. No.	162674
Seq. ID	LIB3177-048-P1-K1-H10
Method	BLASTX
NCBI GI	g282865
BLAST score	428
E value	3.0e-42
Match length	147
% identity	56
NCBI Description	chlorophyll a/b-binding protein - Arabidopsis thaliana >gi_16207_emb_CAA39534_ (X56062) chlorophyll A/B-binding protein [Arabidopsis thaliana] >gi_166644 (M85150) chlorophyll a/b-binding protein [Arabidopsis thaliana] >gi_4678304_emb_CAB41095.1_ (AL049655) chlorophyll a/b-binding protein [Arabidopsis thaliana]

Seq. No.	162675
Seq. ID	LIB3177-048-P1-K1-H11
Method	BLASTX
NCBI GI	g1173104
BLAST score	344
E value	2.0e-32
Match length	137
% identity	53
NCBI Description	RIBONUCLEASE 2 PRECURSOR >gi_289210 (M98336) ribonuclease [Arabidopsis thaliana] >gi_2642160 (AC003000) ribonuclease, RNS2 [Arabidopsis thaliana]

Seq. No.	162676
Seq. ID	LIB3177-048-P1-K1-H12
Method	BLASTN
NCBI GI	g2244747
BLAST score	63
E value	7.0e-27
Match length	225
% identity	85
NCBI Description	Arabidopsis thaliana DNA chromosome 4, ESSA I contig fragment No

Seq. No.	162677
Seq. ID	LIB3177-048-P1-K1-H7
Method	BLASTN
NCBI GI	g4539378
BLAST score	80
E value	6.0e-37
Match length	168
% identity	87
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F28A21 (ESSA project)

Seq. No.	162678
Seq. ID	LIB3177-048-P1-K1-H9
Method	BLASTX
NCBI GI	g3550519

BLAST score	143
E value	7.0e-09
Match length	130
% identity	29
NCBI Description	(AJ007630) oxygenase [Nicotiana tabacum]

Seq. No.	162679
Seq. ID	LIB3177-049-P1-K1-A1
Method	BLASTX
NCBI GI	g2119846
BLAST score	336
E value	8.0e-32
Match length	88
% identity	74
NCBI Description	chlorophyll a/b-binding protein type I precursor Lhb1B2 - Arabidopsis thaliana >gi_16364_emb_CAA45790_ (X64460) photosystem II type I chlorophyll a /b binding protein [Arabidopsis thaliana] >gi_3128230 (AC004077) photosystem II type I chlorophyll a/b binding protein [Arabidopsis thaliana] >gi_3337371 (AC004481) photosystem II type I chlorophyll a/b binding protein [Arabidopsis thaliana]

Seq. No.	162680
Seq. ID	LIB3177-049-P1-K1-A2
Method	BLASTN
NCBI GI	g4206762
BLAST score	118
E value	7.0e-60
Match length	209
% identity	90
NCBI Description	Arabidopsis thaliana cell wall-plasma membrane linker protein homolog (CWLP) mRNA, complete cds

Seq. No.	162681
Seq. ID	LIB3177-049-P1-K1-A3
Method	BLASTN
NCBI GI	g3608494
BLAST score	71
E value	5.0e-32
Match length	135
% identity	88
NCBI Description	Arabidopsis thaliana plastid division protein FtsZ mRNA, complete cds

Seq. No.	162682
Seq. ID	LIB3177-049-P1-K1-A4
Method	BLASTN
NCBI GI	g2264304
BLAST score	96
E value	1.0e-46
Match length	192
% identity	88
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MBG8, complete sequence [Arabidopsis thaliana]

Seq. No.	162683
Seq. ID	LIB3177-049-P1-K1-A5

Method	BLASTN
NCBI GI	g4713943
BLAST score	94
E value	2.0e-45
Match length	250
% identity	84
NCBI Description	Arabidopsis thaliana chromosome 1 BAC T8K14 sequence, complete sequence

Seq. No.	162684
Seq. ID	LIB3177-049-P1-K1-A7
Method	BLASTN
NCBI GI	g1145698
BLAST score	35
E value	2.0e-10
Match length	87
% identity	85
NCBI Description	Arabidopsis thaliana delta tonoplast integral protein gene, partial cds

Seq. No.	162685
Seq. ID	LIB3177-049-P1-K1-B1
Method	BLASTX
NCBI GI	g102278
BLAST score	282
E value	2.0e-25
Match length	85
% identity	10
NCBI Description	ubiquitin 14 - slime mold (Dictyostelium discoideum)

Seq. No.	162686
Seq. ID	LIB3177-049-P1-K1-B11
Method	BLASTX
NCBI GI	g1170089
BLAST score	262
E value	4.0e-23
Match length	86
% identity	64
NCBI Description	GLUTATHIONE S-TRANSFERASE ERD13 (CLASS PHI) >gi_481822_pir__S39542 probable glutathione transferase (EC 2.5.1.18) (clone ERD13) - Arabidopsis thaliana >gi_497789_dbj_BAA04554_ (D17673) glutathione S-transferase [Arabidopsis thaliana] >gi_3201614 (AC004669) glutathione S-transferase [Arabidopsis thaliana]

Seq. No.	162687
Seq. ID	LIB3177-049-P1-K1-B3
Method	BLASTX
NCBI GI	g3695383
BLAST score	267
E value	2.0e-23
Match length	115
% identity	55
NCBI Description	(AF096370) similar to inorganic pyrophosphatase (Pfam: PF00719 Pyrophosphatase, E-value: 2.7e-88) [Arabidopsis thaliana]

Seq. No.	162688
Seq. ID	LIB3177-049-P1-K1-B4
Method	BLASTN
NCBI GI	g2264316
BLAST score	67
E value	2.0e-29
Match length	306
% identity	58
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MRO11, complete sequence [Arabidopsis thaliana]

Seq. No.	162689
Seq. ID	LIB3177-049-P1-K1-B9
Method	BLASTN
NCBI GI	g3228389
BLAST score	117
E value	4.0e-59
Match length	265
% identity	86
NCBI Description	Genomic sequence for Arabidopsis thaliana BAC F17L21, complete sequence [Arabidopsis thaliana]

Seq. No.	162690
Seq. ID	LIB3177-049-P1-K1-C1
Method	BLASTX
NCBI GI	g115778
BLAST score	136
E value	3.0e-10
Match length	111
% identity	44
NCBI Description	CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR (CAB-1) (LHCP) >gi_282896_pir__S22511 chlorophyll a/b-binding protein (cab-1) - white mustard >gi_21138_emb_CAA34459_ (X16436) chlorophyll a/b-binding protein (AA 1-266) [Sinapis alba] >gi_21140_emb_CAA33903_ (X15894) chlorophyll a/b-binding polypeptide [Sinapis alba]

Seq. No.	162691
Seq. ID	LIB3177-049-P1-K1-C11
Method	BLASTX
NCBI GI	g2982299
BLAST score	180
E value	2.0e-13
Match length	84
% identity	48
NCBI Description	(AF051234) transcription factor BTF3 homolog [Picea mariana]

Seq. No.	162692
Seq. ID	LIB3177-049-P1-K1-C2
Method	BLASTX
NCBI GI	g2160168
BLAST score	251
E value	9.0e-22
Match length	98
% identity	60
NCBI Description	(AC000132) Strong similarity to R. communis

	phosphoglycerate mutase (gb_X70652). ESTs gb_T41853,gb_T76648 come from this gene. [Arabidopsis thaliana]
Seq. No.	162693
Seq. ID	LIB3177-049-P1-K1-C3
Method	BLASTX
NCBI GI	g3831470
BLAST score	262
E value	4.0e-23
Match length	76
% identity	72
NCBI Description	(AC005700) unknown protein, 3' partial [Arabidopsis thaliana]
Seq. No.	162694
Seq. ID	LIB3177-049-P1-K1-C4
Method	BLASTN
NCBI GI	g2245073
BLAST score	70
E value	4.0e-31
Match length	300
% identity	82
NCBI Description	Arabidopsis thaliana DNA chromosome 4, ESSA I contig fragment No
Seq. No.	162695
Seq. ID	LIB3177-049-P1-K1-D11
Method	BLASTX
NCBI GI	g2500959
BLAST score	126
E value	1.0e-09
Match length	104
% identity	33
NCBI Description	ALANYL-TRNA SYNTHETASE (ALANINE--TRNA LIGASE) (ALARS) >gi_1653611_dbj_BAA18523_ (D90915) alanyl-tRNA synthetase [Synechocystis sp.]
Seq. No.	162696
Seq. ID	LIB3177-049-P1-K1-D12
Method	BLASTN
NCBI GI	g2789659
BLAST score	92
E value	3.0e-44
Match length	261
% identity	83
NCBI Description	Arabidopsis thaliana p105 mRNA, complete cds
Seq. No.	162697
Seq. ID	LIB3177-049-P1-K1-D3
Method	BLASTX
NCBI GI	g2499973
BLAST score	271
E value	5.0e-24
Match length	82
% identity	70
NCBI Description	PHOTOSYSTEM II 5 KD PROTEIN PRECURSOR (PSII-T)

>gi_1465366_emb_CAA66701_ (X98078) photosystem II [Arabidopsis thaliana]

Seq. No.	162698
Seq. ID	LIB3177-049-P1-K1-D4
Method	BLASTX
NCBI GI	g2529665
BLAST score	227
E value	4.0e-19
Match length	78
% identity	64
NCBI Description	(AC002535) putative ribosomal protein L7A [Arabidopsis thaliana]

Seq. No.	162699
Seq. ID	LIB3177-049-P1-K1-D5
Method	BLASTN
NCBI GI	g4741939
BLAST score	53
E value	3.0e-21
Match length	154
% identity	82
NCBI Description	Arabidopsis thaliana Lhca2 protein (Lhca2) mRNA, complete cds

Seq. No.	162700
Seq. ID	LIB3177-049-P1-K1-E1
Method	BLASTX
NCBI GI	g4454036
BLAST score	213
E value	2.0e-17
Match length	82
% identity	57
NCBI Description	(AL035394) putative major latex protein [Arabidopsis thaliana]

Seq. No.	162701
Seq. ID	LIB3177-049-P1-K1-E12
Method	BLASTX
NCBI GI	g2317731
BLAST score	177
E value	2.0e-13
Match length	61
% identity	59
NCBI Description	(AF013628) reversibly glycosylated polypeptide-2 [Arabidopsis thaliana]

Seq. No.	162702
Seq. ID	LIB3177-049-P1-K1-E2
Method	BLASTX
NCBI GI	g4467099
BLAST score	186
E value	2.0e-14
Match length	56
% identity	71
NCBI Description	(AL035538) glycine hydroxymethyltransferase like protein [Arabidopsis thaliana]

Seq. No.	162703
Seq. ID	LIB3177-049-P1-K1-E3
Method	BLASTN
NCBI GI	g4539309
BLAST score	86
E value	1.0e-40
Match length	306
% identity	82
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F19H22 (ESSA project)

Seq. No.	162704
Seq. ID	LIB3177-049-P1-K1-F1
Method	BLASTX
NCBI GI	g1732572
BLAST score	139
E value	1.0e-08
Match length	67
% identity	51
NCBI Description	(U72154) beta-glucosidase [Brassica nigra]

Seq. No.	162705
Seq. ID	LIB3177-049-P1-K1-F2
Method	BLASTN
NCBI GI	g4584351
BLAST score	119
E value	3.0e-60
Match length	338
% identity	84
NCBI Description	Arabidopsis thaliana chromosome II BAC T12H3 genomic sequence, complete sequence

Seq. No.	162706
Seq. ID	LIB3177-049-P1-K1-F3
Method	BLASTX
NCBI GI	g1170028
BLAST score	175
E value	8.0e-13
Match length	73
% identity	55
NCBI Description	GLUTAMATE-1-SEMIALDEHYDE 2,1-AMINOMUTASE 1 PRECURSOR (GSA 1) (GLUTAMATE-1-SEMIALDEHYDE AMINOTRANSFERASE 1) (GSA-AT 1) >gi_454357 (U03773) glutamate-1-semialdehyde-2,1-aminomutase [Arabidopsis thaliana]

Seq. No.	162707
Seq. ID	LIB3177-049-P1-K1-F4
Method	BLASTN
NCBI GI	g2231164
BLAST score	67
E value	3.0e-29
Match length	175
% identity	85
NCBI Description	Oryza sativa integral membrane protein (OsNramp2) mRNA, complete cds

Seq. No.	162708
Seq. ID	LIB3177-049-P1-K1-F5
Method	BLASTN
NCBI GI	g4220635
BLAST score	61
E value	8.0e-26
Match length	251
% identity	89
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MDB19, complete sequence [Arabidopsis thaliana]

Seq. No.	162709
Seq. ID	LIB3177-049-P1-K1-F7
Method	BLASTX
NCBI GI	g2058456
BLAST score	142
E value	2.0e-09
Match length	47
% identity	64
NCBI Description	(U66408) GTP-binding protein [Arabidopsis thaliana] >gi_2345150_gb_AAB67830_ (AF014822) developmentally regulated GTP binding protein [Arabidopsis thaliana]

Seq. No.	162710
Seq. ID	LIB3177-049-P1-K1-G1
Method	BLASTN
NCBI GI	g166695
BLAST score	139
E value	3.0e-72
Match length	283
% identity	87
NCBI Description	Arabidopsis thaliana recombination and DNA-damage resistance protein (DRT112) mRNA, complete cds

Seq. No.	162711
Seq. ID	LIB3177-049-P1-K1-G10
Method	BLASTN
NCBI GI	g4454022
BLAST score	35
E value	2.0e-10
Match length	75
% identity	87
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F9D16 (ESSAII project)

Seq. No.	162712
Seq. ID	LIB3177-049-P1-K1-G2
Method	BLASTX
NCBI GI	g452470
BLAST score	273
E value	3.0e-24
Match length	88
% identity	68
NCBI Description	(U05218) ATP sulfurylase [Arabidopsis thaliana]

Seq. No.	162713

Seq. ID	LIB3177-049-P1-K1-G3
Method	BLASTX
NCBI GI	g4336758
BLAST score	375
E value	4.0e-36
Match length	96
% identity	74
NCBI Description	(AF104454) catalase [Brassica juncea]

Seq. No.	162714
Seq. ID	LIB3177-049-P1-K1-G8
Method	BLASTX
NCBI GI	g4512682
BLAST score	332
E value	4.0e-31
Match length	112
% identity	64
NCBI Description	(AC006931) unknown protein [Arabidopsis thaliana]

Seq. No.	162715
Seq. ID	LIB3177-049-P1-K1-H1
Method	BLASTX
NCBI GI	g4218120
BLAST score	268
E value	1.0e-23
Match length	105
% identity	58
NCBI Description	(AL035353) Proline-rich APG-like protein [Arabidopsis thaliana]

Seq. No.	162716
Seq. ID	LIB3177-049-P1-K1-H2
Method	BLASTX
NCBI GI	g2190259
BLAST score	141
E value	9.0e-09
Match length	81
% identity	37
NCBI Description	(D86385) A-type cyclin [Catharanthus roseus]

Seq. No.	162717
Seq. ID	LIB3177-049-P1-K1-H8
Method	BLASTX
NCBI GI	g4741952
BLAST score	142
E value	4.0e-09
Match length	59
% identity	49
NCBI Description	(AF134126) Lhcb3 protein [Arabidopsis thaliana]

Seq. No.	162718
Seq. ID	LIB3177-049-P1-K2-A1
Method	BLASTX
NCBI GI	g115767
BLAST score	717
E value	3.0e-76
Match length	134

% identity	99
NCBI Description	CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR (CAB-165/180) (LHCP) >gi_81603_pir__A29280 chlorophyll a/b-binding protein ab165 - Arabidopsis thaliana >gi_16368_emb_CAA27540_ (X03907) chlorophyll a/b binding protein (LHCP AB 65) [Arabidopsis thaliana] >gi_16372_emb_CAA27541_ (X03908) chlorophyll a/b binding protein (LHCP AB 180) [Arabidopsis thaliana]
Seq. No.	162719
Seq. ID	LIB3177-049-P1-K2-A10
Method	BLASTX
NCBI GI	g2492517
BLAST score	123
E value	2.0e-48
Match length	135
% identity	76
NCBI Description	26S PROTEASE REGULATORY SUBUNIT 6B (TAT-BINDING PROTEIN-7) (TBP-7) >gi_1395186_dbj_BAA09340_ (D50695) proteasomal ATPase (Tat-binding protein7) [Rattus norvegicus]
Seq. No.	162720
Seq. ID	LIB3177-049-P1-K2-A2
Method	BLASTN
NCBI GI	g4206762
BLAST score	123
E value	1.0e-62
Match length	337
% identity	83
NCBI Description	Arabidopsis thaliana cell wall-plasma membrane linker protein homolog (CWLP) mRNA, complete cds
Seq. No.	162721
Seq. ID	LIB3177-049-P1-K2-A4
Method	BLASTX
NCBI GI	g4455225
BLAST score	470
E value	3.0e-47
Match length	106
% identity	78
NCBI Description	(AL035440) putative protein [Arabidopsis thaliana]
Seq. No.	162722
Seq. ID	LIB3177-049-P1-K2-B1
Method	BLASTX
NCBI GI	g1076708
BLAST score	596
E value	6.0e-62
Match length	120
% identity	28
NCBI Description	seed tetraubiquitin - common sunflower >gi_303901_dbj_BAA03764_ (D16248) ubiquitin [Glycine max] >gi_456714_dbj_BAA05670_ (D28123) Ubiquitin [Glycine max] >gi_556688_emb_CAA84440_ (Z34988) seed tetraubiquitin [Helianthus annuus] >gi_994785_dbj_BAA05085_ (D26092) Ubiquitin [Glycine max] >gi_4263514_gb_AAD15340_ (AC004044) putative polyubiquitin [Arabidopsis thaliana]

>gi_1096513_prf__2111434A tetraubiquitin [Helianthus annuus]

Seq. No.	162723
Seq. ID	LIB3177-049-P1-K2-B11
Method	BLASTX
NCBI GI	g1170089
BLAST score	621
E value	6.0e-65
Match length	127
% identity	97
NCBI Description	GLUTATHIONE S-TRANSFERASE ERD13 (CLASS PHI) >gi_481822_pir__S39542 probable glutathione transferase (EC 2.5.1.18) (clone ERD13) - Arabidopsis thaliana >gi_497789_dbj_BAA04554_ (D17673) glutathione S-transferase [Arabidopsis thaliana] >gi_3201614 (AC004669) glutathione S-transferase [Arabidopsis thaliana]

Seq. No.	162724
Seq. ID	LIB3177-049-P1-K2-B3
Method	BLASTX
NCBI GI	g3510259
BLAST score	173
E value	4.0e-31
Match length	91
% identity	76
NCBI Description	(AC005310) putative inorganic pyrophosphatase [Arabidopsis thaliana] >gi_3522960 (AC004411) putative inorganic pyrophosphatase [Arabidopsis thaliana]

Seq. No.	162725
Seq. ID	LIB3177-049-P1-K2-B4
Method	BLASTN
NCBI GI	g2264316
BLAST score	92
E value	4.0e-44
Match length	405
% identity	36
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MRO11, complete sequence [Arabidopsis thaliana]

Seq. No.	162726
Seq. ID	LIB3177-049-P1-K2-B6
Method	BLASTX
NCBI GI	g3024022
BLAST score	396
E value	1.0e-38
Match length	84
% identity	88
NCBI Description	INITIATION FACTOR 5A-5 (EIF-5A) (EIF-4D) >gi_2225885_dbj_BAA20879_ (AB004826) eukaryotic initiation factor 5A5 [Solanum tuberosum]

Seq. No.	162727
Seq. ID	LIB3177-049-P1-K2-B8
Method	BLASTX
NCBI GI	g1710780

BLAST score	181
E value	1.0e-13
Match length	58
% identity	66
NCBI Description	40S RIBOSOMAL PROTEIN S9 (S7) >gi_1321917_emb_CAA65433_ (X96613) cytoplasmic ribosomal protein S7 [Podospora anserina]

Seq. No.	162728
Seq. ID	LIB3177-049-P1-K2-B9
Method	BLASTN
NCBI GI	g3228389
BLAST score	184
E value	5.0e-99
Match length	280
% identity	96
NCBI Description	Genomic sequence for Arabidopsis thaliana BAC F17L21, complete sequence [Arabidopsis thaliana]

Seq. No.	162729
Seq. ID	LIB3177-049-P1-K2-C1
Method	BLASTX
NCBI GI	g115767
BLAST score	495
E value	2.0e-50
Match length	95
% identity	99
NCBI Description	CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR (CAB-165/180) (LHCP) >gi_81603_pir__A29280 chlorophyll a/b-binding protein ab165 - Arabidopsis thaliana >gi_16368_emb_CAA27540_ (X03907) chlorophyll a/b binding protein (LHCP AB 65) [Arabidopsis thaliana] >gi_16372_emb_CAA27541_ (X03908) chlorophyll a/b binding protein (LHCP AB 180) [Arabidopsis thaliana]

Seq. No.	162730
Seq. ID	LIB3177-049-P1-K2-C11
Method	BLASTX
NCBI GI	g2982299
BLAST score	251
E value	2.0e-21
Match length	92
% identity	60
NCBI Description	(AF051234) transcription factor BTF3 homolog [Picea mariana]

Seq. No.	162731
Seq. ID	LIB3177-049-P1-K2-C12
Method	BLASTX
NCBI GI	g1737218
BLAST score	42
E value	1.0e-50
Match length	123
% identity	84
NCBI Description	(U79959) vacuolar sorting receptor homolog [Arabidopsis thaliana]

Seq. No.	162732
Seq. ID	LIB3177-049-P1-K2-C3
Method	BLASTX
NCBI GI	g3831470
BLAST score	400
E value	5.0e-39
Match length	128
% identity	70
NCBI Description	(AC005700) unknown protein, 3' partial [Arabidopsis thaliana]

Seq. No.	162733
Seq. ID	LIB3177-049-P1-K2-C4
Method	BLASTN
NCBI GI	g2245073
BLAST score	190
E value	1.0e-102
Match length	409
% identity	93
NCBI Description	Arabidopsis thaliana DNA chromosome 4, ESSA I contig fragment No

Seq. No.	162734
Seq. ID	LIB3177-049-P1-K2-C6
Method	BLASTX
NCBI GI	g1732572
BLAST score	81
E value	2.0e-18
Match length	71
% identity	72
NCBI Description	(U72154) beta-glucosidase [Brassica nigra]

Seq. No.	162735
Seq. ID	LIB3177-049-P1-K2-D1
Method	BLASTX
NCBI GI	g170354
BLAST score	588
E value	5.0e-61
Match length	118
% identity	22
NCBI Description	(M74156) pentameric polyubiquitin [Nicotiana sylvestris]

Seq. No.	162736
Seq. ID	LIB3177-049-P1-K2-D12
Method	BLASTX
NCBI GI	g2789660
BLAST score	370
E value	2.0e-35
Match length	99
% identity	75
NCBI Description	(AF040102) p105 [Arabidopsis thaliana]

Seq. No.	162737
Seq. ID	LIB3177-049-P1-K2-D2
Method	BLASTN
NCBI GI	g515373
BLAST score	172

E value	7.0e-92
Match length	176
% identity	99
NCBI Description	Arabidopsis thaliana chloroplast DNA

Seq. No.	162738
Seq. ID	LIB3177-049-P1-K2-D3
Method	BLASTX
NCBI GI	g2499973
BLAST score	316
E value	2.0e-29
Match length	76
% identity	93
NCBI Description	PHOTOSYSTEM II 5 KD PROTEIN PRECURSOR (PSII-T) >gi_1465366_emb_CAA66701_ (X98078) photosystem II [Arabidopsis thaliana]

Seq. No.	162739
Seq. ID	LIB3177-049-P1-K2-D4
Method	BLASTX
NCBI GI	g2529665
BLAST score	560
E value	1.0e-57
Match length	135
% identity	83
NCBI Description	(AC002535) putative ribosomal protein L7A [Arabidopsis thaliana]

Seq. No.	162740
Seq. ID	LIB3177-049-P1-K2-D5
Method	BLASTX
NCBI GI	g4741940
BLAST score	576
E value	1.0e-59
Match length	133
% identity	58
NCBI Description	(AF134120) Lhca2 protein [Arabidopsis thaliana]

Seq. No.	162741
Seq. ID	LIB3177-049-P1-K2-D6
Method	BLASTN
NCBI GI	g4741939
BLAST score	62
E value	2.0e-26
Match length	200
% identity	82
NCBI Description	Arabidopsis thaliana Lhca2 protein (Lhca2) mRNA, complete cds

Seq. No.	162742
Seq. ID	LIB3177-049-P1-K2-D7
Method	BLASTX
NCBI GI	g4585935
BLAST score	539
E value	3.0e-55
Match length	117
% identity	87

NCBI Description	(AC007211) putative chlorophyll A/B binding protein [Arabidopsis thaliana] >gi_4741946_gb_AAD28770.1_AF134123_1 (AF134123) Lhcb2 protein [Arabidopsis thaliana]
Seq. No.	162743
Seq. ID	LIB3177-049-P1-K2-D8
Method	BLASTX
NCBI GI	g2119846
BLAST score	710
E value	2.0e-75
Match length	135
% identity	99
NCBI Description	chlorophyll a/b-binding protein type I precursor Lhb1B2 - Arabidopsis thaliana >gi_16364_emb_CAA45790_ (X64460) photosystem II type I chlorophyll a /b binding protein [Arabidopsis thaliana] >gi_3128230 (AC004077) photosystem II type I chlorophyll a/b binding protein [Arabidopsis thaliana] >gi_3337371 (AC004481) photosystem II type I chlorophyll a/b binding protein [Arabidopsis thaliana]
Seq. No.	162744
Seq. ID	LIB3177-049-P1-K2-E1
Method	BLASTX
NCBI GI	g4454036
BLAST score	657
E value	4.0e-69
Match length	135
% identity	91
NCBI Description	(AL035394) putative major latex protein [Arabidopsis thaliana]
Seq. No.	162745
Seq. ID	LIB3177-049-P1-K2-E10
Method	BLASTX
NCBI GI	g4585966
BLAST score	474
E value	1.0e-47
Match length	122
% identity	75
NCBI Description	(AC005287) Putative dihyrdolipoamide acetyltransferase [Arabidopsis thaliana]
Seq. No.	162746
Seq. ID	LIB3177-049-P1-K2-E12
Method	BLASTN
NCBI GI	g2317730
BLAST score	44
E value	3.0e-16
Match length	60
% identity	93
NCBI Description	Arabidopsis thaliana reversibly glycosylated polypeptide-2 (AtRGP) mRNA, complete cds
Seq. No.	162747
Seq. ID	LIB3177-049-P1-K2-E2
Method	BLASTX
NCBI GI	g4467099

BLAST score	665
E value	5.0e-70
Match length	133
% identity	98
NCBI Description	(AL035538) glycine hydroxymethyltransferase like protein [Arabidopsis thaliana]

Seq. No.	162748
Seq. ID	LIB3177-049-P1-K2-E3
Method	BLASTN
NCBI GI	g4539309
BLAST score	295
E value	1.0e-165
Match length	421
% identity	99
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F19H22 (ESSA project)

Seq. No.	162749
Seq. ID	LIB3177-049-P1-K2-E6
Method	BLASTN
NCBI GI	g3309085
BLAST score	103
E value	8.0e-51
Match length	119
% identity	97
NCBI Description	Arabidopsis thaliana calcineurin B-like protein 3 (CBL3) mRNA, complete cds

Seq. No.	162750
Seq. ID	LIB3177-049-P1-K2-E8
Method	BLASTN
NCBI GI	g4589440
BLAST score	54
E value	1.0e-21
Match length	62
% identity	97
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MSD21, complete sequence

Seq. No.	162751
Seq. ID	LIB3177-049-P1-K2-F1
Method	BLASTX
NCBI GI	g1732570
BLAST score	340
E value	5.0e-32
Match length	96
% identity	81
NCBI Description	(U72153) beta-glucosidase [Arabidopsis thaliana]

Seq. No.	162752
Seq. ID	LIB3177-049-P1-K2-F10
Method	BLASTN
NCBI GI	g4753645
BLAST score	185
E value	1.0e-99
Match length	428

% identity	99
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F17N18 (ESSA project)
Seq. No.	162753
Seq. ID	LIB3177-049-P1-K2-F2
Method	BLASTN
NCBI GI	g4584351
BLAST score	349
E value	0.0e+00
Match length	349
% identity	100
NCBI Description	Arabidopsis thaliana chromosome II BAC T12H3 genomic sequence, complete sequence
Seq. No.	162754
Seq. ID	LIB3177-049-P1-K2-F3
Method	BLASTX
NCBI GI	g1170028
BLAST score	547
E value	3.0e-56
Match length	125
% identity	86
NCBI Description	GLUTAMATE-1-SEMIALDEHYDE 2,1-AMINOMUTASE 1 PRECURSOR (GSA 1) (GLUTAMATE-1-SEMIALDEHYDE AMINOTRANSFERASE 1) (GSA-AT 1) >gi_454357 (U03773) glutamate-1-semialdehyde-2,1-aminomutase [Arabidopsis thaliana]
Seq. No.	162755
Seq. ID	LIB3177-049-P1-K2-F4
Method	BLASTX
NCBI GI	g2231149
BLAST score	416
E value	4.0e-41
Match length	87
% identity	99
NCBI Description	(L81152) integral membrane protein [Oryza sativa]
Seq. No.	162756
Seq. ID	LIB3177-049-P1-K2-F6
Method	BLASTX
NCBI GI	g129915
BLAST score	102
E value	1.0e-19
Match length	76
% identity	62
NCBI Description	PHOSPHOGLYCERATE KINASE, CHLOROPLAST PRECURSOR >gi_66912_pir__TVWTGC phosphoglycerate kinase (EC 2.7.2.3) precursor, chloroplast - wheat >gi_21833_emb_CAA33303_ (X15233) phosphoglycerate kinase (AA 1 - 480) [Triticum aestivum] >gi_3293043_emb_CAA51931_ (X73528) phosphoglycerate kinase [Triticum aestivum]
Seq. No.	162757
Seq. ID	LIB3177-049-P1-K2-F7
Method	BLASTX

NCBI GI	g2058456
BLAST score	354
E value	2.0e-41
Match length	119
% identity	75
NCBI Description	(U66408) GTP-binding protein [Arabidopsis thaliana] >gi_2345150_gb_AAB67830_ (AF014822) developmentally regulated GTP binding protein [Arabidopsis thaliana]

Seq. No.	162758
Seq. ID	LIB3177-049-P1-K2-F8
Method	BLASTX
NCBI GI	g4539459
BLAST score	352
E value	2.0e-33
Match length	137
% identity	47
NCBI Description	(AL049500) putative protein [Arabidopsis thaliana]

Seq. No.	162759
Seq. ID	LIB3177-049-P1-K2-F9
Method	BLASTX
NCBI GI	g2781354
BLAST score	571
E value	5.0e-59
Match length	134
% identity	82
NCBI Description	(AC003113) F24O1.10 [Arabidopsis thaliana]

Seq. No.	162760
Seq. ID	LIB3177-049-P1-K2-G1
Method	BLASTX
NCBI GI	g1169201
BLAST score	444
E value	4.0e-44
Match length	113
% identity	81
NCBI Description	DNA-DAMAGE-REPAIR/TOLERATION PROTEIN DRT112 PRECURSOR >gi_421830_pir__S33707 DRT112 protein - Arabidopsis thaliana >gi_166696 (M98456) DRT112 [Arabidopsis thaliana]

Seq. No.	162761
Seq. ID	LIB3177-049-P1-K2-G10
Method	BLASTX
NCBI GI	g4454037
BLAST score	490
E value	1.0e-49
Match length	92
% identity	97
NCBI Description	(AL035394) putative major latex protein [Arabidopsis thaliana]

Seq. No.	162762
Seq. ID	LIB3177-049-P1-K2-G12
Method	BLASTN
NCBI GI	g4309747
BLAST score	40

E value	2.0e-13
Match length	118
% identity	88
NCBI Description	Arabidopsis thaliana chromosome II BAC T13E11 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	162763
Seq. ID	LIB3177-049-P1-K2-G2
Method	BLASTX
NCBI GI	g452470
BLAST score	131
E value	2.0e-07
Match length	120
% identity	82
NCBI Description	(U05218) ATP sulfurylase [Arabidopsis thaliana]

Seq. No.	162764
Seq. ID	LIB3177-049-P1-K2-G3
Method	BLASTX
NCBI GI	g4336756
BLAST score	527
E value	5.0e-54
Match length	100
% identity	99
NCBI Description	(AF104453) catalase [Brassica juncea]

Seq. No.	162765
Seq. ID	LIB3177-049-P1-K2-G4
Method	BLASTN
NCBI GI	g405130
BLAST score	217
E value	1.0e-119
Match length	285
% identity	94
NCBI Description	Arabidopsis thaliana nuclear-encoded chloroplast stromal cyclophilin (ROC4) mRNA, complete cds

Seq. No.	162766
Seq. ID	LIB3177-049-P1-K2-G5
Method	BLASTX
NCBI GI	g4585935
BLAST score	590
E value	3.0e-61
Match length	115
% identity	97
NCBI Description	(AC007211) putative chlorophyll A/B binding protein [Arabidopsis thaliana] >gi_4741946_gb_AAD28770.1_AF134123_1 (AF134123) Lhcb2 protein [Arabidopsis thaliana]

Seq. No.	162767
Seq. ID	LIB3177-049-P1-K2-G8
Method	BLASTX
NCBI GI	g4512682
BLAST score	658
E value	3.0e-69
Match length	135
% identity	96

NCBI Description	(AC006931) unknown protein [Arabidopsis thaliana]
Seq. No.	162768
Seq. ID	LIB3177-049-P1-K2-H1
Method	BLASTX
NCBI GI	g4218120
BLAST score	473
E value	1.0e-47
Match length	121
% identity	76
NCBI Description	(AL035353) Proline-rich APG-like protein [Arabidopsis thaliana]
Seq. No.	162769
Seq. ID	LIB3177-049-P1-K2-H12
Method	BLASTX
NCBI GI	g3024898
BLAST score	154
E value	4.0e-10
Match length	54
% identity	50
NCBI Description	PUTATIVE PRE-MRNA SPLICING FACTOR ATP-DEPENDENT RNA HELICASE KIAA0224 (HA4657) >gi_1504028_dbj_BAA13213_ (D86977) similar to putative ATP-dependent RNA helicase K03H1.2 of C.elegans(S41025) [Homo sapiens] >gi_3123906 (AF038391) pre-mRNA splicing factor [Homo sapiens]
Seq. No.	162770
Seq. ID	LIB3177-049-P1-K2-H2
Method	BLASTX
NCBI GI	g4218120
BLAST score	258
E value	2.0e-22
Match length	119
% identity	50
NCBI Description	(AL035353) Proline-rich APG-like protein [Arabidopsis thaliana]
Seq. No.	162771
Seq. ID	LIB3177-049-P1-K2-H3
Method	BLASTX
NCBI GI	g2119848
BLAST score	508
E value	1.0e-51
Match length	111
% identity	87
NCBI Description	chlorophyll a/b-binding protein type I precursor Lhb1B1 - Arabidopsis thaliana >gi_16366_emb_CAA45789_ (X64459) photosystem II type I chlorophyll a /b binding protein [Arabidopsis thaliana] >gi_3128229 (AC004077) putative photosystem II type I chlorophyll a/b binding protein [Arabidopsis thaliana] >gi_3337372 (AC004481) putative photosystem II type I chlorophyll a/b binding protein [Arabidopsis thaliana]
Seq. No.	162772
Seq. ID	LIB3177-049-P1-K2-H5

Method	BLASTX
NCBI GI	g282865
BLAST score	506
E value	2.0e-51
Match length	121
% identity	81
NCBI Description	chlorophyll a/b-binding protein - Arabidopsis thaliana >gi_16207_emb_CAA39534_ (X56062) chlorophyll A/B-binding protein [Arabidopsis thaliana] >gi_166644 (M85150) chlorophyll a/b-binding protein [Arabidopsis thaliana] >gi_4678304_emb_CAB41095.1_ (AL049655) chlorophyll a/b-binding protein [Arabidopsis thaliana]

Seq. No.	162773
Seq. ID	LIB3177-049-P1-K2-H7
Method	BLASTN
NCBI GI	g1419473
BLAST score	127
E value	3.0e-65
Match length	191
% identity	92
NCBI Description	A.thaliana chloroplast ndhA gene

Seq. No.	162774
Seq. ID	LIB3177-049-P1-K2-H8
Method	BLASTX
NCBI GI	g4741952
BLAST score	641
E value	3.0e-67
Match length	119
% identity	75
NCBI Description	(AF134126) Lhcb3 protein [Arabidopsis thaliana]

Seq. No.	162775
Seq. ID	LIB3177-050-P1-K1-A1
Method	BLASTX
NCBI GI	g4587525
BLAST score	175
E value	1.0e-12
Match length	125
% identity	33
NCBI Description	(AC007060) Contains the PF_00650 CRAL/TRIO phosphatidyl-inositol-transfer protein domain. ESTs gb_T76582, gb_N06574 and gb_Z25700 come from this gene. [Arabidopsis thaliana]

Seq. No.	162776
Seq. ID	LIB3177-050-P1-K1-A10
Method	BLASTX
NCBI GI	g2832683
BLAST score	331
E value	6.0e-31
Match length	117
% identity	62
NCBI Description	(AL021712) putative protein [Arabidopsis thaliana]

Seq. No.	162777

Seq. ID	LIB3177-050-P1-K1-A2
Method	BLASTN
NCBI GI	g3327922
BLAST score	84
E value	2.0e-39
Match length	184
% identity	86
NCBI Description	Arabidopsis thaliana chromosome II BAC T31E10 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	162778
Seq. ID	LIB3177-050-P1-K1-A4
Method	BLASTX
NCBI GI	g1172977
BLAST score	307
E value	4.0e-28
Match length	129
% identity	54
NCBI Description	60S RIBOSOMAL PROTEIN L18 >gi_606970 (U15741) cytoplasmic ribosomal protein L18 [Arabidopsis thaliana]

Seq. No.	162779
Seq. ID	LIB3177-050-P1-K1-A6
Method	BLASTX
NCBI GI	g541667
BLAST score	171
E value	4.0e-12
Match length	142
% identity	23
NCBI Description	(X79339) musashi [Drosophila melanogaster]

Seq. No.	162780
Seq. ID	LIB3177-050-P1-K1-B1
Method	BLASTN
NCBI GI	g3449334
BLAST score	62
E value	3.0e-26
Match length	206
% identity	85
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MYH9, complete sequence [Arabidopsis thaliana]

Seq. No.	162781
Seq. ID	LIB3177-050-P1-K1-B11
Method	BLASTX
NCBI GI	g2119846
BLAST score	321
E value	9.0e-30
Match length	110
% identity	58
NCBI Description	chlorophyll a/b-binding protein type I precursor Lhb1B2 - Arabidopsis thaliana >gi_16364_emb_CAA45790_ (X64460) photosystem II type I chlorophyll a /b binding protein [Arabidopsis thaliana] >gi_3128230 (AC004077) photosystem II type I chlorophyll a/b binding protein [Arabidopsis thaliana] >gi_3337371 (AC004481) photosystem II type I chlorophyll a/b binding protein [Arabidopsis thaliana]

Seq. No.	162782
Seq. ID	LIB3177-050-P1-K1-B2
Method	BLASTX
NCBI GI	g2199574
BLAST score	245
E value	8.0e-21
Match length	82
% identity	60
NCBI Description	(AF004293) aquaporin [Brassica rapa]

Seq. No.	162783
Seq. ID	LIB3177-050-P1-K1-B3
Method	BLASTX
NCBI GI	g267073
BLAST score	191
E value	1.0e-14
Match length	98
% identity	45
NCBI Description	TUBULIN BETA-2/BETA-3 CHAIN >gi_320184_pir__JQ1587 tubulin beta chain - Arabidopsis thaliana >gi_166898 (M84700) beta-2 tubulin [Arabidopsis thaliana] >gi_166900 (M84701) beta-3 tubulin [Arabidopsis thaliana]

Seq. No.	162784
Seq. ID	LIB3177-050-P1-K1-B4
Method	BLASTX
NCBI GI	g2252827
BLAST score	367
E value	4.0e-35
Match length	110
% identity	67
NCBI Description	(AF013293) No definition line found [Arabidopsis thaliana]

Seq. No.	162785
Seq. ID	LIB3177-050-P1-K1-B6
Method	BLASTX
NCBI GI	g4240116
BLAST score	277
E value	1.0e-24
Match length	106
% identity	58
NCBI Description	(AB007799) NADH-cytochrome b5 reductase [Arabidopsis thaliana] >gi_4240118_dbj_BAA74838_ (AB007800) NADH-cytochrome b5 reductase [Arabidopsis thaliana]

Seq. No.	162786
Seq. ID	LIB3177-050-P1-K1-B7
Method	BLASTX
NCBI GI	g2262173
BLAST score	240
E value	3.0e-20
Match length	90
% identity	52
NCBI Description	(AC002329) NADPH thioredoxin reductase [Arabidopsis thaliana]

Seq. No.	162787
Seq. ID	LIB3177-050-P1-K1-B8
Method	BLASTX
NCBI GI	g3789942
BLAST score	402
E value	3.0e-39
Match length	132
% identity	13
NCBI Description	(AF093505) polyubiquitin [Saccharum hybrid cultivar H32-8560]

Seq. No.	162788
Seq. ID	LIB3177-050-P1-K1-C2
Method	BLASTX
NCBI GI	g115783
BLAST score	357
E value	7.0e-34
Match length	126
% identity	60
NCBI Description	CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR (CAB-140) (LHCP) >gi_16376_emb_CAA27543_ (X03909) chlorophyll a/b binding protein (LHCP AB 140) [Arabidopsis thaliana]

Seq. No.	162789
Seq. ID	LIB3177-050-P1-K1-C3
Method	BLASTX
NCBI GI	g2245138
BLAST score	185
E value	8.0e-14
Match length	55
% identity	69
NCBI Description	(Z97344) hypothetical protein [Arabidopsis thaliana]

Seq. No.	162790
Seq. ID	LIB3177-050-P1-K1-C4
Method	BLASTX
NCBI GI	g119975
BLAST score	292
E value	2.0e-26
Match length	96
% identity	67
NCBI Description	FERREDOXIN PRECURSOR >gi_99692_pir__S09979 ferredoxin [2Fe-2S] precursor - Arabidopsis thaliana >gi_16437_emb_CAA35754_ (X51370) ferredoxin precursor [Arabidopsis thaliana] >gi_166698 (M35868) ferrodoxin A [Arabidopsis thaliana]

Seq. No.	162791
Seq. ID	LIB3177-050-P1-K1-C5
Method	BLASTX
NCBI GI	g2062161
BLAST score	486
E value	5.0e-49
Match length	136
% identity	36
NCBI Description	(AC001645) jasmonate inducible protein isolog [Arabidopsis

thaliana]

Seq. No.	162792
Seq. ID	LIB3177-050-P1-K1-C6
Method	BLASTX
NCBI GI	g166702
BLAST score	174
E value	2.0e-12
Match length	78
% identity	53
NCBI Description	(M64114) glyceraldehyde 3-phosphate dehydrogenase A subunit [Arabidopsis thaliana]

Seq. No.	162793
Seq. ID	LIB3177-050-P1-K1-C8
Method	BLASTX
NCBI GI	g115767
BLAST score	169
E value	6.0e-12
Match length	95
% identity	38
NCBI Description	CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR (CAB-165/180) (LHCP) >gi_81603_pir__A29280 chlorophyll a/b-binding protein ab165 - Arabidopsis thaliana >gi_16368_emb_CAA27540_ (X03907) chlorophyll a/b binding protein (LHCP AB 65) [Arabidopsis thaliana] >gi_16372_emb_CAA27541_ (X03908) chlorophyll a/b binding protein (LHCP AB 180) [Arabidopsis thaliana]

Seq. No.	162794
Seq. ID	LIB3177-050-P1-K1-D2
Method	BLASTX
NCBI GI	g2982469
BLAST score	241
E value	3.0e-20
Match length	141
% identity	44
NCBI Description	(AL022223) putative protein [Arabidopsis thaliana]

Seq. No.	162795
Seq. ID	LIB3177-050-P1-K1-D3
Method	BLASTX
NCBI GI	g132074
BLAST score	203
E value	3.0e-16
Match length	83
% identity	53
NCBI Description	RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN 1A PRECURSOR (RUBISCO SMALL SUBUNIT 1A) >gi_68063_pir__RKMUA1 ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain A1 precursor - Arabidopsis thaliana

Seq. No.	162796
Seq. ID	LIB3177-050-P1-K1-D4
Method	BLASTN
NCBI GI	g4038029
BLAST score	48

E value	6.0e-18
Match length	161
% identity	93
NCBI Description	Arabidopsis thaliana chromosome II BAC F5O4 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	162797
Seq. ID	LIB3177-050-P1-K1-D5
Method	BLASTX
NCBI GI	g2661422
BLAST score	323
E value	5.0e-30
Match length	119
% identity	59
NCBI Description	(AJ001342) Putative S-phase-specific ribosomal protein [Arabidopsis thaliana] >gi_3096936_emb_CAA18846.1_ (AL023094) Putative S-phase-specific ribosomal protein [Arabidopsis thaliana]

Seq. No.	162798
Seq. ID	LIB3177-050-P1-K1-D6
Method	BLASTX
NCBI GI	g1363487
BLAST score	165
E value	2.0e-11
Match length	54
% identity	57
NCBI Description	IAA7 protein - Arabidopsis thaliana >gi_972917 (U18409) IAA7 [Arabidopsis thaliana]

Seq. No.	162799
Seq. ID	LIB3177-050-P1-K1-D7
Method	BLASTX
NCBI GI	g2581783
BLAST score	301
E value	2.0e-27
Match length	124
% identity	54
NCBI Description	(U94998) class 1 non-symbiotic hemoglobin [Arabidopsis thaliana] >gi_4678203_gb_AAD26949.1_AC007134_7 (AC007134) class 1 non-symbiotic hemoglobin (AHB1) [Arabidopsis thaliana]

Seq. No.	162800
Seq. ID	LIB3177-050-P1-K1-E10
Method	BLASTX
NCBI GI	g4539419
BLAST score	167
E value	1.0e-11
Match length	75
% identity	48
NCBI Description	(AL049171) putative ribosomal protein [Arabidopsis thaliana]

Seq. No.	162801
Seq. ID	LIB3177-050-P1-K1-E2
Method	BLASTX

NCBI GI	g3928092
BLAST score	296
E value	8.0e-27
Match length	126
% identity	52
NCBI Description	(AC005770) unknown protein [Arabidopsis thaliana]

Seq. No.	162802
Seq. ID	LIB3177-050-P1-K1-E4
Method	BLASTN
NCBI GI	g4206766
BLAST score	32
E value	1.0e-08
Match length	52
% identity	90
NCBI Description	Arabidopsis thaliana glycine-rich protein 3 short isoform (GRP3S) mRNA, complete cds

Seq. No.	162803
Seq. ID	LIB3177-050-P1-K1-E7
Method	BLASTX
NCBI GI	g2921094
BLAST score	142
E value	8.0e-09
Match length	58
% identity	64
NCBI Description	(AF018174) thioredoxin-f [Brassica napus]

Seq. No.	162804
Seq. ID	LIB3177-050-P1-K1-F1
Method	BLASTX
NCBI GI	g100196
BLAST score	177
E value	8.0e-13
Match length	72
% identity	49
NCBI Description	chlorophyll a/b-binding protein (cab-11) - tomato

Seq. No.	162805
Seq. ID	LIB3177-050-P1-K1-F2
Method	BLASTX
NCBI GI	g4585935
BLAST score	333
E value	4.0e-31
Match length	125
% identity	53
NCBI Description	(AC007211) putative chlorophyll A/B binding protein [Arabidopsis thaliana] >gi_4741946_gb_AAD28770.1_AF134123_1 (AF134123) Lhcb2 protein [Arabidopsis thaliana]

Seq. No.	162806
Seq. ID	LIB3177-050-P1-K1-F4
Method	BLASTX
NCBI GI	g1175013
BLAST score	218
E value	1.0e-17
Match length	121

% identity	44
NCBI Description	PLASMA MEMBRANE INTRINSIC PROTEIN 2A >gi_629542_pir__S44084 plasma membrane intrinsic protein 2a - Arabidopsis thaliana >gi_472877_emb_CAA53477_ (X75883) plasma membrane intrinsic protein 2a [Arabidopsis thaliana]
Seq. No.	162807
Seq. ID	LIB3177-050-P1-K1-F7
Method	BLASTX
NCBI GI	g541858
BLAST score	286
E value	1.0e-25
Match length	128
% identity	52
NCBI Description	endoxyloglucan transferase - Arabidopsis thaliana >gi_469484_dbj_BAA03921_ (D16454) endo-xyloglucan transferase [Arabidopsis thaliana] >gi_4063757 (AC005561) endo-xyloglucan transferase [Arabidopsis thaliana]
Seq. No.	162808
Seq. ID	LIB3177-050-P1-K1-F8
Method	BLASTX
NCBI GI	g1345594
BLAST score	173
E value	2.0e-12
Match length	112
% identity	38
NCBI Description	14-3-3-LIKE PROTEIN GF14 KAPPA >gi_1022780 (U36447) GF14 Kappa isoform [Arabidopsis thaliana]
Seq. No.	162809
Seq. ID	LIB3177-050-P1-K1-F9
Method	BLASTX
NCBI GI	g4741960
BLAST score	307
E value	5.0e-28
Match length	113
% identity	56
NCBI Description	(AF134130) Lhcb6 protein [Arabidopsis thaliana]
Seq. No.	162810
Seq. ID	LIB3177-050-P1-K1-G1
Method	BLASTX
NCBI GI	g1389699
BLAST score	198
E value	3.0e-15
Match length	129
% identity	39
NCBI Description	(U38845) nitrilase 1 [Arabidopsis thaliana]
Seq. No.	162811
Seq. ID	LIB3177-050-P1-K1-G10
Method	BLASTX
NCBI GI	g3402684
BLAST score	252
E value	1.0e-21
Match length	108

% identity	56
NCBI Description	(AC004697) hypothetical protein [Arabidopsis thaliana]
Seq. No.	162812
Seq. ID	LIB3177-050-P1-K1-G11
Method	BLASTX
NCBI GI	g507808
BLAST score	229
E value	5.0e-19
Match length	112
% identity	47
NCBI Description	(D13987) phosphoenolpyruvate carboxylase [Brassica napus] >gi_743641_prf__2013218A phosphoenolpyruvate carboxylase [Brassica napus]
Seq. No.	162813
Seq. ID	LIB3177-050-P1-K1-G12
Method	BLASTX
NCBI GI	g1350680
BLAST score	266
E value	2.0e-23
Match length	112
% identity	54
NCBI Description	60S RIBOSOMAL PROTEIN L1
Seq. No.	162814
Seq. ID	LIB3177-050-P1-K1-G2
Method	BLASTX
NCBI GI	g2213595
BLAST score	325
E value	3.0e-30
Match length	122
% identity	54
NCBI Description	(AC000348) T7N9.15 [Arabidopsis thaliana]
Seq. No.	162815
Seq. ID	LIB3177-050-P1-K1-G4
Method	BLASTX
NCBI GI	g1934726
BLAST score	319
E value	2.0e-29
Match length	123
% identity	59
NCBI Description	(U95034) germin-like protein [Arabidopsis thaliana]
Seq. No.	162816
Seq. ID	LIB3177-050-P1-K1-G6
Method	BLASTN
NCBI GI	g3449314
BLAST score	48
E value	7.0e-18
Match length	288
% identity	79
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K22F20, complete sequence [Arabidopsis thaliana]
Seq. No.	162817

Seq. ID	LIB3177-050-P1-K1-G7
Method	BLASTX
NCBI GI	g2497733
BLAST score	211
E value	8.0e-17
Match length	114
% identity	43
NCBI Description	NONSPECIFIC LIPID-TRANSFER PROTEIN 1 PRECURSOR (LTP 1) >gi_1177796 (M80567) non-specific lipid transfer protein [Arabidopsis thaliana] >gi_3786018 (AC005499) unknown protein [Arabidopsis thaliana]

Seq. No.	162818
Seq. ID	LIB3177-050-P1-K1-H10
Method	BLASTN
NCBI GI	g2245031
BLAST score	120
E value	8.0e-61
Match length	288
% identity	85
NCBI Description	Arabidopsis thaliana DNA chromosome 4, ESSA I contig fragment No

Seq. No.	162819
Seq. ID	LIB3177-050-P1-K1-H11
Method	BLASTX
NCBI GI	g3128210
BLAST score	142
E value	1.0e-08
Match length	40
% identity	70
NCBI Description	(AC004077) putative cytochrome P450 protein [Arabidopsis thaliana] >gi_3337378 (AC004481) putative cytochrome P450 protein [Arabidopsis thaliana]

Seq. No.	162820
Seq. ID	LIB3177-050-P1-K1-H4
Method	BLASTX
NCBI GI	g4510407
BLAST score	60
E value	6.0e-11
Match length	65
% identity	62
NCBI Description	(AC006587) unknown protein [Arabidopsis thaliana]

Seq. No.	162821
Seq. ID	LIB3177-050-P1-K1-H5
Method	BLASTN
NCBI GI	g2696018
BLAST score	47
E value	3.0e-17
Match length	291
% identity	78
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MXC9, complete sequence [Arabidopsis thaliana]

Seq. No. 162822

Seq. ID LIB3177-050-P1-K1-H7
Method BLASTX
NCBI GI g1707008
BLAST score 278
E value 1.0e-24
Match length 115
% identity 53
NCBI Description (U78721) 30S ribosomal protein S5 isolog [Arabidopsis thaliana]

Seq. No. 162823
Seq. ID LIB3177-050-P1-K1-H8
Method BLASTX
NCBI GI g1169201
BLAST score 243
E value 1.0e-20
Match length 122
% identity 49
NCBI Description DNA-DAMAGE-REPAIR/TOLERATION PROTEIN DRT112 PRECURSOR >gi_421830_pir__S33707 DRT112 protein - Arabidopsis thaliana >gi_166696 (M98456) DRT112 [Arabidopsis thaliana]

Seq. No. 162824
Seq. ID LIB3177-050-P1-K2-A11
Method BLASTX
NCBI GI g4454014
BLAST score 527
E value 8.0e-54
Match length 126
% identity 87
NCBI Description (AL035396) putative protein [Arabidopsis thaliana]

Seq. No. 162825
Seq. ID LIB3177-050-P1-K2-A2
Method BLASTX
NCBI GI g3128213
BLAST score 729
E value 1.0e-77
Match length 143
% identity 99
NCBI Description (AC004077) hypothetical protein [Arabidopsis thaliana]

Seq. No. 162826
Seq. ID LIB3177-050-P1-K2-A3
Method BLASTX
NCBI GI g4337175
BLAST score 451
E value 3.0e-45
Match length 90
% identity 98
NCBI Description (AC006416) ESTs gb_T20589, gb_T04648, gb_AA597906, gb_T04111, gb_R84180, gb_R65428, gb_T44439, gb_T76570, gb_R90004, gb_T45020, gb_T42457, gb_T20921, gb_AA042762 and gb_AA720210 come from this gene. [Arabidopsis thaliana]

Seq. No. 162827
Seq. ID LIB3177-050-P1-K2-B11

Method	BLASTX
NCBI GI	g2119846
BLAST score	259
E value	7.0e-23
Match length	73
% identity	70
NCBI Description	chlorophyll a/b-binding protein type I precursor Lhb1B2 - Arabidopsis thaliana >gi_16364_emb_CAA45790_ (X64460) photosystem II type I chlorophyll a /b binding protein [Arabidopsis thaliana] >gi_3128230 (AC004077) photosystem II type I chlorophyll a/b binding protein [Arabidopsis thaliana] >gi_3337371 (AC004481) photosystem II type I chlorophyll a/b binding protein [Arabidopsis thaliana]

Seq. No.	162828
Seq. ID	LIB3177-050-P1-K2-B2
Method	BLASTX
NCBI GI	g1175011
BLAST score	396
E value	9.0e-39
Match length	77
% identity	97
NCBI Description	PLASMA MEMBRANE INTRINSIC PROTEIN 1B (TRANSMEMBRANE PROTEIN A) (TMP-A) >gi_296085_emb_CAA48356_ (X68293) transmembrane protein [Arabidopsis thaliana] >gi_3386599 (AC004665) plasma membrane intrinsic protein 1B [Arabidopsis thaliana]

Seq. No.	162829
Seq. ID	LIB3177-050-P1-K2-B7
Method	BLASTX
NCBI GI	g2262173
BLAST score	526
E value	9.0e-54
Match length	136
% identity	79
NCBI Description	(AC002329) NADPH thioredoxin reductase [Arabidopsis thaliana]

Seq. No.	162830
Seq. ID	LIB3177-050-P1-K2-C12
Method	BLASTN
NCBI GI	g4455168
BLAST score	108
E value	7.0e-54
Match length	281
% identity	94
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F10M10 (ESSAII project)

Seq. No.	162831
Seq. ID	LIB3177-050-P1-K2-C2
Method	BLASTX
NCBI GI	g115783
BLAST score	456
E value	1.0e-45
Match length	95
% identity	92

NCBI Description	CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR (CAB-140) (LHCP) >gi_16376_emb_CAA27543_ (X03909) chlorophyll a/b binding protein (LHCP AB 140) [Arabidopsis thaliana]
Seq. No.	162832
Seq. ID	LIB3177-050-P1-K2-C3
Method	BLASTN
NCBI GI	g2245126
BLAST score	124
E value	2.0e-63
Match length	302
% identity	96
NCBI Description	Arabidopsis thaliana DNA chromosome 4, ESSA I contig fragment No
Seq. No.	162833
Seq. ID	LIB3177-050-P1-K2-C5
Method	BLASTN
NCBI GI	g2062153
BLAST score	44
E value	7.0e-16
Match length	127
% identity	43
NCBI Description	Arabidopsis thaliana chromosome III BAC T02O04 genomic sequence, complete sequence [Arabidopsis thaliana]
Seq. No.	162834
Seq. ID	LIB3177-050-P1-K2-C6
Method	BLASTX
NCBI GI	g166702
BLAST score	151
E value	2.0e-10
Match length	50
% identity	64
NCBI Description	(M64114) glyceraldehyde 3-phosphate dehydrogenase A subunit [Arabidopsis thaliana]
Seq. No.	162835
Seq. ID	LIB3177-050-P1-K2-C8
Method	BLASTX
NCBI GI	g16374
BLAST score	502
E value	6.0e-51
Match length	95
% identity	100
NCBI Description	(X03908) chlorophyll a/b binding protein (LHCP AB 180) [Arabidopsis thaliana]
Seq. No.	162836
Seq. ID	LIB3177-050-P1-K2-D11
Method	BLASTX
NCBI GI	g115767
BLAST score	615
E value	3.0e-64
Match length	129
% identity	89

NCBI Description	CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR (CAB-165/180) (LHCP) >gi_81603_pir__A29280 chlorophyll a/b-binding protein ab165 - Arabidopsis thaliana >gi_16368_emb_CAA27540_ (X03907) chlorophyll a/b binding protein (LHCP AB 65) [Arabidopsis thaliana] >gi_16372_emb_CAA27541_ (X03908) chlorophyll a/b binding protein (LHCP AB 180) [Arabidopsis thaliana]
Seq. No.	162837
Seq. ID	LIB3177-050-P1-K2-D2
Method	BLASTN
NCBI GI	g4468103
BLAST score	65
E value	8.0e-29
Match length	77
% identity	96
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone M3E9 (ESSA project)
Seq. No.	162838
Seq. ID	LIB3177-050-P1-K2-D3
Method	BLASTX
NCBI GI	g132074
BLAST score	685
E value	2.0e-72
Match length	135
% identity	95
NCBI Description	RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN 1A PRECURSOR (RUBISCO SMALL SUBUNIT 1A) >gi_68063_pir__RKMUA1 ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain A1 precursor - Arabidopsis thaliana
Seq. No.	162839
Seq. ID	LIB3177-050-P1-K2-D4
Method	BLASTN
NCBI GI	g4038029
BLAST score	65
E value	4.0e-28
Match length	287
% identity	97
NCBI Description	Arabidopsis thaliana chromosome II BAC F5O4 genomic sequence, complete sequence [Arabidopsis thaliana]
Seq. No.	162840
Seq. ID	LIB3177-050-P1-K2-D5
Method	BLASTX
NCBI GI	g2661422
BLAST score	355
E value	9.0e-34
Match length	120
% identity	68
NCBI Description	(AJ001342) Putative S-phase-specific ribosomal protein [Arabidopsis thaliana] >gi_3096936_emb_CAA18846.1_ (AL023094) Putative S-phase-specific ribosomal protein [Arabidopsis thaliana]
Seq. No.	162841

Seq. ID	LIB3177-050-P1-K2-D7
Method	BLASTX
NCBI GI	g2581783
BLAST score	235
E value	7.0e-39
Match length	96
% identity	91
NCBI Description	(U94998) class 1 non-symbiotic hemoglobin [Arabidopsis thaliana] >gi_4678203_gb_AAD26949.1_AC007134_7 (AC007134) class 1 non-symbiotic hemoglobin (AHB1) [Arabidopsis thaliana]

Seq. No.	162842
Seq. ID	LIB3177-050-P1-K2-E2
Method	BLASTN
NCBI GI	g3928074
BLAST score	153
E value	1.0e-80
Match length	339
% identity	98
NCBI Description	Arabidopsis thaliana chromosome II BAC T7F6 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	162843
Seq. ID	LIB3177-050-P1-K2-E4
Method	BLASTN
NCBI GI	g4206766
BLAST score	97
E value	2.0e-47
Match length	169
% identity	89
NCBI Description	Arabidopsis thaliana glycine-rich protein 3 short isoform (GRP3S) mRNA, complete cds

Seq. No.	162844
Seq. ID	LIB3177-050-P1-K2-E7
Method	BLASTX
NCBI GI	g2921094
BLAST score	479
E value	5.0e-50
Match length	120
% identity	88
NCBI Description	(AF018174) thioredoxin-f [Brassica napus]

Seq. No.	162845
Seq. ID	LIB3177-050-P1-K2-E8
Method	BLASTX
NCBI GI	g1063415
BLAST score	195
E value	1.0e-15
Match length	44
% identity	89
NCBI Description	(L40948) K+ channel protein [Arabidopsis thaliana]

Seq. No.	162846
Seq. ID	LIB3177-050-P1-K2-F1
Method	BLASTX

NCBI GI	g115385
BLAST score	282
E value	2.0e-25
Match length	69
% identity	75
NCBI Description	CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR (CAB-4) (LHCP) >gi_166646 (M63931) light-harvesting chlorophyll a/b binding protein [Arabidopsis thaliana]

Seq. No.	162847
Seq. ID	LIB3177-050-P1-K2-F11
Method	BLASTX
NCBI GI	g1769905
BLAST score	99
E value	1.0e-26
Match length	128
% identity	59
NCBI Description	(X98108) 23 kDa polypeptide of oxygen-evolving comlex (OEC) [Arabidopsis thaliana]

Seq. No.	162848
Seq. ID	LIB3177-050-P1-K2-F12
Method	BLASTN
NCBI GI	g1916612
BLAST score	47
E value	1.0e-17
Match length	143
% identity	90
NCBI Description	Arabidopsis thaliana acetyl-CoA carboxylase biotin-containing subunit (CAC1) gene, nuclear gene encoding chloroplast protein, complete cds

Seq. No.	162849
Seq. ID	LIB3177-050-P1-K2-F2
Method	BLASTX
NCBI GI	g4585935
BLAST score	571
E value	4.0e-59
Match length	112
% identity	95
NCBI Description	(AC007211) putative chlorophyll A/B binding protein [Arabidopsis thaliana] >gi_4741946_gb_AAD28770.1_AF134123_1 (AF134123) Lhcb2 protein [Arabidopsis thaliana]

Seq. No.	162850
Seq. ID	LIB3177-050-P1-K2-F3
Method	BLASTN
NCBI GI	g4589434
BLAST score	135
E value	9.0e-70
Match length	443
% identity	99
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MNJ7, complete sequence

Seq. No.	162851
Seq. ID	LIB3177-050-P1-K2-F4

Method	BLASTX
NCBI GI	g1175013
BLAST score	168
E value	4.0e-12
Match length	74
% identity	54
NCBI Description	PLASMA MEMBRANE INTRINSIC PROTEIN 2A >gi_629542_pir__S44084 plasma membrane intrinsic protein 2a - Arabidopsis thaliana >gi_472877_emb_CAA53477_ (X75883) plasma membrane intrinsic protein 2a [Arabidopsis thaliana]

Seq. No.	162852
Seq. ID	LIB3177-050-P1-K2-F5
Method	BLASTX
NCBI GI	g231660
BLAST score	329
E value	1.0e-30
Match length	146
% identity	47
NCBI Description	HYPOTHETICAL 226 KD PROTEIN (ORF 1901)

Seq. No.	162853
Seq. ID	LIB3177-050-P1-K2-F6
Method	BLASTX
NCBI GI	g231660
BLAST score	155
E value	2.0e-10
Match length	57
% identity	47
NCBI Description	HYPOTHETICAL 226 KD PROTEIN (ORF 1901)

Seq. No.	162854
Seq. ID	LIB3177-050-P1-K2-F7
Method	BLASTX
NCBI GI	g541858
BLAST score	280
E value	8.0e-34
Match length	90
% identity	78
NCBI Description	endoxyloglucan transferase - Arabidopsis thaliana >gi_469484_dbj_BAA03921_ (D16454) endo-xyloglucan transferase [Arabidopsis thaliana] >gi_4063757 (AC005561) endo-xyloglucan transferase [Arabidopsis thaliana]

Seq. No.	162855
Seq. ID	LIB3177-050-P1-K2-F8
Method	BLASTN
NCBI GI	g1022779
BLAST score	34
E value	2.0e-10
Match length	66
% identity	88
NCBI Description	Arabidopsis thaliana GF14 Kappa isoform mRNA, complete cds

Seq. No.	162856
Seq. ID	LIB3177-050-P1-K2-F9
Method	BLASTN

NCBI GI	g4741959
BLAST score	95
E value	4.0e-46
Match length	234
% identity	90
NCBI Description	Arabidopsis thaliana Lhcb6 protein (Lhcb6) mRNA, complete cds

Seq. No.	162857
Seq. ID	LIB3177-050-P1-K2-G1
Method	BLASTX
NCBI GI	g417381
BLAST score	503
E value	4.0e-53
Match length	125
% identity	90
NCBI Description	NITRILASE 1 >gi_99738_pir__S22398 nitrilase (EC 3.5.5.1) - Arabidopsis thaliana >gi_16400_emb_CAA45041_ (X63445) nitrilase I [Arabidopsis thaliana]

Seq. No.	162858
Seq. ID	LIB3177-050-P1-K2-G10
Method	BLASTX
NCBI GI	g3402684
BLAST score	532
E value	8.0e-62
Match length	143
% identity	87
NCBI Description	(AC004697) hypothetical protein [Arabidopsis thaliana]

Seq. No.	162859
Seq. ID	LIB3177-050-P1-K2-G11
Method	BLASTX
NCBI GI	g3402684
BLAST score	235
E value	7.0e-20
Match length	95
% identity	57
NCBI Description	(AC004697) hypothetical protein [Arabidopsis thaliana]

Seq. No.	162860
Seq. ID	LIB3177-050-P1-K2-G12
Method	BLASTX
NCBI GI	g1350680
BLAST score	356
E value	7.0e-38
Match length	118
% identity	75
NCBI Description	60S RIBOSOMAL PROTEIN L1

Seq. No.	162861
Seq. ID	LIB3177-050-P1-K2-G2
Method	BLASTX
NCBI GI	g2213595
BLAST score	604
E value	7.0e-63
Match length	143

% identity	83
NCBI Description	(AC000348) T7N9.15 [Arabidopsis thaliana]

Seq. No.	162862
Seq. ID	LIB3177-050-P1-K2-G4
Method	BLASTX
NCBI GI	g1934726
BLAST score	481
E value	2.0e-48
Match length	111
% identity	87
NCBI Description	(U95034) germin-like protein [Arabidopsis thaliana]

Seq. No.	162863
Seq. ID	LIB3177-050-P1-K2-G6
Method	BLASTX
NCBI GI	g3123295
BLAST score	391
E value	1.0e-51
Match length	133
% identity	56
NCBI Description	CALMODULIN-RELATED PROTEIN 2, TOUCH-INDUCED >gi_2583169 (AF026473) calmodulin-related protein [Arabidopsis thaliana]

Seq. No.	162864
Seq. ID	LIB3177-050-P1-K2-G7
Method	BLASTX
NCBI GI	g2497733
BLAST score	525
E value	1.0e-53
Match length	118
% identity	87
NCBI Description	NONSPECIFIC LIPID-TRANSFER PROTEIN 1 PRECURSOR (LTP 1) >gi_1177796 (M80567) non-specific lipid transfer protein [Arabidopsis thaliana] >gi_3786018 (AC005499) unknown protein [Arabidopsis thaliana]

Seq. No.	162865
Seq. ID	LIB3177-050-P1-K2-G8
Method	BLASTX
NCBI GI	g1750190
BLAST score	139
E value	1.0e-08
Match length	26
% identity	96
NCBI Description	(U79744) putative serine/threonine protein kinase [Arabidopsis thaliana]

Seq. No.	162866
Seq. ID	LIB3177-050-P1-K2-H10
Method	BLASTN
NCBI GI	g2245031
BLAST score	48
E value	1.0e-18
Match length	71
% identity	93

NCBI Description	Arabidopsis thaliana DNA chromosome 4, ESSA I contig fragment No
Seq. No.	162867
Seq. ID	LIB3177-050-P1-K2-H11
Method	BLASTX
NCBI GI	g3128210
BLAST score	307
E value	4.0e-28
Match length	65
% identity	95
NCBI Description	(AC004077) putative cytochrome P450 protein [Arabidopsis thaliana] >gi_3337378 (AC004481) putative cytochrome P450 protein [Arabidopsis thaliana]
Seq. No.	162868
Seq. ID	LIB3177-050-P1-K2-H3
Method	BLASTN
NCBI GI	g3746567
BLAST score	141
E value	8.0e-74
Match length	167
% identity	96
NCBI Description	Arabidopsis thaliana branched-chain alpha-keto acid decarboxylase E1 beta subunit (BCDH beta1) mRNA, complete cds
Seq. No.	162869
Seq. ID	LIB3177-050-P1-K2-H4
Method	BLASTN
NCBI GI	g4510392
BLAST score	80
E value	1.0e-37
Match length	80
% identity	100
NCBI Description	Arabidopsis thaliana chromosome II BAC T17D12 genomic sequence, complete sequence
Seq. No.	162870
Seq. ID	LIB3177-050-P1-K2-H8
Method	BLASTX
NCBI GI	g1169201
BLAST score	548
E value	3.0e-56
Match length	137
% identity	83
NCBI Description	DNA-DAMAGE-REPAIR/TOLERATION PROTEIN DRT112 PRECURSOR >gi_421830_pir__S33707 DRT112 protein - Arabidopsis thaliana >gi_166696 (M98456) DRT112 [Arabidopsis thaliana]
Seq. No.	162871
Seq. ID	LIB3177-050-P1-K2-H9
Method	BLASTX
NCBI GI	g1169201
BLAST score	323
E value	6.0e-30
Match length	99

% identity	71
NCBI Description	DNA-DAMAGE-REPAIR/TOLERATION PROTEIN DRT112 PRECURSOR >gi_421830_pir__S33707 DRT112 protein - Arabidopsis thaliana >gi_166696 (M98456) DRT112 [Arabidopsis thaliana]

Seq. No.	162872
Seq. ID	LIB3177-052-P1-K1-A1
Method	BLASTX
NCBI GI	g2119846
BLAST score	442
E value	3.0e-44
Match length	83
% identity	100
NCBI Description	chlorophyll a/b-binding protein type I precursor Lhb1B2 - Arabidopsis thaliana >gi_16364_emb_CAA45790_ (X64460) photosystem II type I chlorophyll a /b binding protein [Arabidopsis thaliana] >gi_3128230 (AC004077) photosystem II type I chlorophyll a/b binding protein [Arabidopsis thaliana] >gi_3337371 (AC004481) photosystem II type I chlorophyll a/b binding protein [Arabidopsis thaliana]

Seq. No.	162873
Seq. ID	LIB3177-052-P1-K1-A2
Method	BLASTX
NCBI GI	g4204285
BLAST score	401
E value	4.0e-39
Match length	124
% identity	60
NCBI Description	(AC003027) lcl_prt_seq No definition line found [Arabidopsis thaliana]

Seq. No.	162874
Seq. ID	LIB3177-052-P1-K1-A3
Method	BLASTN
NCBI GI	g3985955
BLAST score	199
E value	1.0e-108
Match length	333
% identity	94
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MTH16, complete sequence [Arabidopsis thaliana]

Seq. No.	162875
Seq. ID	LIB3177-052-P1-K1-A4
Method	BLASTX
NCBI GI	g117238
BLAST score	590
E value	3.0e-61
Match length	137
% identity	87
NCBI Description	MAGNESIUM-CHELATASE SUBUNIT CHLI PRECURSOR (PROTEIN CS/CH-42) (MG-PROTOPORPHYRIN IX CHELATASE) >gi_81656_pir__S12785 protein ch-42 precursor, chloroplast - Arabidopsis thaliana >gi_1020100_emb_CAA62754_ (X91411) protoporphyrin-IX Mg-chetalase [Arabidopsis thaliana] >gi_2832653_emb_CAA16728_ (AL021710) protein ch-42

	precursor, chloroplast [Arabidopsis thaliana] >gi_4490290_emb_CAB38561.1_ (X51799) chloroplast protein [Arabidopsis thaliana] >gi_228771_prf__1811226A ccsA gene [Euglena gracilis]
Seq. No.	162876
Seq. ID	LIB3177-052-P1-K1-A8
Method	BLASTX
NCBI GI	g4006898
BLAST score	510
E value	5.0e-52
Match length	108
% identity	94
NCBI Description	(Z99708) splicing factor-like protein [Arabidopsis thaliana]
Seq. No.	162877
Seq. ID	LIB3177-052-P1-K1-B1
Method	BLASTX
NCBI GI	g543841
BLAST score	508
E value	1.0e-51
Match length	103
% identity	96
NCBI Description	ADP-RIBOSYLATION FACTOR 1 >gi_322518_pir__S28875 ADP-ribosylation factor 1 - Arabidopsis thaliana >gi_166586 (M95166) ADP-ribosylation factor [Arabidopsis thaliana] >gi_2275195 (AC002337) ADP-ribosylation factor [Arabidopsis thaliana] >gi_4630747_gb_AAD26597.1_AC007236_2 (AC007236) ADP-ribosylation factor [Arabidopsis thaliana]
Seq. No.	162878
Seq. ID	LIB3177-052-P1-K1-B10
Method	BLASTX
NCBI GI	g4503503
BLAST score	228
E value	6.0e-19
Match length	116
% identity	42
NCBI Description	eukaryotic translation initiation factor 2B >gi_2494303_sp_Q14232_E2BA_HUMAN TRANSLATION INITIATION FACTOR EIF-2B ALPHA SUBUNIT (EIF-2B GDP-GTP EXCHANGE FACTOR) >gi_1200232_emb_CAA64950_ (X95648) alfa subunit [Homo sapiens]
Seq. No.	162879
Seq. ID	LIB3177-052-P1-K1-B12
Method	BLASTX
NCBI GI	g1076367
BLAST score	652
E value	2.0e-68
Match length	133
% identity	91
NCBI Description	peptidylprolyl isomerase (EC 5.2.1.8) ROC1 - Arabidopsis thaliana
Seq. No.	162880

Seq. ID	LIB3177-052-P1-K1-B2
Method	BLASTX
NCBI GI	g115767
BLAST score	678
E value	4.0e-72
Match length	141
% identity	99
NCBI Description	CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR (CAB-165/180) (LHCP) >gi_81603_pir__A29280 chlorophyll a/b-binding protein ab165 - Arabidopsis thaliana >gi_16368_emb_CAA27540_ (X03907) chlorophyll a/b binding protein (LHCP AB 65) [Arabidopsis thaliana] >gi_16372_emb_CAA27541_ (X03908) chlorophyll a/b binding protein (LHCP AB 180) [Arabidopsis thaliana]

Seq. No.	162881
Seq. ID	LIB3177-052-P1-K1-B3
Method	BLASTX
NCBI GI	g4204260
BLAST score	275
E value	3.0e-24
Match length	63
% identity	87
NCBI Description	(AC005223) 25568 [Arabidopsis thaliana]

Seq. No.	162882
Seq. ID	LIB3177-052-P1-K1-B4
Method	BLASTX
NCBI GI	g2498887
BLAST score	161
E value	5.0e-11
Match length	78
% identity	40
NCBI Description	3-OXO-5-ALPHA-STEROID 4-DEHYDROGENASE 1 (STEROID 5-ALPHA-REDUCTASE 1) (SR TYPE 1) >gi_999036_bbs_164548 (S77162) steroid 5 alpha-reductase type 1 isoenzyme, SR type 1 [Cynomolgus monkeys, prostate, Peptide, 263 aa] [Macaca fascicularis]

Seq. No.	162883
Seq. ID	LIB3177-052-P1-K1-B6
Method	BLASTX
NCBI GI	g4512625
BLAST score	671
E value	1.0e-70
Match length	137
% identity	99
NCBI Description	(AC004793) ESTs gb_T20423, gb_AA712864, gb_H76323 and gb_Z25560 come from this gene. [Arabidopsis thaliana]

Seq. No.	162884
Seq. ID	LIB3177-052-P1-K1-B7
Method	BLASTX
NCBI GI	g132110
BLAST score	658
E value	3.0e-69
Match length	122

% identity	98
NCBI Description	RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN 3B PRECURSOR (RUBISCO SMALL SUBUNIT 3B) >gi_68060_pir__RKMUB3 ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain B3 precursor - Arabidopsis thaliana >gi_16195_emb_CAA32702_ (X14564) ribulose bisphosphate carboxylase [Arabidopsis thaliana]
Seq. No.	162885
Seq. ID	LIB3177-052-P1-K1-B9
Method	BLASTX
NCBI GI	g2062156
BLAST score	416
E value	6.0e-41
Match length	108
% identity	30
NCBI Description	(AC001645) jasmonate inducible protein isolog [Arabidopsis thaliana]
Seq. No.	162886
Seq. ID	LIB3177-052-P1-K1-C1
Method	BLASTX
NCBI GI	g4741940
BLAST score	578
E value	8.0e-60
Match length	110
% identity	66
NCBI Description	(AF134120) Lhca2 protein [Arabidopsis thaliana]
Seq. No.	162887
Seq. ID	LIB3177-052-P1-K1-C10
Method	BLASTN
NCBI GI	g3241926
BLAST score	137
E value	4.0e-71
Match length	297
% identity	95
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MSG15, complete sequence [Arabidopsis thaliana]
Seq. No.	162888
Seq. ID	LIB3177-052-P1-K1-C11
Method	BLASTX
NCBI GI	g1362162
BLAST score	542
E value	1.0e-55
Match length	157
% identity	64
NCBI Description	beta-glucosidase BGQ60 precursor - barley >gi_804656 (L41869) beta-glucosidase [Hordeum vulgare]
Seq. No.	162889
Seq. ID	LIB3177-052-P1-K1-C12
Method	BLASTX
NCBI GI	g4204274
BLAST score	729
E value	2.0e-77

Match length	133
% identity	98
NCBI Description	(AC004146) ribulose bisphosphate carboxylase, small subunit [Arabidopsis thaliana]

Seq. No.	162890
Seq. ID	LIB3177-052-P1-K1-C2
Method	BLASTX
NCBI GI	g1737218
BLAST score	714
E value	7.0e-76
Match length	120
% identity	100
NCBI Description	(U79959) vacuolar sorting receptor homolog [Arabidopsis thaliana]

Seq. No.	162891
Seq. ID	LIB3177-052-P1-K1-C3
Method	BLASTX
NCBI GI	g3292836
BLAST score	457
E value	9.0e-46
Match length	100
% identity	94
NCBI Description	(AL031018) gamma-glutamylcysteine synthetase [Arabidopsis thaliana] >gi_4262277_gb_AAD14544_ (AF068299) gamma-glutamylcysteine synthetase [Arabidopsis thaliana]

Seq. No.	162892
Seq. ID	LIB3177-052-P1-K1-D1
Method	BLASTX
NCBI GI	g3286693
BLAST score	741
E value	6.0e-79
Match length	148
% identity	99
NCBI Description	(Y15433) 33 kDa polypeptide of oxygen-evolving complex (OEC) in photosystem II [Arabidopsis thaliana]

Seq. No.	162893
Seq. ID	LIB3177-052-P1-K1-D10
Method	BLASTX
NCBI GI	g4586256
BLAST score	584
E value	2.0e-60
Match length	146
% identity	79
NCBI Description	(AL049640) probable photosystem I chain XI precursor [Arabidopsis thaliana]

Seq. No.	162894
Seq. ID	LIB3177-052-P1-K1-D11
Method	BLASTX
NCBI GI	g3928103
BLAST score	405
E value	1.0e-39
Match length	98

% identity	85
NCBI Description	(AC005770) putative water channel protein [Arabidopsis thaliana]
Seq. No.	162895
Seq. ID	LIB3177-052-P1-K1-D2
Method	BLASTX
NCBI GI	g131381
BLAST score	436
E value	2.0e-43
Match length	109
% identity	84
NCBI Description	OXYGEN-EVOLVING ENHANCER PROTEIN 1 PRECURSOR (OEE1) (33 KD SUBUNIT OF OXYGEN EVOLVING SYSTEM OF PHOTOSYSTEM II) (33 KD THYLAKOID MEMBRANE PROTEIN) >gi_99745_pir__S11852 photosystem II oxygen-evolving complex protein 1 precursor - Arabidopsis thaliana >gi_22571_emb_CAA36675_ (X52428) 33 kDa oxygen-evolving protein [Arabidopsis thaliana]
Seq. No.	162896
Seq. ID	LIB3177-052-P1-K1-D3
Method	BLASTN
NCBI GI	g2264312
BLAST score	191
E value	1.0e-103
Match length	464
% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MOK16, complete sequence [Arabidopsis thaliana]
Seq. No.	162897
Seq. ID	LIB3177-052-P1-K1-D4
Method	BLASTX
NCBI GI	g4006913
BLAST score	209
E value	2.0e-16
Match length	59
% identity	64
NCBI Description	(Z99708) hypothetical protein [Arabidopsis thaliana]
Seq. No.	162898
Seq. ID	LIB3177-052-P1-K1-D6
Method	BLASTN
NCBI GI	g4006885
BLAST score	200
E value	1.0e-108
Match length	297
% identity	95
NCBI Description	Arabidopsis thaliana DNA chromosome 4, ESSA I AP2 contig fragment No
Seq. No.	162899
Seq. ID	LIB3177-052-P1-K1-D7
Method	BLASTX
NCBI GI	g132102
BLAST score	626
E value	2.0e-65

Match length	124
% identity	94
NCBI Description	RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN 2B PRECURSOR (RUBISCO SMALL SUBUNIT 2B) >gi_68061_pir__RKMUB2 ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain B2 precursor - Arabidopsis thaliana >gi_16194_emb_CAA32701_ (X14564) ribulose bisphosphate carboxylase [Arabidopsis thaliana]

Seq. No.	162900
Seq. ID	LIB3177-052-P1-K1-D8
Method	BLASTX
NCBI GI	g4371284
BLAST score	52
E value	1.0e-64
Match length	129
% identity	98
NCBI Description	(AC006260) putative plasma membrane intrinsic protein 2B [Arabidopsis thaliana]

Seq. No.	162901
Seq. ID	LIB3177-052-P1-K1-D9
Method	BLASTX
NCBI GI	g2244847
BLAST score	671
E value	1.0e-70
Match length	153
% identity	87
NCBI Description	(Z97337) hydroxyproline-rich glycoprotein homolog [Arabidopsis thaliana]

Seq. No.	162902
Seq. ID	LIB3177-052-P1-K1-E10
Method	BLASTX
NCBI GI	g4589964
BLAST score	555
E value	4.0e-57
Match length	101
% identity	99
NCBI Description	(AC007169) delta 9 desaturase [Arabidopsis thaliana]

Seq. No.	162903
Seq. ID	LIB3177-052-P1-K1-E11
Method	BLASTX
NCBI GI	g417381
BLAST score	853
E value	5.0e-92
Match length	156
% identity	99
NCBI Description	NITRILASE 1 >gi_99738_pir__S22398 nitrilase (EC 3.5.5.1) - Arabidopsis thaliana >gi_16400_emb_CAA45041_ (X63445) nitrilase I [Arabidopsis thaliana]

Seq. No.	162904
Seq. ID	LIB3177-052-P1-K1-E4
Method	BLASTX
NCBI GI	g282865

BLAST score	652
E value	2.0e-68
Match length	133
% identity	92
NCBI Description	chlorophyll a/b-binding protein - Arabidopsis thaliana >gi_16207_emb_CAA39534_ (X56062) chlorophyll A/B-binding protein [Arabidopsis thaliana] >gi_166644 (M85150) chlorophyll a/b-binding protein [Arabidopsis thaliana] >gi_4678304_emb_CAB41095.1_ (AL049655) chlorophyll a/b-binding protein [Arabidopsis thaliana]

Seq. No.	162905
Seq. ID	LIB3177-052-P1-K1-E6
Method	BLASTX
NCBI GI	g3914442
BLAST score	545
E value	7.0e-56
Match length	145
% identity	75
NCBI Description	PHOTOSYSTEM I REACTION CENTRE SUBUNIT VI PRECURSOR (LIGHT-HARVESTING COMPLEX I 11 KD PROTEIN) (PSI-H) >gi_1916350 (U92504) PSI-H subunit [Brassica rapa]

Seq. No.	162906
Seq. ID	LIB3177-052-P1-K1-E7
Method	BLASTX
NCBI GI	g2827469
BLAST score	248
E value	4.0e-21
Match length	144
% identity	35
NCBI Description	(AF044255) NOSA [Dictyostelium discoideum]

Seq. No.	162907
Seq. ID	LIB3177-052-P1-K1-E9
Method	BLASTX
NCBI GI	g2275216
BLAST score	274
E value	3.0e-24
Match length	64
% identity	83
NCBI Description	(AC002337) cytochrome c oxidase Vc subunit isolog [Arabidopsis thaliana]

Seq. No.	162908
Seq. ID	LIB3177-052-P1-K1-F11
Method	BLASTX
NCBI GI	g166702
BLAST score	319
E value	7.0e-30
Match length	78
% identity	83
NCBI Description	(M64114) glyceraldehyde 3-phosphate dehydrogenase A subunit [Arabidopsis thaliana]

Seq. No.	162909
Seq. ID	LIB3177-052-P1-K1-F2

Method	BLASTN
NCBI GI	g4757414
BLAST score	363
E value	0.0e+00
Match length	445
% identity	95
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MYF24, complete sequence

Seq. No.	162910
Seq. ID	LIB3177-052-P1-K1-F3
Method	BLASTX
NCBI GI	g3158376
BLAST score	285
E value	2.0e-25
Match length	91
% identity	62
NCBI Description	(AF035385) unknown [Arabidopsis thaliana]

Seq. No.	162911
Seq. ID	LIB3177-052-P1-K1-F4
Method	BLASTX
NCBI GI	g3688799
BLAST score	693
E value	3.0e-73
Match length	140
% identity	99
NCBI Description	(AF057137) gamma tonoplast intrinsic protein 2 [Arabidopsis thaliana]

Seq. No.	162912
Seq. ID	LIB3177-052-P1-K1-G10
Method	BLASTX
NCBI GI	g81601
BLAST score	148
E value	5.0e-10
Match length	52
% identity	65
NCBI Description	chaperonin 60 beta - Arabidopsis thaliana

Seq. No.	162913
Seq. ID	LIB3177-052-P1-K1-G11
Method	BLASTX
NCBI GI	g421826
BLAST score	628
E value	1.0e-65
Match length	143
% identity	83
NCBI Description	chlorophyll a/b-binding protein CP29 - Arabidopsis thaliana >gi_298036_emb_CAA50712_ (X71878) CP29 [Arabidopsis thaliana]

Seq. No.	162914
Seq. ID	LIB3177-052-P1-K1-G12
Method	BLASTN
NCBI GI	g3063438
BLAST score	110

E value	3.0e-55
Match length	165
% identity	90
NCBI Description	Complete sequence of Arabidopsis F22013, complete sequence [Arabidopsis thaliana]

Seq. No.	162915
Seq. ID	LIB3177-052-P1-K1-G2
Method	BLASTX
NCBI GI	g4512709
BLAST score	550
E value	2.0e-56
Match length	145
% identity	79
NCBI Description	(AC006569) putative photosystem I reaction center subunit IV precursor [Arabidopsis thaliana]

Seq. No.	162916
Seq. ID	LIB3177-052-P1-K1-G3
Method	BLASTX
NCBI GI	g2288981
BLAST score	529
E value	5.0e-54
Match length	147
% identity	71
NCBI Description	(AC002335) calcium binding protein isolog [Arabidopsis thaliana] >gi_3763938 (AC004450) putative calcium binding protein [Arabidopsis thaliana]

Seq. No.	162917
Seq. ID	LIB3177-052-P1-K1-G4
Method	BLASTX
NCBI GI	g4633131
BLAST score	398
E value	1.0e-38
Match length	76
% identity	100
NCBI Description	(AF110407) ATP sulfurylase precursor [Arabidopsis thaliana] >gi_4803653_emb_CAB42640.1_ (AJ012586) sulfate adenylyltransferase [Arabidopsis thaliana]

Seq. No.	162918
Seq. ID	LIB3177-052-P1-K1-G5
Method	BLASTN
NCBI GI	g3176701
BLAST score	223
E value	1.0e-122
Match length	444
% identity	99
NCBI Description	Arabidopsis thaliana chromosome II BAC T20K24 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	162919
Seq. ID	LIB3177-052-P1-K1-G8
Method	BLASTX
NCBI GI	g1703200
BLAST score	284

E value	2.0e-25
Match length	97
% identity	63
NCBI Description	PROTEIN KINASE AFC2 >gi_601789 (U16177) protein kinase [Arabidopsis thaliana] >gi_642130_dbj_BAA08214_ (D45353) protein kinase [Arabidopsis thaliana] >gi_4220516_emb_CAA22989_ (AL035356) protein kinase (AFC2) [Arabidopsis thaliana]

Seq. No.	162920
Seq. ID	LIB3177-052-P1-K1-G9
Method	BLASTX
NCBI GI	g115767
BLAST score	666
E value	4.0e-70
Match length	150
% identity	85
NCBI Description	CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR (CAB-165/180) (LHCP) >gi_81603_pir__A29280 chlorophyll a/b-binding protein ab165 - Arabidopsis thaliana >gi_16368_emb_CAA27540_ (X03907) chlorophyll a/b binding protein (LHCP AB 65) [Arabidopsis thaliana] >gi_16372_emb_CAA27541_ (X03908) chlorophyll a/b binding protein (LHCP AB 180) [Arabidopsis thaliana]

Seq. No.	162921
Seq. ID	LIB3177-052-P1-K1-H1
Method	BLASTX
NCBI GI	g4309736
BLAST score	665
E value	6.0e-70
Match length	145
% identity	91
NCBI Description	(AC006439) hypothetical protein [Arabidopsis thaliana]

Seq. No.	162922
Seq. ID	LIB3177-052-P1-K1-H10
Method	BLASTX
NCBI GI	g119723
BLAST score	230
E value	2.0e-19
Match length	65
% identity	77
NCBI Description	FRUCTOSE-1,6-BISPHOSPHATASE, CHLOROPLAST PRECURSOR (D-FRUCTOSE-1,6-BISPHOSPHATE 1-PHOSPHOHYDROLASE) (FBPASE) >gi_99693_pir__S16582 fructose-bisphosphatase (EC 3.1.3.11) precursor, chloroplast - Arabidopsis thaliana >gi_11242_emb_CAA41154_ (X58148) fructose-bisphosphatase [Arabidopsis thaliana]

Seq. No.	162923
Seq. ID	LIB3177-052-P1-K1-H11
Method	BLASTX
NCBI GI	g2827662
BLAST score	379
E value	2.0e-36
Match length	126

% identity	57
NCBI Description	(AL021637) Phosphoribosylanthranilate transferase [Arabidopsis thaliana]

Seq. No.	162924
Seq. ID	LIB3177-052-P1-K1-H12
Method	BLASTX
NCBI GI	g2789660
BLAST score	643
E value	2.0e-67
Match length	157
% identity	82
NCBI Description	(AF040102) p105 [Arabidopsis thaliana]

Seq. No.	162925
Seq. ID	LIB3177-052-P1-K1-H2
Method	BLASTX
NCBI GI	g4586049
BLAST score	720
E value	2.0e-76
Match length	130
% identity	100
NCBI Description	(AC007020) hypothetical protein [Arabidopsis thaliana]

Seq. No.	162926
Seq. ID	LIB3177-052-P1-K1-H3
Method	BLASTX
NCBI GI	g3914442
BLAST score	136
E value	2.0e-29
Match length	126
% identity	61
NCBI Description	PHOTOSYSTEM I REACTION CENTRE SUBUNIT VI PRECURSOR (LIGHT-HARVESTING COMPLEX I 11 KD PROTEIN) (PSI-H) >gi_1916350 (U92504) PSI-H subunit [Brassica rapa]

Seq. No.	162927
Seq. ID	LIB3177-052-P1-K1-H6
Method	BLASTX
NCBI GI	g4586049
BLAST score	448
E value	9.0e-45
Match length	95
% identity	91
NCBI Description	(AC007020) hypothetical protein [Arabidopsis thaliana]

Seq. No.	162928
Seq. ID	LIB3177-052-P1-K1-H7
Method	BLASTX
NCBI GI	g4580466
BLAST score	61
E value	1.0e-78
Match length	151
% identity	99
NCBI Description	(AC006081) putative 50S ribosomal protein L4 [Arabidopsis thaliana]

Seq. No.	162929
Seq. ID	LIB3177-052-P1-K1-H8
Method	BLASTX
NCBI GI	g4191778
BLAST score	250
E value	6.0e-28
Match length	81
% identity	89
NCBI Description	(AC005917) putative nucleosome assembly protein I [Arabidopsis thaliana]

Seq. No.	162930
Seq. ID	LIB3177-053-P1-K1-A1
Method	BLASTX
NCBI GI	g115767
BLAST score	404
E value	4.0e-43
Match length	88
% identity	99
NCBI Description	CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR (CAB-165/180) (LHCP) >gi_81603_pir__A29280 chlorophyll a/b-binding protein ab165 - Arabidopsis thaliana >gi_16368_emb_CAA27540_ (X03907) chlorophyll a/b binding protein (LHCP AB 65) [Arabidopsis thaliana] >gi_16372_emb_CAA27541_ (X03908) chlorophyll a/b binding protein (LHCP AB 180) [Arabidopsis thaliana]

Seq. No.	162931
Seq. ID	LIB3177-053-P1-K1-A2
Method	BLASTX
NCBI GI	g4138581
BLAST score	205
E value	4.0e-16
Match length	150
% identity	21
NCBI Description	(X98474) mitochondrial energy transfer protein [Solanum tuberosum]

Seq. No.	162932
Seq. ID	LIB3177-053-P1-K1-A3
Method	BLASTX
NCBI GI	g1168256
BLAST score	753
E value	2.0e-80
Match length	146
% identity	100
NCBI Description	ASPARTATE AMINOTRANSFERASE, MITOCHONDRIAL PRECURSOR (TRANSAMINASE A) >gi_693688 (U15026) aspartate aminotransferase [Arabidopsis thaliana] >gi_3201622 (AC004669) aspartate aminotransferase [Arabidopsis thaliana]

Seq. No.	162933
Seq. ID	LIB3177-053-P1-K1-A4
Method	BLASTX
NCBI GI	g1710581
BLAST score	43

E value	1.0e-59
Match length	137
% identity	93
NCBI Description	60S RIBOSOMAL PROTEIN L9 >gi_2129720_pir__S71255 ribosomal protein L9 - Arabidopsis thaliana >gi_1107489_emb_CAA63024_ (X91958) 60S ribosomal protein L9 [Arabidopsis thaliana]

Seq. No.	162934
Seq. ID	LIB3177-053-P1-K1-A6
Method	BLASTN
NCBI GI	g3559806
BLAST score	336
E value	0.0e+00
Match length	396
% identity	96
NCBI Description	Arabidopsis thaliana mRNA for nuclear protein HCF136

Seq. No.	162935
Seq. ID	LIB3177-053-P1-K1-A7
Method	BLASTX
NCBI GI	g728882
BLAST score	599
E value	3.0e-62
Match length	116
% identity	99
NCBI Description	ADP-RIBOSYLATION FACTOR 3 >gi_541846_pir__S41938 ADP-ribosylation factor 3 - Arabidopsis thaliana >gi_453191_emb_CAA54564_ (X77385) ADP-ribosylation factor 3 [Arabidopsis thaliana]

Seq. No.	162936
Seq. ID	LIB3177-053-P1-K1-A8
Method	BLASTX
NCBI GI	g2760834
BLAST score	200
E value	2.0e-15
Match length	150
% identity	73
NCBI Description	(AC003105) putative nitrate transporter [Arabidopsis thaliana]

Seq. No.	162937
Seq. ID	LIB3177-053-P1-K1-A9
Method	BLASTX
NCBI GI	g1168256
BLAST score	121
E value	6.0e-25
Match length	118
% identity	61
NCBI Description	ASPARTATE AMINOTRANSFERASE, MITOCHONDRIAL PRECURSOR (TRANSAMINASE A) >gi_693688 (U15026) aspartate aminotransferase [Arabidopsis thaliana] >gi_3201622 (AC004669) aspartate aminotransferase [Arabidopsis thaliana]

Seq. No.	162938
Seq. ID	LIB3177-053-P1-K1-B1

Method	BLASTX
NCBI GI	g3688799
BLAST score	588
E value	5.0e-61
Match length	124
% identity	96
NCBI Description	(AF057137) gamma tonoplast intrinsic protein 2 [Arabidopsis thaliana]

Seq. No.	162939
Seq. ID	LIB3177-053-P1-K1-B10
Method	BLASTN
NCBI GI	g4185128
BLAST score	66
E value	8.0e-29
Match length	220
% identity	92
NCBI Description	Arabidopsis thaliana chromosome II P1 MSF3 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	162940
Seq. ID	LIB3177-053-P1-K1-B11
Method	BLASTN
NCBI GI	g4510360
BLAST score	161
E value	2.0e-85
Match length	400
% identity	97
NCBI Description	Arabidopsis thaliana chromosome II BAC F11F19 genomic sequence, complete sequence

Seq. No.	162941
Seq. ID	LIB3177-053-P1-K1-B2
Method	BLASTX
NCBI GI	g3386546
BLAST score	752
E value	3.0e-80
Match length	142
% identity	99
NCBI Description	(AF079503) H-protein promoter binding factor-2a [Arabidopsis thaliana]

Seq. No.	162942
Seq. ID	LIB3177-053-P1-K1-B3
Method	BLASTX
NCBI GI	g4415930
BLAST score	64
E value	2.0e-41
Match length	122
% identity	74
NCBI Description	(AC006418) unknown protein [Arabidopsis thaliana] >gi_4559389_gb_AAD23049.1_AC006526_14 (AC006526) unknown protein [Arabidopsis thaliana]

Seq. No.	162943
Seq. ID	LIB3177-053-P1-K1-B4
Method	BLASTX

NCBI GI	g1172969
BLAST score	538
E value	2.0e-55
Match length	107
% identity	100
NCBI Description	60S RIBOSOMAL PROTEIN L11 (L16) >gi_629552_pir__S49033 ribosomal protein L11.e - Arabidopsis thaliana >gi_550544_emb_CAA57394_ (X81798) ribosomal protein L16 [Arabidopsis thaliana]

Seq. No.	162944
Seq. ID	LIB3177-053-P1-K1-B5
Method	BLASTN
NCBI GI	g2583106
BLAST score	97
E value	2.0e-47
Match length	137
% identity	93
NCBI Description	Arabidopsis thaliana chromosome II BAC F4L23 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	162945
Seq. ID	LIB3177-053-P1-K1-B8
Method	BLASTX
NCBI GI	g1175011
BLAST score	586
E value	8.0e-61
Match length	112
% identity	98
NCBI Description	PLASMA MEMBRANE INTRINSIC PROTEIN 1B (TRANSMEMBRANE PROTEIN A) (TMP-A) >gi_296085_emb_CAA48356_ (X68293) transmembrane protein [Arabidopsis thaliana] >gi_3386599 (AC004665) plasma membrane intrinsic protein 1B [Arabidopsis thaliana]

Seq. No.	162946
Seq. ID	LIB3177-053-P1-K1-B9
Method	BLASTX
NCBI GI	g4741948
BLAST score	596
E value	6.0e-62
Match length	115
% identity	97
NCBI Description	(AF134124) Lhcb2 protein [Arabidopsis thaliana]

Seq. No.	162947
Seq. ID	LIB3177-053-P1-K1-C10
Method	BLASTX
NCBI GI	g4585882
BLAST score	501
E value	8.0e-51
Match length	98
% identity	98
NCBI Description	(AC005850) PSI type III chlorophyll a/b-binding protein [Arabidopsis thaliana]

Seq. No.	162948
Seq. ID	LIB3177-053-P1-K1-C11

Method	BLASTX
NCBI GI	g125576
BLAST score	468
E value	6.0e-47
Match length	108
% identity	86
NCBI Description	PHOSPHORIBULOKINASE PRECURSOR (PHOSPHOPENTOKINASE) (PRKASE) (PRK) >gi_99744_pir__S16583 phosphoribulokinase (EC 2.7.1.19) precursor - Arabidopsis thaliana >gi_16441_emb_CAA41155_ (X58149) Ribulose-5-phosphate kinase [Arabidopsis thaliana]

Seq. No.	162949
Seq. ID	LIB3177-053-P1-K1-C3
Method	BLASTX
NCBI GI	g4337175
BLAST score	266
E value	1.0e-46
Match length	101
% identity	99
NCBI Description	(AC006416) ESTs gb_T20589, gb_T04648, gb_AA597906, gb_T04111, gb_R84180, gb_R65428, gb_T44439, gb_T76570, gb_R90004, gb_T45020, gb_T42457, gb_T20921, gb_AA042762 and gb_AA720210 come from this gene. [Arabidopsis thaliana]

Seq. No.	162950
Seq. ID	LIB3177-053-P1-K1-C4
Method	BLASTX
NCBI GI	g4107101
BLAST score	616
E value	3.0e-64
Match length	126
% identity	96
NCBI Description	(AB015142) AHP2 [Arabidopsis thaliana] >gi_4156241_dbj_BAA37110_ (AB012568) ATHP1 [Arabidopsis thaliana]

Seq. No.	162951
Seq. ID	LIB3177-053-P1-K1-C6
Method	BLASTX
NCBI GI	g2781394
BLAST score	251
E value	8.0e-22
Match length	72
% identity	78
NCBI Description	(U70424) O-methyltransferase 1 [Arabidopsis thaliana]

Seq. No.	162952
Seq. ID	LIB3177-053-P1-K1-D1
Method	BLASTX
NCBI GI	g4467095
BLAST score	484
E value	7.0e-49
Match length	133
% identity	77
NCBI Description	(AL035538) putative protein [Arabidopsis thaliana]

Seq. No.	162953
Seq. ID	LIB3177-053-P1-K1-D10
Method	BLASTX
NCBI GI	g133872
BLAST score	354
E value	1.0e-33
Match length	94
% identity	70
NCBI Description	30S RIBOSOMAL PROTEIN S1, CHLOROPLAST PRECURSOR (CS1) >gi_282838_pir__S26494 ribosomal protein S1, chloroplast - spinach >gi_322404_pir__A44121 small subunit ribosomal protein CS1, CS-S2 - spinach >gi_18060_emb_CAA46927_ (X66135) ribosomal protein S1 [Spinacia oleracea] >gi_170143 (M82923) chloroplast ribosomal protein S1 [Spinacia oleracea]

Seq. No.	162954
Seq. ID	LIB3177-053-P1-K1-D3
Method	BLASTX
NCBI GI	g4689386
BLAST score	308
E value	3.0e-28
Match length	128
% identity	53
NCBI Description	(AF139468) photosystem I reaction center subunit III [Vigna radiata]

Seq. No.	162955
Seq. ID	LIB3177-053-P1-K1-D4
Method	BLASTX
NCBI GI	g3288821
BLAST score	517
E value	1.0e-52
Match length	115
% identity	87
NCBI Description	(AF063901) alanine:glyoxylate aminotransferase; transaminase [Arabidopsis thaliana] >gi_4733989_gb_AAD28669.1_AC007209_5 (AC007209) alanine-glyoxylate aminotransferase [Arabidopsis thaliana]

Seq. No.	162956
Seq. ID	LIB3177-053-P1-K1-D5
Method	BLASTX
NCBI GI	g1710114
BLAST score	167
E value	5.0e-12
Match length	85
% identity	51
NCBI Description	(U53865) PRH26 [Arabidopsis thaliana]

Seq. No.	162957
Seq. ID	LIB3177-053-P1-K1-E1
Method	BLASTX
NCBI GI	g3599491
BLAST score	324
E value	4.0e-30
Match length	100

% identity	63
NCBI Description	(AF085149) putative aminotransferase [Capsicum chinense]

Seq. No.	162958
Seq. ID	LIB3177-053-P1-K1-E10
Method	BLASTX
NCBI GI	g2062161
BLAST score	287
E value	8.0e-26
Match length	55
% identity	50
NCBI Description	(AC001645) jasmonate inducible protein isolog [Arabidopsis thaliana]

Seq. No.	162959
Seq. ID	LIB3177-053-P1-K1-E11
Method	BLASTN
NCBI GI	g2062153
BLAST score	179
E value	5.0e-96
Match length	216
% identity	18
NCBI Description	Arabidopsis thaliana chromosome III BAC T02O04 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	162960
Seq. ID	LIB3177-053-P1-K1-E2
Method	BLASTN
NCBI GI	g2828183
BLAST score	377
E value	0.0e+00
Match length	443
% identity	98
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MPL12, complete sequence [Arabidopsis thaliana]

Seq. No.	162961
Seq. ID	LIB3177-053-P1-K1-E3
Method	BLASTX
NCBI GI	g421826
BLAST score	618
E value	2.0e-64
Match length	141
% identity	82
NCBI Description	chlorophyll a/b-binding protein CP29 - Arabidopsis thaliana >gi_298036_emb_CAA50712_ (X71878) CP29 [Arabidopsis thaliana]

Seq. No.	162962
Seq. ID	LIB3177-053-P1-K1-E6
Method	BLASTX
NCBI GI	g135467
BLAST score	107
E value	5.0e-61
Match length	131
% identity	92
NCBI Description	TUBULIN BETA-4 CHAIN >gi_2129546_pir__S68122 beta-tubulin 4

- Arabidopsis thaliana >gi_166640 (M21415) beta-tubulin [Arabidopsis thaliana]

Seq. No.	162963
Seq. ID	LIB3177-053-P1-K1-E9
Method	BLASTN
NCBI GI	g3510336
BLAST score	36
E value	2.0e-11
Match length	76
% identity	87
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K18J17, complete sequence [Arabidopsis thaliana]

Seq. No.	162964
Seq. ID	LIB3177-053-P1-K1-F12
Method	BLASTX
NCBI GI	g1143427
BLAST score	147
E value	2.0e-09
Match length	36
% identity	81
NCBI Description	(X73961) heat shock protein 70 [Cucumis sativus]

Seq. No.	162965
Seq. ID	LIB3177-053-P1-K1-F2
Method	BLASTX
NCBI GI	g166834
BLAST score	44
E value	6.0e-58
Match length	132
% identity	90
NCBI Description	(M86720) ribulose bisphosphate carboxylase/oxygenase activase [Arabidopsis thaliana] >gi_2642155 (AC003000) Rubisco activase [Arabidopsis thaliana]

Seq. No.	162966
Seq. ID	LIB3177-053-P1-K1-F3
Method	BLASTX
NCBI GI	g3157924
BLAST score	213
E value	5.0e-17
Match length	41
% identity	100
NCBI Description	(AC002131) Contains homology to extensin-like protein gb_D83227 from Populus nigra. ESTs gb_H76425, gb_T13883, gb_T45348, gb_H37743, gb_AA042634, gb_Z26960 and gb_Z25951 come from this gene. There is a similar ORF on the opposite strand. [... >gi_4063707 (AF104327) extensin-like protein [Arabidopsis thaliana]

Seq. No.	162967
Seq. ID	LIB3177-053-P1-K1-F4
Method	BLASTX
NCBI GI	g2462840
BLAST score	602
E value	1.0e-62

Match length	114
% identity	99
NCBI Description	(AF000657) cytochrome C [Arabidopsis thaliana]

Seq. No.	162968
Seq. ID	LIB3177-053-P1-K1-F6
Method	BLASTX
NCBI GI	g2618721
BLAST score	397
E value	1.0e-38
Match length	95
% identity	85
NCBI Description	(U49072) IAA16 [Arabidopsis thaliana]

Seq. No.	162969
Seq. ID	LIB3177-053-P1-K1-F7
Method	BLASTX
NCBI GI	g99696
BLAST score	508
E value	1.0e-51
Match length	131
% identity	77
NCBI Description	glutamate--ammonia ligase (EC 6.3.1.2) precursor, chloroplast (clone lambdaAtgsl1) - Arabidopsis thaliana >gi_240070_bbs_69728 (S69727) light-regulated glutamine synthetase isoenzyme [Arabidopsis thaliana, Peptide, 430 aa] [Arabidopsis thaliana] >gi_228453_prf__1804333A Gln synthetase [Arabidopsis thaliana]

Seq. No.	162970
Seq. ID	LIB3177-053-P1-K1-F8
Method	BLASTX
NCBI GI	g2618721
BLAST score	473
E value	1.0e-47
Match length	109
% identity	86
NCBI Description	(U49072) IAA16 [Arabidopsis thaliana]

Seq. No.	162971
Seq. ID	LIB3177-053-P1-K1-G10
Method	BLASTX
NCBI GI	g1086252
BLAST score	405
E value	1.0e-39
Match length	137
% identity	55
NCBI Description	sucrose cleavage protein - Potato >gi_707001_bbs_157931 (S74161) sucrolytic enzyme/ferredoxin homolog [Solanum tuberosum=potatoes, cv. Cara, leaf, Peptide, 322 aa] [Solanum tuberosum]

Seq. No.	162972
Seq. ID	LIB3177-053-P1-K1-G4
Method	BLASTX
NCBI GI	g3786017
BLAST score	395

E value	2.0e-38
Match length	116
% identity	74
NCBI Description	(AC005499) putative non-green plastid inner envelope membrane protein [Arabidopsis thaliana]

Seq. No.	162973
Seq. ID	LIB3177-053-P1-K1-G5
Method	BLASTX
NCBI GI	g4105782
BLAST score	477
E value	6.0e-48
Match length	120
% identity	78
NCBI Description	(AF049922) PGP169-12 [Petunia x hybrida]

Seq. No.	162974
Seq. ID	LIB3177-053-P1-K1-G6
Method	BLASTX
NCBI GI	g4262156
BLAST score	630
E value	6.0e-66
Match length	149
% identity	85
NCBI Description	(AC005275) putative component of cytochrome B6-F complex [Arabidopsis thaliana]

Seq. No.	162975
Seq. ID	LIB3177-053-P1-K1-G7
Method	BLASTX
NCBI GI	g3122914
BLAST score	682
E value	5.0e-72
Match length	141
% identity	87
NCBI Description	VALYL-TRNA SYNTHETASE (VALINE--TRNA LIGASE) (VALRS) >gi_1890130 (U89986) valyl tRNA synthetase [Arabidopsis thaliana]

Seq. No.	162976
Seq. ID	LIB3177-053-P1-K1-G9
Method	BLASTN
NCBI GI	g1209241
BLAST score	238
E value	1.0e-131
Match length	283
% identity	95
NCBI Description	Arabidopsis thaliana metallothionein mRNA sequence

Seq. No.	162977
Seq. ID	LIB3177-053-P1-K1-H10
Method	BLASTX
NCBI GI	g4741960
BLAST score	632
E value	3.0e-66
Match length	115
% identity	100

NCBI Description	(AF134130) Lhcb6 protein [Arabidopsis thaliana]
Seq. No.	162978
Seq. ID	LIB3177-053-P1-K1-H11
Method	BLASTN
NCBI GI	g3241916
BLAST score	210
E value	1.0e-114
Match length	397
% identity	99
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K15N18, complete sequence [Arabidopsis thaliana]
Seq. No.	162979
Seq. ID	LIB3177-053-P1-K1-H2
Method	BLASTX
NCBI GI	g2829899
BLAST score	330
E value	9.0e-31
Match length	109
% identity	61
NCBI Description	(AC002311) similar to ripening-induced protein, gp_AJ001449_2465015 and major#latex protein, gp_X91961_1107495 [Arabidopsis thaliana]
Seq. No.	162980
Seq. ID	LIB3177-053-P1-K1-H3
Method	BLASTX
NCBI GI	g1363489
BLAST score	669
E value	2.0e-70
Match length	123
% identity	99
NCBI Description	thioglucosidase (EC 3.2.3.1) 3D precursor - Arabidopsis thaliana >gi_984052_emb_CAA61592_ (X89413) thioglucoside glucohydrolase [Arabidopsis thaliana]
Seq. No.	162981
Seq. ID	LIB3177-053-P1-K1-H4
Method	BLASTX
NCBI GI	g4585935
BLAST score	714
E value	9.0e-76
Match length	134
% identity	100
NCBI Description	(AC007211) putative chlorophyll A/B binding protein [Arabidopsis thaliana] >gi_4741946_gb_AAD28770.1_AF134123_1 (AF134123) Lhcb2 protein [Arabidopsis thaliana]
Seq. No.	162982
Seq. ID	LIB3177-053-P1-K1-H5
Method	BLASTX
NCBI GI	g3914442
BLAST score	541
E value	2.0e-55
Match length	145
% identity	74

NCBI Description	PHOTOSYSTEM I REACTION CENTRE SUBUNIT VI PRECURSOR (LIGHT-HARVESTING COMPLEX I 11 KD PROTEIN) (PSI-H) >gi_1916350 (U92504) PSI-H subunit [Brassica rapa]
Seq. No.	162983
Seq. ID	LIB3177-053-P1-K1-H9
Method	BLASTX
NCBI GI	g100535
BLAST score	268
E value	2.0e-23
Match length	80
% identity	64
NCBI Description	hypothetical protein - swollen duckweed >gi_1929057_emb_CAA32236_ (X14075) longest ORF (1) [Lemna gibba]
Seq. No.	162984
Seq. ID	LIB3177-055-P1-K1-A1
Method	BLASTX
NCBI GI	g4262241
BLAST score	334
E value	2.0e-31
Match length	110
% identity	68
NCBI Description	(AC006200) unknown protein [Arabidopsis thaliana]
Seq. No.	162985
Seq. ID	LIB3177-055-P1-K1-A10
Method	BLASTN
NCBI GI	g435678
BLAST score	60
E value	2.0e-25
Match length	80
% identity	94
NCBI Description	L.esculentum Mill (cv. Rutgers) mRNA for ribosomal protein S25
Seq. No.	162986
Seq. ID	LIB3177-055-P1-K1-A12
Method	BLASTX
NCBI GI	g3024431
BLAST score	565
E value	2.0e-58
Match length	134
% identity	85
NCBI Description	26S PROTEASE REGULATORY SUBUNIT 6A HOMOLOG (TAT-BINDING PROTEIN HOMOLOG 1) (TBP-1) >gi_2342675 (AC000106) Similar to probable Mg-dependent ATPase (pir_S56671). ESTs gb_T46782,gb_AA04798 come from this gene. [Arabidopsis thaliana]
Seq. No.	162987
Seq. ID	LIB3177-055-P1-K1-A2
Method	BLASTX
NCBI GI	g4103154
BLAST score	341
E value	5.0e-32

Match length	115
% identity	60
NCBI Description	(AF020717) histidyl-tRNA synthetase [Triticum aestivum]

Seq. No.	162988
Seq. ID	LIB3177-055-P1-K1-A3
Method	BLASTX
NCBI GI	g4454036
BLAST score	751
E value	4.0e-80
Match length	137
% identity	100
NCBI Description	(AL035394) putative major latex protein [Arabidopsis thaliana]

Seq. No.	162989
Seq. ID	LIB3177-055-P1-K1-A4
Method	BLASTX
NCBI GI	g2829133
BLAST score	224
E value	3.0e-18
Match length	45
% identity	96
NCBI Description	(AF043351) adenosine-5'-phosphosulfate-kinase [Arabidopsis thaliana] >gi_4490745_emb_CAB38907.1_ (AL035708) adenosine-5'-phosphosulfate-kinase [Arabidopsis thaliana]

Seq. No.	162990
Seq. ID	LIB3177-055-P1-K1-A5
Method	BLASTX
NCBI GI	g267069
BLAST score	624
E value	3.0e-65
Match length	117
% identity	99
NCBI Description	TUBULIN ALPHA-2/ALPHA-4 CHAIN >gi_320183_pir__JQ1594 tubulin alpha chain - Arabidopsis thaliana >gi_166914 (M84696) apha-2 tubulin [Arabidopsis thaliana] >gi_166916 (M84697) alpha-4 tubulin [Arabidopsis thaliana]

Seq. No.	162991
Seq. ID	LIB3177-055-P1-K1-A8
Method	BLASTX
NCBI GI	g4185509
BLAST score	342
E value	2.0e-32
Match length	72
% identity	94
NCBI Description	(AF102821) actin depolymerizing factor 3 [Arabidopsis thaliana]

Seq. No.	162992
Seq. ID	LIB3177-055-P1-K1-A9
Method	BLASTN
NCBI GI	g4584351
BLAST score	93
E value	5.0e-45

Match length	125
% identity	94
NCBI Description	Arabidopsis thaliana chromosome II BAC T12H3 genomic sequence, complete sequence

Seq. No.	162993
Seq. ID	LIB3177-055-P1-K1-B1
Method	BLASTN
NCBI GI	g4510338
BLAST score	387
E value	0.0e+00
Match length	395
% identity	99
NCBI Description	Arabidopsis thaliana chromosome II BAC F2H17 genomic sequence, complete sequence

Seq. No.	162994
Seq. ID	LIB3177-055-P1-K1-B10
Method	BLASTN
NCBI GI	g4220627
BLAST score	116
E value	1.0e-58
Match length	217
% identity	93
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K20J1, complete sequence [Arabidopsis thaliana]

Seq. No.	162995
Seq. ID	LIB3177-055-P1-K1-B11
Method	BLASTX
NCBI GI	g3319349
BLAST score	669
E value	2.0e-70
Match length	137
% identity	96
NCBI Description	(AF077407) No definition line found [Arabidopsis thaliana]

Seq. No.	162996
Seq. ID	LIB3177-055-P1-K1-B12
Method	BLASTX
NCBI GI	g3319349
BLAST score	319
E value	5.0e-32
Match length	89
% identity	84
NCBI Description	(AF077407) No definition line found [Arabidopsis thaliana]

Seq. No.	162997
Seq. ID	LIB3177-055-P1-K1-B2
Method	BLASTX
NCBI GI	g2828267
BLAST score	166
E value	5.0e-18
Match length	114
% identity	54
NCBI Description	(Y14044) geranylgeranyl reductase [Arabidopsis thaliana]

Seq. No.	162998
Seq. ID	LIB3177-055-P1-K1-B5
Method	BLASTX
NCBI GI	g131398
BLAST score	549
E value	2.0e-56
Match length	139
% identity	81
NCBI Description	PHOTOSYSTEM II 10 KD POLYPEPTIDE PRECURSOR >gi_72714_pir__F2MU10 photosystem II 10K protein precursor - Arabidopsis thaliana >gi_16447_emb_CAA39441_ (X55970) photosystem II 10 kDa polypeptide [Arabidopsis thaliana] >gi_3152571 (AC002986) Match to photosystem II 10kDa polypeptide gb_X55970. ESTs gb_Z17693, gb_N37616, gb_T41858, gb_T88021, gb_R37531, gb_T04679, gb_N37520, gb_N64965, gb_Z17592 and gb_N65338, gb_N37466 and gb_T45400 come from this gene. [Arabidopsis

Seq. No.	162999
Seq. ID	LIB3177-055-P1-K1-B6
Method	BLASTX
NCBI GI	g2702272
BLAST score	535
E value	9.0e-55
Match length	150
% identity	26
NCBI Description	(AC003033) hypothetical protein [Arabidopsis thaliana]

Seq. No.	163000
Seq. ID	LIB3177-055-P1-K1-B7
Method	BLASTX
NCBI GI	g3287685
BLAST score	213
E value	7.0e-24
Match length	66
% identity	51
NCBI Description	(AC003979) Strong similarity to hypothetical protein gb_Y09823 from A. thaliana. ESTs gb_T76118, gb_T04263 and gb_ATYU9823 come from this gene. [Arabidopsis thaliana]

Seq. No.	163001
Seq. ID	LIB3177-055-P1-K1-C10
Method	BLASTX
NCBI GI	g3935145
BLAST score	255
E value	6.0e-22
Match length	87
% identity	59
NCBI Description	(AC005106) T25N20.9 [Arabidopsis thaliana]

Seq. No.	163002
Seq. ID	LIB3177-055-P1-K1-C12
Method	BLASTX
NCBI GI	g1769907
BLAST score	686
E value	1.0e-72
Match length	131

% identity	98
NCBI Description	(X92975) xyloglucan endo-transglycosylase [Arabidopsis thaliana]
Seq. No.	163003
Seq. ID	LIB3177-055-P1-K1-C2
Method	BLASTX
NCBI GI	g121075
BLAST score	590
E value	4.0e-61
Match length	149
% identity	80
NCBI Description	GLYCINE CLEAVAGE SYSTEM H PROTEIN PRECURSOR >gi_166725 (M82921) H-Protein precursor [Arabidopsis thaliana] >gi_861215 (U27144) glycine decarboxylase complex H-protein precursor [Arabidopsis thaliana] >gi_3608151 (AC005314) glycine decarboxylase complex H-protein [Arabidopsis thaliana] >gi_445119_prf__1908425A Gly decarboxylase:SUBUNIT=H protein [Arabidopsis thaliana]
Seq. No.	163004
Seq. ID	LIB3177-055-P1-K1-C3
Method	BLASTN
NCBI GI	g1877523
BLAST score	232
E value	1.0e-127
Match length	458
% identity	100
NCBI Description	Arabidopsis thaliana BAC T7I23, complete sequence [Arabidopsis thaliana]
Seq. No.	163005
Seq. ID	LIB3177-055-P1-K1-C4
Method	BLASTX
NCBI GI	g4432870
BLAST score	490
E value	9.0e-50
Match length	99
% identity	95
NCBI Description	(AC006300) putative selenium-binding protein, 3' partial [Arabidopsis thaliana]
Seq. No.	163006
Seq. ID	LIB3177-055-P1-K1-C7
Method	BLASTX
NCBI GI	g421826
BLAST score	784
E value	6.0e-84
Match length	150
% identity	98
NCBI Description	chlorophyll a/b-binding protein CP29 - Arabidopsis thaliana >gi_298036_emb_CAA50712_ (X71878) CP29 [Arabidopsis thaliana]
Seq. No.	163007
Seq. ID	LIB3177-055-P1-K1-C8
Method	BLASTX

NCBI GI	g132074
BLAST score	434
E value	3.0e-43
Match length	95
% identity	85
NCBI Description	RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN 1A PRECURSOR (RUBISCO SMALL SUBUNIT 1A) >gi_68063_pir__RKMUA1 ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain A1 precursor - Arabidopsis thaliana

Seq. No.	163008
Seq. ID	LIB3177-055-P1-K1-C9
Method	BLASTX
NCBI GI	g2245032
BLAST score	218
E value	1.0e-17
Match length	116
% identity	41
NCBI Description	(Z97342) gibberellin oxidase homolog [Arabidopsis thaliana]

Seq. No.	163009
Seq. ID	LIB3177-055-P1-K1-D1
Method	BLASTX
NCBI GI	g131162
BLAST score	451
E value	7.0e-45
Match length	81
% identity	99
NCBI Description	PHOTOSYSTEM I IRON-SULFUR CENTER 1 (PHOTOSYSTEM I SUBUNIT VII-1) (9 KD POLYPEPTIDE 1) (PSI-C-1) >gi_131163_sp_P07136_PSAC_TOBAC PHOTOSYSTEM I IRON-SULFUR CENTER (PHOTOSYSTEM I SUBUNIT VII) (9 KD POLYPEPTIDE) (PSI-C) >gi_97657_pir__S14967 photosystem I iron-sulfur protein psaC - Synechocystis sp. (PCC 6803) >gi_100391_pir__S07170 photosystem I iron-sulfur protein psaC - common tobacco chloroplast >gi_11792_emb_CAA29304_ (X05881) 9kd polypeptide (psaC gene product, AA 1 - 81) [Nicotiana tabacum] >gi_47596_emb_CAA37836_ (X53842) 8.9kDa iron-sulfur containing subunit of Photosystem I [Synechocystis sp.] >gi_2924280_emb_CAA77433_ (Z00044) PSI 9kD protein [Nicotiana tabacum]

Seq. No.	163010
Seq. ID	LIB3177-055-P1-K1-D10
Method	BLASTX
NCBI GI	g4741962
BLAST score	416
E value	6.0e-47
Match length	140
% identity	56
NCBI Description	(AF134131) PsbS protein [Arabidopsis thaliana]

Seq. No.	163011
Seq. ID	LIB3177-055-P1-K1-D11
Method	BLASTX
NCBI GI	g2645999
BLAST score	476

E value	1.0e-71
Match length	145
% identity	97
NCBI Description	(AF034631) chlorophyll a/b binding protein of LHCII type I precursor [Panax ginseng]

Seq. No.	163012
Seq. ID	LIB3177-055-P1-K1-D12
Method	BLASTX
NCBI GI	g4263525
BLAST score	664
E value	7.0e-70
Match length	153
% identity	86
NCBI Description	(AC004044) putative photosystem I reaction center subunit II precursor [Arabidopsis thaliana]

Seq. No.	163013
Seq. ID	LIB3177-055-P1-K1-D2
Method	BLASTX
NCBI GI	g461550
BLAST score	437
E value	3.0e-43
Match length	122
% identity	75
NCBI Description	ATP SYNTHASE GAMMA CHAIN 1, CHLOROPLAST PRECURSOR >gi_81635_pir__B39732 H+-transporting ATP synthase (EC 3.6.1.34) gamma-1 chain precursor, chloroplast - Arabidopsis thaliana >gi_166632 (M61741) ATP synthase gamma-subunit [Arabidopsis thaliana]

Seq. No.	163014
Seq. ID	LIB3177-055-P1-K1-D3
Method	BLASTX
NCBI GI	g3983125
BLAST score	666
E value	4.0e-70
Match length	148
% identity	90
NCBI Description	(AF097648) phosphate/triose-phosphate translocator precursor [Arabidopsis thaliana]

Seq. No.	163015
Seq. ID	LIB3177-055-P1-K1-D4
Method	BLASTX
NCBI GI	g2632254
BLAST score	338
E value	1.0e-31
Match length	115
% identity	56
NCBI Description	(Y12465) serine/threonine kinase [Sorghum bicolor]

Seq. No.	163016
Seq. ID	LIB3177-055-P1-K1-D5
Method	BLASTX
NCBI GI	g4587564
BLAST score	676

E value	3.0e-71
Match length	136
% identity	99
NCBI Description	(AC006550) Strong similarity to gb_X14017 photosystem I reaction centre subunit II precursor (psaD) from Spinacia oleracea. ESTs gb_R30423, gb_T42998, gb_Z18178, gb_T14133, gb_N65521, gb_T42498, gb_T41918, gb_N38024

Seq. No.	163017
Seq. ID	LIB3177-055-P1-K1-D7
Method	BLASTX
NCBI GI	g4100433
BLAST score	211
E value	9.0e-17
Match length	62
% identity	63
NCBI Description	(AF000378) beta-glucosidase [Glycine max]

Seq. No.	163018
Seq. ID	LIB3177-055-P1-K1-D8
Method	BLASTN
NCBI GI	g1871173
BLAST score	210
E value	1.0e-115
Match length	243
% identity	96
NCBI Description	Arabidopsis thaliana chromosome II BAC T06D20 genomic sequence, complete sequence

Seq. No.	163019
Seq. ID	LIB3177-055-P1-K1-D9
Method	BLASTX
NCBI GI	g3688799
BLAST score	651
E value	2.0e-68
Match length	130
% identity	99
NCBI Description	(AF057137) gamma tonoplast intrinsic protein 2 [Arabidopsis thaliana]

Seq. No.	163020
Seq. ID	LIB3177-055-P1-K1-E1
Method	BLASTX
NCBI GI	g4585992
BLAST score	301
E value	2.0e-27
Match length	55
% identity	100
NCBI Description	(AC005287) Hypothetical protein [Arabidopsis thaliana]

Seq. No.	163021
Seq. ID	LIB3177-055-P1-K1-E11
Method	BLASTX
NCBI GI	g1076393
BLAST score	589
E value	3.0e-61
Match length	121

% identity	99
NCBI Description	RCI14A protein - Arabidopsis thaliana >gi_540559_emb_CAA52237_ (X74140) RCI14A [Arabidopsis thaliana]

Seq. No.	163022
Seq. ID	LIB3177-055-P1-K1-E2
Method	BLASTN
NCBI GI	g4093156
BLAST score	350
E value	0.0e+00
Match length	353
% identity	100
NCBI Description	Arabidopsis thaliana phytochrome-associated protein 2 (PAP2) mRNA, complete cds

Seq. No.	163023
Seq. ID	LIB3177-055-P1-K1-E3
Method	BLASTX
NCBI GI	g2129559
BLAST score	489
E value	2.0e-49
Match length	121
% identity	78
NCBI Description	cellulase homolog OR16pep - Arabidopsis thaliana >gi_1022807 (U37702) cellulase [Arabidopsis thaliana] >gi_3493633 (AF074092) cellulase [Arabidopsis thaliana] >gi_3598956 (AF074375) cellulase [Arabidopsis thaliana] >gi_3978258 (AF073875) endo-1,4-beta-D-glucanase KORRIGAN [Arabidopsis thaliana]

Seq. No.	163024
Seq. ID	LIB3177-055-P1-K1-E5
Method	BLASTX
NCBI GI	g132110
BLAST score	353
E value	1.0e-33
Match length	84
% identity	86
NCBI Description	RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN 3B PRECURSOR (RUBISCO SMALL SUBUNIT 3B) >gi_68060_pir__RKMUB3 ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain B3 precursor - Arabidopsis thaliana >gi_16195_emb_CAA32702_ (X14564) ribulose bisphosphate carboxylase [Arabidopsis thaliana]

Seq. No.	163025
Seq. ID	LIB3177-055-P1-K1-E6
Method	BLASTX
NCBI GI	g1172873
BLAST score	246
E value	1.0e-45
Match length	100
% identity	95
NCBI Description	CYSTEINE PROTEINASE RD21A PRECURSOR >gi_541857_pir__JN0719 drought-inducible cysteine proteinase (EC 3.4.22.-) RD21A precursor - Arabidopsis thaliana >gi_435619_dbj_BAA02374_

(D13043) thiol protease [Arabidopsis thaliana]

Seq. No.	163026
Seq. ID	LIB3177-055-P1-K1-E7
Method	BLASTX
NCBI GI	g133028
BLAST score	630
E value	7.0e-66
Match length	128
% identity	100
NCBI Description	50S RIBOSOMAL PROTEIN L9, CHLOROPLAST PRECURSOR (CL9) >gi_71257_pir__R5MUL9 ribosomal protein L9 precursor, chloroplast - Arabidopsis thaliana >gi_16499_emb_CAA77480_ (Z11129) plastid ribosomal protein CL9 [Arabidopsis thaliana] >gi_16501_emb_CAA77594_ (Z11509) Chloroplast ribosomal protein CL9 [Arabidopsis thaliana]

Seq. No.	163027
Seq. ID	LIB3177-055-P1-K1-E8
Method	BLASTX
NCBI GI	g166835
BLAST score	481
E value	1.0e-48
Match length	99
% identity	93
NCBI Description	(M86720) ribulose bisphosphate carboxylase/oxygenase activase [Arabidopsis thaliana] >gi_2642170 (AC003000) Rubisco activase [Arabidopsis thaliana]

Seq. No.	163028
Seq. ID	LIB3177-055-P1-K1-E9
Method	BLASTX
NCBI GI	g120675
BLAST score	413
E value	7.0e-42
Match length	110
% identity	82
NCBI Description	GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE, CYTOSOLIC >gi_66011_pir__DEIS3C glyceraldehyde-3-phosphate dehydrogenase (EC 1.2.1.12), cytosolic - white mustard >gi_21143_emb_CAA27844_ (X04301) GAPDH (aa 1-338) [Sinapis alba]

Seq. No.	163029
Seq. ID	LIB3177-055-P1-K1-F1
Method	BLASTX
NCBI GI	g4741950
BLAST score	805
E value	2.0e-86
Match length	150
% identity	100
NCBI Description	(AF134125) Lhcb2 protein [Arabidopsis thaliana]

Seq. No.	163030
Seq. ID	LIB3177-055-P1-K1-F10
Method	BLASTX
NCBI GI	g265974

BLAST score	486
E value	5.0e-49
Match length	135
% identity	73
NCBI Description	RD29A=responsive-to-dessication protein [Arabidopsis thaliana, Columbia ecotype, Peptide, 710 aa] >gi_303504_dbj_BAA02376_ (D13044) RD29A [Arabidopsis thaliana] >gi_445065_prf__1908381A rd29A gene [Arabidopsis thaliana]

Seq. No.	163031
Seq. ID	LIB3177-055-P1-K1-F11
Method	BLASTX
NCBI GI	g3212866
BLAST score	217
E value	9.0e-18
Match length	102
% identity	49
NCBI Description	(AC004005) unknown protein [Arabidopsis thaliana]

Seq. No.	163032
Seq. ID	LIB3177-055-P1-K1-F12
Method	BLASTX
NCBI GI	g2499973
BLAST score	235
E value	1.0e-19
Match length	105
% identity	53
NCBI Description	PHOTOSYSTEM II 5 KD PROTEIN PRECURSOR (PSII-T) >gi_1465366_emb_CAA66701_ (X98078) photosystem II [Arabidopsis thaliana]

Seq. No.	163033
Seq. ID	LIB3177-055-P1-K1-F2
Method	BLASTX
NCBI GI	g3860261
BLAST score	289
E value	3.0e-26
Match length	62
% identity	100
NCBI Description	(AC005824) putative acidic ribosomal protein [Arabidopsis thaliana]

Seq. No.	163034
Seq. ID	LIB3177-055-P1-K1-F3
Method	BLASTN
NCBI GI	g3153204
BLAST score	156
E value	2.0e-82
Match length	345
% identity	99
NCBI Description	Arabidopsis thaliana serine/threonine protein phosphatase type one (TOPP8) gene, complete cds

Seq. No.	163035
Seq. ID	LIB3177-055-P1-K1-F4
Method	BLASTX

NCBI GI	g1001603
BLAST score	170
E value	6.0e-12
Match length	58
% identity	53
NCBI Description	(D64000) hypothetical protein [Synechocystis sp.]

Seq. No.	163036
Seq. ID	LIB3177-055-P1-K1-F5
Method	BLASTX
NCBI GI	g4586256
BLAST score	350
E value	5.0e-33
Match length	153
% identity	52
NCBI Description	(AL049640) probable photosystem I chain XI precursor [Arabidopsis thaliana]

Seq. No.	163037
Seq. ID	LIB3177-055-P1-K1-F6
Method	BLASTX
NCBI GI	g3789942
BLAST score	121
E value	3.0e-06
Match length	110
% identity	7
NCBI Description	(AF093505) polyubiquitin [Saccharum hybrid cultivar H32-8560]

Seq. No.	163038
Seq. ID	LIB3177-055-P1-K1-F7
Method	BLASTX
NCBI GI	g100525
BLAST score	383
E value	4.0e-37
Match length	91
% identity	20
NCBI Description	ubiquitin precursor UbB2 - common sunflower (fragment) >gi_18803_emb_CAA40323_ (X57003) polyubiquitin protein [Helianthus annuus]

Seq. No.	163039
Seq. ID	LIB3177-055-P1-K1-F8
Method	BLASTX
NCBI GI	g2119848
BLAST score	317
E value	9.0e-30
Match length	65
% identity	94
NCBI Description	chlorophyll a/b-binding protein type I precursor Lhb1B1 - Arabidopsis thaliana >gi_16366_emb_CAA45789_ (X64459) photosystem II type I chlorophyll a /b binding protein [Arabidopsis thaliana] >gi_3128229 (AC004077) putative photosystem II type I chlorophyll a/b binding protein [Arabidopsis thaliana] >gi_3337372 (AC004481) putative photosystem II type I chlorophyll a/b binding protein [Arabidopsis thaliana]

Seq. No.	163040
Seq. ID	LIB3177-055-P1-K1-F9
Method	BLASTX
NCBI GI	g3201613
BLAST score	726
E value	4.0e-77
Match length	151
% identity	95
NCBI Description	(AC004669) glutathione S-transferase [Arabidopsis thaliana]

Seq. No.	163041
Seq. ID	LIB3177-055-P1-K1-G1
Method	BLASTX
NCBI GI	g132074
BLAST score	748
E value	1.0e-79
Match length	136
% identity	100
NCBI Description	RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN 1A PRECURSOR (RUBISCO SMALL SUBUNIT 1A) >gi_68063_pir__RKMUA1 ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain A1 precursor - Arabidopsis thaliana

Seq. No.	163042
Seq. ID	LIB3177-055-P1-K1-G10
Method	BLASTX
NCBI GI	g4539292
BLAST score	477
E value	5.0e-48
Match length	92
% identity	97
NCBI Description	(AL049480) putative ribosomal protein S10 [Arabidopsis thaliana]

Seq. No.	163043
Seq. ID	LIB3177-055-P1-K1-G12
Method	BLASTN
NCBI GI	g4678258
BLAST score	33
E value	5.0e-09
Match length	75
% identity	95
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F6I7 (ESSA project)

Seq. No.	163044
Seq. ID	LIB3177-055-P1-K1-G3
Method	BLASTX
NCBI GI	g729479
BLAST score	378
E value	2.0e-36
Match length	97
% identity	72
NCBI Description	FERREDOXIN--NADP REDUCTASE PRECURSOR (FNR) >gi_551131 (U14956) ferredoxin NADP+ reductase precursor [Vicia faba]

Seq. No.	163045
Seq. ID	LIB3177-055-P1-K1-G4
Method	BLASTX
NCBI GI	g4678921
BLAST score	718
E value	3.0e-76
Match length	140
% identity	69
NCBI Description	(AL049711) putative calmodulin [Arabidopsis thaliana]

Seq. No.	163046
Seq. ID	LIB3177-055-P1-K1-G5
Method	BLASTX
NCBI GI	g2246621
BLAST score	441
E value	9.0e-44
Match length	98
% identity	84
NCBI Description	(AF004393) salt-stress induced tonoplast intrinsic protein [Arabidopsis thaliana]

Seq. No.	163047
Seq. ID	LIB3177-055-P1-K1-G6
Method	BLASTX
NCBI GI	g4467099
BLAST score	446
E value	2.0e-44
Match length	91
% identity	99
NCBI Description	(AL035538) glycine hydroxymethyltransferase like protein [Arabidopsis thaliana]

Seq. No.	163048
Seq. ID	LIB3177-055-P1-K1-G7
Method	BLASTX
NCBI GI	g135467
BLAST score	391
E value	3.0e-38
Match length	75
% identity	97
NCBI Description	TUBULIN BETA-4 CHAIN >gi_2129546_pir__S68122 beta-tubulin 4 - Arabidopsis thaliana >gi_166640 (M21415) beta-tubulin [Arabidopsis thaliana]

Seq. No.	163049
Seq. ID	LIB3177-055-P1-K1-G9
Method	BLASTX
NCBI GI	g2262170
BLAST score	388
E value	1.0e-37
Match length	77
% identity	99
NCBI Description	(AC002329) predicted glycosyl hydrolase [Arabidopsis thaliana]

Seq. No.	163050
Seq. ID	LIB3177-055-P1-K1-H10

Method	BLASTX
NCBI GI	g2911085
BLAST score	437
E value	3.0e-43
Match length	154
% identity	63
NCBI Description	(AL021960) photosystem II oxygen-evolving complex protein 3-like [Arabidopsis thaliana] >gi_3402748_emb_CAA20194.1_ (AL031187) photosystem II oxygen-evolving complex protein 3 - like [Arabidopsis thaliana]

Seq. No.	163051
Seq. ID	LIB3177-055-P1-K1-H11
Method	BLASTX
NCBI GI	g4583542
BLAST score	295
E value	1.0e-26
Match length	123
% identity	58
NCBI Description	(Y16847) 16 kDa polypeptide of oxygen-evolving complex [Arabidopsis thaliana]

Seq. No.	163052
Seq. ID	LIB3177-055-P1-K1-H12
Method	BLASTX
NCBI GI	g3980238
BLAST score	206
E value	2.0e-16
Match length	68
% identity	59
NCBI Description	(Z21677) ribosomal protein L18 [Thermotoga maritima]

Seq. No.	163053
Seq. ID	LIB3177-055-P1-K1-H2
Method	BLASTX
NCBI GI	g2062157
BLAST score	760
E value	4.0e-81
Match length	154
% identity	29
NCBI Description	(AC001645) jasmonate inducible protein isolog [Arabidopsis thaliana]

Seq. No.	163054
Seq. ID	LIB3177-055-P1-K1-H3
Method	BLASTX
NCBI GI	g3219858
BLAST score	601
E value	2.0e-62
Match length	116
% identity	100
NCBI Description	DNA-DIRECTED RNA POLYMERASE II 13.6 KD POLYPEPTIDE >gi_2129724_pir__S71204 RNA polymerase II 13.6 kDa chain - Arabidopsis thaliana >gi_881501 (U28048) RNA polymerase II 13.6 kDa subunit [Arabidopsis thaliana] >gi_4678938_emb_CAB41329.1_ (AL049711) DNA-directed RNA polymerase II 13.6K chain [Arabidopsis thaliana]

Seq. No.	163055
Seq. ID	LIB3177-055-P1-K1-H5
Method	BLASTX
NCBI GI	g1171993
BLAST score	649
E value	3.0e-68
Match length	140
% identity	94
NCBI Description	PHENYLALANINE AMMONIA-LYASE 2 >gi_1076370_pir__S52991 phenylalanine ammonia-lyase (EC 4.3.1.5) - Arabidopsis thaliana >gi_497421 (L33678) phenylalanine ammonia lyase [Arabidopsis thaliana]

Seq. No.	163056
Seq. ID	LIB3177-055-P1-K1-H6
Method	BLASTN
NCBI GI	g4584531
BLAST score	119
E value	2.0e-60
Match length	269
% identity	95
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone T9E8 (ESSA project)

Seq. No.	163057
Seq. ID	LIB3177-055-P1-K1-H8
Method	BLASTN
NCBI GI	g1063683
BLAST score	100
E value	2.0e-49
Match length	108
% identity	98
NCBI Description	Arabidopsis thaliana glycine-rich protein (AtGRP2b) mRNA, complete cds

Seq. No.	163058
Seq. ID	LIB3177-055-P1-K1-H9
Method	BLASTN
NCBI GI	g2829132
BLAST score	412
E value	0.0e+00
Match length	424
% identity	99
NCBI Description	Arabidopsis thaliana adenosine-5'-phosphosulfate-kinase (akn2) mRNA, complete cds

Seq. No.	163059
Seq. ID	LIB3177-056-P1-K1-A1
Method	BLASTX
NCBI GI	g231586
BLAST score	238
E value	5.0e-20
Match length	107
% identity	53
NCBI Description	ATP SYNTHASE BETA CHAIN, MITOCHONDRIAL PRECURSOR >gi_82027_pir__S20504 H+-transporting ATP synthase (EC

3.6.1.34) beta chain, mitochondrial - Para rubber tree >gi_18831_emb_CAA41401_ (X58498) mitochondrial ATP synthase beta-subunit [Hevea brasiliensis]

Seq. No.	163060
Seq. ID	LIB3177-056-P1-K1-A10
Method	BLASTN
NCBI GI	g1107482
BLAST score	212
E value	1.0e-115
Match length	386
% identity	90
NCBI Description	A.thaliana mRNA for 30S ribosomal protein S13

Seq. No.	163061
Seq. ID	LIB3177-056-P1-K1-A12
Method	BLASTN
NCBI GI	g4325340
BLAST score	86
E value	5.0e-41
Match length	165
% identity	96
NCBI Description	Arabidopsis thaliana BAC T1J1

Seq. No.	163062
Seq. ID	LIB3177-056-P1-K1-A2
Method	BLASTX
NCBI GI	g2584721
BLAST score	296
E value	4.0e-27
Match length	80
% identity	75
NCBI Description	(Y10157) sulfite reductase [Arabidopsis thaliana]

Seq. No.	163063
Seq. ID	LIB3177-056-P1-K1-A4
Method	BLASTX
NCBI GI	g2618725
BLAST score	718
E value	3.0e-76
Match length	145
% identity	97
NCBI Description	(U49074) IAA18 [Arabidopsis thaliana]

Seq. No.	163064
Seq. ID	LIB3177-056-P1-K1-A5
Method	BLASTX
NCBI GI	g1363489
BLAST score	292
E value	9.0e-27
Match length	60
% identity	92
NCBI Description	thioglucosidase (EC 3.2.3.1) 3D precursor - Arabidopsis thaliana >gi_984052_emb_CAA61592_ (X89413) thioglucoside glucohydrolase [Arabidopsis thaliana]

Seq. No. 163065

Seq. ID	LIB3177-056-P1-K1-A6
Method	BLASTX
NCBI GI	g2117612
BLAST score	214
E value	9.0e-18
Match length	52
% identity	85
NCBI Description	catalase (EC 1.11.1.6) 3 - Arabidopsis thaliana

Seq. No.	163066
Seq. ID	LIB3177-056-P1-K1-A7
Method	BLASTN
NCBI GI	g3798730
BLAST score	39
E value	1.0e-12
Match length	87
% identity	86
NCBI Description	Arabidopsis thaliana transgenic line C DNA

Seq. No.	163067
Seq. ID	LIB3177-056-P1-K1-A8
Method	BLASTX
NCBI GI	g1170373
BLAST score	48
E value	1.0e-17
Match length	83
% identity	77
NCBI Description	HEAT SHOCK COGNATE 70 KD PROTEIN 1 >gi_1072473_pir__S46302 heat shock cognate protein 70-1 - Arabidopsis thaliana >gi_397482_emb_CAA52684_ (X74604) heat shock protein 70 cognate [Arabidopsis thaliana]

Seq. No.	163068
Seq. ID	LIB3177-056-P1-K1-A9
Method	BLASTN
NCBI GI	g2821960
BLAST score	180
E value	8.0e-97
Match length	233
% identity	94
NCBI Description	Arabidopsis thaliana mRNA for spermidine synthase, partial cds

Seq. No.	163069
Seq. ID	LIB3177-056-P1-K1-B1
Method	BLASTN
NCBI GI	g2821960
BLAST score	229
E value	1.0e-126
Match length	254
% identity	97
NCBI Description	Arabidopsis thaliana mRNA for spermidine synthase, partial cds

Seq. No.	163070
Seq. ID	LIB3177-056-P1-K1-B10
Method	BLASTX

NCBI GI	g1710780
BLAST score	451
E value	6.0e-45
Match length	120
% identity	72
NCBI Description	40S RIBOSOMAL PROTEIN S9 (S7) >gi_1321917_emb_CAA65433_ (X96613) cytoplasmic ribosomal protein S7 [Podospora anserina]

Seq. No.	163071
Seq. ID	LIB3177-056-P1-K1-B11
Method	BLASTX
NCBI GI	g3135611
BLAST score	530
E value	3.0e-54
Match length	115
% identity	90
NCBI Description	(AF062485) cellulose synthase [Arabidopsis thaliana]

Seq. No.	163072
Seq. ID	LIB3177-056-P1-K1-B12
Method	BLASTX
NCBI GI	g1710780
BLAST score	509
E value	1.0e-51
Match length	133
% identity	74
NCBI Description	40S RIBOSOMAL PROTEIN S9 (S7) >gi_1321917_emb_CAA65433_ (X96613) cytoplasmic ribosomal protein S7 [Podospora anserina]

Seq. No.	163073
Seq. ID	LIB3177-056-P1-K1-B2
Method	BLASTX
NCBI GI	g4490310
BLAST score	493
E value	8.0e-50
Match length	160
% identity	64
NCBI Description	(AL035678) somatic embryogenesis receptor-like kinase-like protein [Arabidopsis thaliana]

Seq. No.	163074
Seq. ID	LIB3177-056-P1-K1-B3
Method	BLASTX
NCBI GI	g2341034
BLAST score	343
E value	2.0e-32
Match length	87
% identity	83
NCBI Description	(AC000104) F19P19.13 [Arabidopsis thaliana]

Seq. No.	163075
Seq. ID	LIB3177-056-P1-K1-B4
Method	BLASTX
NCBI GI	g115767
BLAST score	764

E value	1.0e-81
Match length	145
% identity	100
NCBI Description	CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR (CAB-165/180) (LHCP) >gi_81603_pir__A29280 chlorophyll a/b-binding protein ab165 - Arabidopsis thaliana >gi_16368_emb_CAA27540_ (X03907) chlorophyll a/b binding protein (LHCP AB 65) [Arabidopsis thaliana] >gi_16372_emb_CAA27541_ (X03908) chlorophyll a/b binding protein (LHCP AB 180) [Arabidopsis thaliana]

Seq. No.	163076
Seq. ID	LIB3177-056-P1-K1-B5
Method	BLASTX
NCBI GI	g140207
BLAST score	156
E value	2.0e-10
Match length	56
% identity	57
NCBI Description	PROBABLE 40S RIBOSOMAL PROTEIN S9 >gi_102109_pir__S12674 ribosomal protein S9.e - Trypanosoma brucei >gi_10399_emb_CAA36818_ (X52586) ald orfU protein (AA 1 - 190) [Trypanosoma brucei]

Seq. No.	163077
Seq. ID	LIB3177-056-P1-K1-B6
Method	BLASTX
NCBI GI	g400983
BLAST score	372
E value	1.0e-35
Match length	76
% identity	95
NCBI Description	50S RIBOSOMAL PROTEIN L11, CHLOROPLAST PRECURSOR (CL11) >gi_279648_pir__R5SP11 ribosomal protein L11 precursor - spinach >gi_21313_emb_CAA39950_ (X56615) ribosomal protein L11 [Spinacia oleracea]

Seq. No.	163078
Seq. ID	LIB3177-056-P1-K1-B7
Method	BLASTN
NCBI GI	g2244901
BLAST score	163
E value	1.0e-86
Match length	356
% identity	89
NCBI Description	Arabidopsis thaliana DNA chromosome 4, ESSA I contig fragment No

Seq. No.	163079
Seq. ID	LIB3177-056-P1-K1-B8
Method	BLASTX
NCBI GI	g3201613
BLAST score	424
E value	1.0e-71
Match length	150
% identity	90
NCBI Description	(AC004669) glutathione S-transferase [Arabidopsis thaliana]

Seq. No.	163080
Seq. ID	LIB3177-056-P1-K1-B9
Method	BLASTX
NCBI GI	g4678944
BLAST score	537
E value	6.0e-55
Match length	119
% identity	53
NCBI Description	(AL049711) putative protein [Arabidopsis thaliana]

Seq. No.	163081
Seq. ID	LIB3177-056-P1-K1-C1
Method	BLASTN
NCBI GI	g2853071
BLAST score	473
E value	0.0e+00
Match length	480
% identity	100
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F24J7 (ESSA project)

Seq. No.	163082
Seq. ID	LIB3177-056-P1-K1-C10
Method	BLASTN
NCBI GI	g4757405
BLAST score	339
E value	0.0e+00
Match length	422
% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MOJ10, complete sequence

Seq. No.	163083
Seq. ID	LIB3177-056-P1-K1-C11
Method	BLASTX
NCBI GI	g2642429
BLAST score	159
E value	1.0e-10
Match length	145
% identity	26
NCBI Description	(AC002391) putative poly(A)-binding protein [Arabidopsis thaliana]

Seq. No.	163084
Seq. ID	LIB3177-056-P1-K1-C2
Method	BLASTX
NCBI GI	g3831445
BLAST score	792
E value	7.0e-85
Match length	150
% identity	100
NCBI Description	(AC005819) unknown protein [Arabidopsis thaliana]

Seq. No.	163085
Seq. ID	LIB3177-056-P1-K1-C3
Method	BLASTN

NCBI GI	g2264316
BLAST score	89
E value	3.0e-42
Match length	438
% identity	38
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MRO11, complete sequence [Arabidopsis thaliana]

Seq. No.	163086
Seq. ID	LIB3177-056-P1-K1-C4
Method	BLASTX
NCBI GI	g1351271
BLAST score	237
E value	8.0e-20
Match length	101
% identity	57
NCBI Description	TRIOSEPHOSPHATE ISOMERASE CHLOROPLAST PRECURSOR (TIM) >gi_1084309_pir__S52032 triose-phosphate isomerase (EC 5.3.1.1) precursor, chloroplast - spinach >gi_806312 (L36387) triosephosphate isomerase, chloroplast isozyme [Spinacia oleracea]

Seq. No.	163087
Seq. ID	LIB3177-056-P1-K1-C6
Method	BLASTN
NCBI GI	g3249094
BLAST score	306
E value	1.0e-172
Match length	338
% identity	98
NCBI Description	Arabidopsis thaliana chromosome 1 BAC T12M4 sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	163088
Seq. ID	LIB3177-056-P1-K1-C7
Method	BLASTX
NCBI GI	g2529370
BLAST score	594
E value	9.0e-62
Match length	128
% identity	88
NCBI Description	(L76552) NADP-dependent glyceraldehydephosphate dehydrogenase subunit A [Spinacia oleracea]

Seq. No.	163089
Seq. ID	LIB3177-056-P1-K1-C8
Method	BLASTX
NCBI GI	g1362162
BLAST score	490
E value	2.0e-49
Match length	119
% identity	76
NCBI Description	beta-glucosidase BGQ60 precursor - barley >gi_804656 (L41869) beta-glucosidase [Hordeum vulgare]

Seq. No.	163090
Seq. ID	LIB3177-056-P1-K1-C9

Method	BLASTX
NCBI GI	g1732570
BLAST score	137
E value	8.0e-23
Match length	60
% identity	95
NCBI Description	(U72153) beta-glucosidase [Arabidopsis thaliana]

Seq. No.	163091
Seq. ID	LIB3177-056-P1-K1-D1
Method	BLASTN
NCBI GI	g16172
BLAST score	55
E value	3.0e-22
Match length	59
% identity	98
NCBI Description	A.thaliana mRNA for ascorbate peroxidase

Seq. No.	163092
Seq. ID	LIB3177-056-P1-K1-D10
Method	BLASTX
NCBI GI	g16374
BLAST score	778
E value	3.0e-83
Match length	150
% identity	100
NCBI Description	(X03908) chlorophyll a/b binding protein (LHCP AB 180) [Arabidopsis thaliana]

Seq. No.	163093
Seq. ID	LIB3177-056-P1-K1-D11
Method	BLASTX
NCBI GI	g3482915
BLAST score	456
E value	2.0e-45
Match length	142
% identity	65
NCBI Description	(AC003970) Similar to 12-oxophytodienoate reductase, gi_2765083 and old-yellow-enzyme homolog, gi_2232254 [Arabidopsis thaliana]

Seq. No.	163094
Seq. ID	LIB3177-056-P1-K1-D3
Method	BLASTX
NCBI GI	g2632254
BLAST score	438
E value	2.0e-43
Match length	133
% identity	60
NCBI Description	(Y12465) serine/threonine kinase [Sorghum bicolor]

Seq. No.	163095
Seq. ID	LIB3177-056-P1-K1-D4
Method	BLASTN
NCBI GI	g304108
BLAST score	268
E value	1.0e-149

Match length	296
% identity	98
NCBI Description	Arabidopsis thaliana poly(A)-binding protein mRNA, complete cds

Seq. No.	163096
Seq. ID	LIB3177-056-P1-K1-D5
Method	BLASTX
NCBI GI	g1336084
BLAST score	598
E value	4.0e-62
Match length	113
% identity	99
NCBI Description	(U56635) Arabidopsis thaliana glutamate dehydrogenase 2 (GDH2) mRNA, complete cds. [Arabidopsis thaliana]

Seq. No.	163097
Seq. ID	LIB3177-056-P1-K1-D6
Method	BLASTX
NCBI GI	g4586256
BLAST score	579
E value	6.0e-60
Match length	146
% identity	79
NCBI Description	(AL049640) probable photosystem I chain XI precursor [Arabidopsis thaliana]

Seq. No.	163098
Seq. ID	LIB3177-056-P1-K1-D7
Method	BLASTX
NCBI GI	g99735
BLAST score	775
E value	7.0e-83
Match length	146
% identity	99
NCBI Description	L-ascorbate peroxidase (EC 1.11.1.11) precursor - Arabidopsis thaliana (fragment)

Seq. No.	163099
Seq. ID	LIB3177-056-P1-K1-E1
Method	BLASTX
NCBI GI	g115767
BLAST score	313
E value	1.0e-31
Match length	90
% identity	83
NCBI Description	CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR (CAB-165/180) (LHCP) >gi_81603_pir__A29280 chlorophyll a/b-binding protein ab165 - Arabidopsis thaliana >gi_16368_emb_CAA27540_ (X03907) chlorophyll a/b binding protein (LHCP AB 65) [Arabidopsis thaliana] >gi_16372_emb_CAA27541_ (X03908) chlorophyll a/b binding protein (LHCP AB 180) [Arabidopsis thaliana]

Seq. No.	163100
Seq. ID	LIB3177-056-P1-K1-E10
Method	BLASTN

NCBI GI	g4585918
BLAST score	47
E value	4.0e-18
Match length	63
% identity	94
NCBI Description	Arabidopsis thaliana chromosome II BAC F1O13 genomic sequence, complete sequence

Seq. No.	163101
Seq. ID	LIB3177-056-P1-K1-E11
Method	BLASTX
NCBI GI	g1769905
BLAST score	398
E value	9.0e-39
Match length	128
% identity	63
NCBI Description	(X98108) 23 kDa polypeptide of oxygen-evolving comlex (OEC) [Arabidopsis thaliana]

Seq. No.	163102
Seq. ID	LIB3177-056-P1-K1-E12
Method	BLASTX
NCBI GI	g4006883
BLAST score	597
E value	5.0e-62
Match length	141
% identity	83
NCBI Description	(Z99707) cysteine proteinase [Arabidopsis thaliana]

Seq. No.	163103
Seq. ID	LIB3177-056-P1-K1-E2
Method	BLASTN
NCBI GI	g2924653
BLAST score	224
E value	1.0e-123
Match length	333
% identity	98
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MDA7, complete sequence [Arabidopsis thaliana]

Seq. No.	163104
Seq. ID	LIB3177-056-P1-K1-E5
Method	BLASTX
NCBI GI	g1850546
BLAST score	271
E value	8.0e-24
Match length	55
% identity	100
NCBI Description	(U88045) syntaxin related protein AtVam3p [Arabidopsis thaliana]

Seq. No.	163105
Seq. ID	LIB3177-056-P1-K1-E6
Method	BLASTN
NCBI GI	g4376087
BLAST score	118
E value	6.0e-60

Match length	142
% identity	96
NCBI Description	Arabidopsis thaliana DNA chromosome 4, ESSA I AP2 contig fragment No

Seq. No.	163106
Seq. ID	LIB3177-056-P1-K1-F10
Method	BLASTX
NCBI GI	g461550
BLAST score	188
E value	3.0e-39
Match length	145
% identity	70
NCBI Description	ATP SYNTHASE GAMMA CHAIN 1, CHLOROPLAST PRECURSOR >gi_81635_pir__B39732 H+-transporting ATP synthase (EC 3.6.1.34) gamma-1 chain precursor, chloroplast - Arabidopsis thaliana >gi_166632 (M61741) ATP synthase gamma-subunit [Arabidopsis thaliana]

Seq. No.	163107
Seq. ID	LIB3177-056-P1-K1-F11
Method	BLASTX
NCBI GI	g730688
BLAST score	676
E value	3.0e-71
Match length	133
% identity	99
NCBI Description	MITOCHONDRIAL 40S RIBOSOMAL PROTEIN S19 PRECURSOR >gi_2129722_pir__S71114 ribosomal protein S19 precursor, mitochondrial - Arabidopsis thaliana >gi_457760_emb_CAA54951_ (X77989) ribosomal protein S19 [Arabidopsis thaliana] >gi_459422_emb_CAA54965_ (X78035) mitochondrial ribosomal protein S19, nuclear encoded [Arabidopsis thaliana]

Seq. No.	163108
Seq. ID	LIB3177-056-P1-K1-F12
Method	BLASTX
NCBI GI	g2688824
BLAST score	243
E value	1.0e-20
Match length	68
% identity	72
NCBI Description	(U93273) putative auxin-repressed protein [Prunus armeniaca]

Seq. No.	163109
Seq. ID	LIB3177-056-P1-K1-F3
Method	BLASTX
NCBI GI	g132110
BLAST score	730
E value	1.0e-77
Match length	135
% identity	99
NCBI Description	RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN 3B PRECURSOR (RUBISCO SMALL SUBUNIT 3B) >gi_68060_pir__RKMUB3 ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain

B3 precursor - Arabidopsis thaliana >gi_16195_emb_CAA32702_ (X14564) ribulose bisphosphate carboxylase [Arabidopsis thaliana]

Seq. No.	163110
Seq. ID	LIB3177-056-P1-K1-F4
Method	BLASTX
NCBI GI	g1848214
BLAST score	365
E value	8.0e-35
Match length	86
% identity	77
NCBI Description	(Y11210) uracil phosphoribosyltransferase [Nicotiana tabacum]

Seq. No.	163111
Seq. ID	LIB3177-056-P1-K1-F5
Method	BLASTX
NCBI GI	g2961372
BLAST score	757
E value	9.0e-81
Match length	143
% identity	100
NCBI Description	(AL022141) putative ribosomal protein L8 [Arabidopsis thaliana] >gi_3036817_emb_CAA18507_ (AL022373) ribosomal protein L2 [Arabidopsis thaliana]

Seq. No.	163112
Seq. ID	LIB3177-056-P1-K1-F6
Method	BLASTN
NCBI GI	g2618601
BLAST score	138
E value	1.0e-71
Match length	170
% identity	96
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MHJ24, complete sequence [Arabidopsis thaliana]

Seq. No.	163113
Seq. ID	LIB3177-056-P1-K1-G1
Method	BLASTX
NCBI GI	g4539008
BLAST score	534
E value	1.0e-54
Match length	150
% identity	77
NCBI Description	(AL049481) lipase-like protein [Arabidopsis thaliana]

Seq. No.	163114
Seq. ID	LIB3177-056-P1-K1-G10
Method	BLASTX
NCBI GI	g2661422
BLAST score	795
E value	3.0e-85
Match length	154
% identity	99
NCBI Description	(AJ001342) Putative S-phase-specific ribosomal protein

[Arabidopsis thaliana] >gi_3096936_emb_CAA18846.1_ (AL023094) Putative S-phase-specific ribosomal protein [Arabidopsis thaliana]

Seq. No.	163115
Seq. ID	LIB3177-056-P1-K1-G11
Method	BLASTX
NCBI GI	g2492863
BLAST score	392
E value	5.0e-38
Match length	97
% identity	68
NCBI Description	ORNITHINE AMINOTRANSFERASE (ORNITHINE--OXO-ACID AMINOTRANSFERASE) >gi_4416517_gb_AAB18259_ (U74303) ornithine transaminase [Emericella nidulans]

Seq. No.	163116
Seq. ID	LIB3177-056-P1-K1-G12
Method	BLASTX
NCBI GI	g132074
BLAST score	758
E value	7.0e-81
Match length	138
% identity	100
NCBI Description	RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN 1A PRECURSOR (RUBISCO SMALL SUBUNIT 1A) >gi_68063_pir__RKMUA1 ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain A1 precursor - Arabidopsis thaliana

Seq. No.	163117
Seq. ID	LIB3177-056-P1-K1-G2
Method	BLASTX
NCBI GI	g4469022
BLAST score	818
E value	6.0e-88
Match length	156
% identity	100
NCBI Description	(AL035602) cytochrome P450-like protein [Arabidopsis thaliana]

Seq. No.	163118
Seq. ID	LIB3177-056-P1-K1-G4
Method	BLASTX
NCBI GI	g3036807
BLAST score	335
E value	2.0e-31
Match length	144
% identity	53
NCBI Description	(AL022373) putative protein [Arabidopsis thaliana]

Seq. No.	163119
Seq. ID	LIB3177-056-P1-K1-G5
Method	BLASTX
NCBI GI	g4539008
BLAST score	399
E value	6.0e-39
Match length	121

% identity	74
NCBI Description	(AL049481) lipase-like protein [Arabidopsis thaliana]
Seq. No.	163120
Seq. ID	LIB3177-056-P1-K1-G6
Method	BLASTX
NCBI GI	g2129672
BLAST score	270
E value	9.0e-24
Match length	102
% identity	56
NCBI Description	photosystem II reaction center protein, 6.1K - Arabidopsis thaliana >gi_950023_emb_CAA62296_ (X90769) component of 6.1 kDa polypeptide of photosystem II reaction center [Arabidopsis thaliana]
Seq. No.	163121
Seq. ID	LIB3177-056-P1-K1-G7
Method	BLASTX
NCBI GI	g1705677
BLAST score	564
E value	4.0e-58
Match length	123
% identity	91
NCBI Description	CELL DIVISION CYCLE PROTEIN 48 HOMOLOG >gi_2118115_pir__S60112 cell division control protein CDC48 homolog - Arabidopsis thaliana >gi_1019904 (U37587) cell division cycle protein [Arabidopsis thaliana]
Seq. No.	163122
Seq. ID	LIB3177-056-P1-K1-G8
Method	BLASTX
NCBI GI	g3281855
BLAST score	182
E value	9.0e-14
Match length	62
% identity	68
NCBI Description	(AL031004) hypothetical protein [Arabidopsis thaliana]
Seq. No.	163123
Seq. ID	LIB3177-056-P1-K1-H1
Method	BLASTX
NCBI GI	g461550
BLAST score	475
E value	1.0e-47
Match length	143
% identity	69
NCBI Description	ATP SYNTHASE GAMMA CHAIN 1, CHLOROPLAST PRECURSOR >gi_81635_pir__B39732 H+-transporting ATP synthase (EC 3.6.1.34) gamma-1 chain precursor, chloroplast - Arabidopsis thaliana >gi_166632 (M61741) ATP synthase gamma-subunit [Arabidopsis thaliana]
Seq. No.	163124
Seq. ID	LIB3177-056-P1-K1-H10
Method	BLASTX
NCBI GI	g3738298

BLAST score	156
E value	2.0e-10
Match length	103
% identity	36
NCBI Description	(AC005309) unknown protein [Arabidopsis thaliana] >gi_4249394 (AC006072) unknown protein [Arabidopsis thaliana]

Seq. No.	163125
Seq. ID	LIB3177-056-P1-K1-H11
Method	BLASTX
NCBI GI	g4741948
BLAST score	731
E value	1.0e-77
Match length	139
% identity	99
NCBI Description	(AF134124) Lhcb2 protein [Arabidopsis thaliana]

Seq. No.	163126
Seq. ID	LIB3177-056-P1-K1-H12
Method	BLASTX
NCBI GI	g1617270
BLAST score	700
E value	4.0e-74
Match length	135
% identity	92
NCBI Description	(X94624) acyl-CoA synthetase [Brassica napus]

Seq. No.	163127
Seq. ID	LIB3177-056-P1-K1-H2
Method	BLASTX
NCBI GI	g2464941
BLAST score	650
E value	3.0e-68
Match length	134
% identity	88
NCBI Description	(Z99708) ubiquitin-conjugating enzyme [Arabidopsis thaliana] >gi_2801446 (AF028340) ubiquitin-conjugating enzyme 17 [Arabidopsis thaliana]

Seq. No.	163128
Seq. ID	LIB3177-056-P1-K1-H3
Method	BLASTN
NCBI GI	g3047100
BLAST score	333
E value	0.0e+00
Match length	420
% identity	100
NCBI Description	Arabidopsis thaliana BAC F6N23

Seq. No.	163129
Seq. ID	LIB3177-056-P1-K1-H4
Method	BLASTN
NCBI GI	g4432811
BLAST score	128
E value	4.0e-66
Match length	144

% identity	97
NCBI Description	Arabidopsis thaliana chromosome II BAC F16D14 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	163130
Seq. ID	LIB3177-056-P1-K1-H5
Method	BLASTX
NCBI GI	g4539008
BLAST score	543
E value	1.0e-55
Match length	153
% identity	77
NCBI Description	(AL049481) lipase-like protein [Arabidopsis thaliana]

Seq. No.	163131
Seq. ID	LIB3177-056-P1-K1-H6
Method	BLASTN
NCBI GI	g3449320
BLAST score	205
E value	1.0e-111
Match length	461
% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MRB17, complete sequence [Arabidopsis thaliana]

Seq. No.	163132
Seq. ID	LIB3177-056-P1-K1-H7
Method	BLASTX
NCBI GI	g166835
BLAST score	580
E value	5.0e-60
Match length	127
% identity	91
NCBI Description	(M86720) ribulose bisphosphate carboxylase/oxygenase activase [Arabidopsis thaliana] >gi_2642170 (AC003000) Rubisco activase [Arabidopsis thaliana]

Seq. No.	163133
Seq. ID	LIB3177-056-P1-K1-H8
Method	BLASTX
NCBI GI	g126766
BLAST score	652
E value	1.0e-68
Match length	133
% identity	93
NCBI Description	MALATE SYNTHASE, GLYOXYSOMAL >gi_68216_pir__SYRPMA malate synthase (EC 4.1.3.2), glyoxysomal - rape >gi_167150 (J04468) malate synthase (EC 4.1.3.2) [Brassica napus]

Seq. No.	163134
Seq. ID	LIB3177-056-P1-K1-H9
Method	BLASTN
NCBI GI	g16200
BLAST score	215
E value	1.0e-117
Match length	306
% identity	97

NCBI Description	A.thaliana gene for auxin-binding protein

Seq. No.	163135
Seq. ID	LIB3177-057-P1-K1-A1
Method	BLASTN
NCBI GI	g2351073
BLAST score	269
E value	1.0e-150
Match length	357
% identity	86
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MYJ24, complete sequence [Arabidopsis thaliana]

Seq. No.	163136
Seq. ID	LIB3177-057-P1-K1-A10
Method	BLASTN
NCBI GI	g3128137
BLAST score	226
E value	1.0e-124
Match length	377
% identity	96
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K9I9, complete sequence [Arabidopsis thaliana]

Seq. No.	163137
Seq. ID	LIB3177-057-P1-K1-A11
Method	BLASTN
NCBI GI	g2275194
BLAST score	162
E value	7.0e-86
Match length	431
% identity	100
NCBI Description	Arabidopsis thaliana chromosome II BAC T08I13 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	163138
Seq. ID	LIB3177-057-P1-K1-A2
Method	BLASTX
NCBI GI	g282865
BLAST score	573
E value	2.0e-59
Match length	109
% identity	73
NCBI Description	chlorophyll a/b-binding protein - Arabidopsis thaliana >gi_16207_emb_CAA39534_ (X56062) chlorophyll A/B-binding protein [Arabidopsis thaliana] >gi_166644 (M85150) chlorophyll a/b-binding protein [Arabidopsis thaliana] >gi_4678304_emb_CAB41095.1_ (AL049655) chlorophyll a/b-binding protein [Arabidopsis thaliana]

Seq. No.	163139
Seq. ID	LIB3177-057-P1-K1-A3
Method	BLASTX
NCBI GI	g4218120
BLAST score	283
E value	1.0e-35
Match length	130

% identity	61
NCBI Description	(AL035353) Proline-rich APG-like protein [Arabidopsis thaliana]

Seq. No.	163140
Seq. ID	LIB3177-057-P1-K1-A4
Method	BLASTX
NCBI GI	g4741940
BLAST score	771
E value	2.0e-82
Match length	145
% identity	97
NCBI Description	(AF134120) Lhca2 protein [Arabidopsis thaliana]

Seq. No.	163141
Seq. ID	LIB3177-057-P1-K1-A5
Method	BLASTX
NCBI GI	g1363489
BLAST score	430
E value	8.0e-43
Match length	84
% identity	98
NCBI Description	thioglucosidase (EC 3.2.3.1) 3D precursor - Arabidopsis thaliana >gi_984052_emb_CAA61592_ (X89413) thioglucoside glucohydrolase [Arabidopsis thaliana]

Seq. No.	163142
Seq. ID	LIB3177-057-P1-K1-A6
Method	BLASTN
NCBI GI	g2244788
BLAST score	62
E value	6.0e-27
Match length	97
% identity	91
NCBI Description	Arabidopsis thaliana DNA chromosome 4, ESSA I contig fragment No

Seq. No.	163143
Seq. ID	LIB3177-057-P1-K1-A8
Method	BLASTX
NCBI GI	g4263525
BLAST score	61
E value	2.0e-40
Match length	115
% identity	75
NCBI Description	(AC004044) putative photosystem I reaction center subunit II precursor [Arabidopsis thaliana]

Seq. No.	163144
Seq. ID	LIB3177-057-P1-K1-A9
Method	BLASTX
NCBI GI	g4582468
BLAST score	206
E value	2.0e-16
Match length	44
% identity	95
NCBI Description	(AC007071) putative 40S ribosomal protein; contains

C-terminal domain [Arabidopsis thaliana]

Seq. No.	163145
Seq. ID	LIB3177-057-P1-K1-B1
Method	BLASTX
NCBI GI	g3913218
BLAST score	255
E value	7.0e-22
Match length	72
% identity	75
NCBI Description	MAGNESIUM-CHELATASE SUBUNIT CHLD PRECURSOR (MG-PROTOPORPHYRIN IX CHELATASE) (MG-CHELATASE SUBUNIT D) >gi_2318117 (AF014399) Mg-chelatase subunit D [Pisum sativum]

Seq. No.	163146
Seq. ID	LIB3177-057-P1-K1-B10
Method	BLASTX
NCBI GI	g120675
BLAST score	510
E value	5.0e-57
Match length	135
% identity	76
NCBI Description	GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE, CYTOSOLIC >gi_66011_pir__DEIS3C glyceraldehyde-3-phosphate dehydrogenase (EC 1.2.1.12), cytosolic - white mustard >gi_21143_emb_CAA27844_ (X04301) GAPDH (aa 1-338) [Sinapis alba]

Seq. No.	163147
Seq. ID	LIB3177-057-P1-K1-B11
Method	BLASTX
NCBI GI	g4741960
BLAST score	503
E value	5.0e-51
Match length	115
% identity	84
NCBI Description	(AF134130) Lhcb6 protein [Arabidopsis thaliana]

Seq. No.	163148
Seq. ID	LIB3177-057-P1-K1-B3
Method	BLASTX
NCBI GI	g3694807
BLAST score	313
E value	4.0e-29
Match length	78
% identity	78
NCBI Description	(AF055898) alanine aminotransferase [Zea mays]

Seq. No.	163149
Seq. ID	LIB3177-057-P1-K1-B4
Method	BLASTN
NCBI GI	g12219
BLAST score	103
E value	7.0e-51
Match length	153
% identity	97

NCBI Description	Mustard chloroplast trnk gene for tRNA-Lys(UUU)
Seq. No.	163150
Seq. ID	LIB3177-057-P1-K1-B5
Method	BLASTX
NCBI GI	g3510256
BLAST score	206
E value	3.0e-16
Match length	76
% identity	49
NCBI Description	(AC005310) unknown protein [Arabidopsis thaliana]
Seq. No.	163151
Seq. ID	LIB3177-057-P1-K1-B7
Method	BLASTX
NCBI GI	g113497
BLAST score	206
E value	8.0e-17
Match length	65
% identity	60
NCBI Description	ALPHA-GALACTOSIDASE PRECURSOR (MELIBIASE) (ALPHA-D-GALACTOSIDE GALACTOHYDROLASE) >gi_99880_pir__S07472 alpha-galactosidase (EC 3.2.1.22) precursor - guar >gi_18292_emb_CAA32772_ (X14619) alpha-galactosidase preproprotein [Cyamopsis tetragonoloba]
Seq. No.	163152
Seq. ID	LIB3177-057-P1-K1-B8
Method	BLASTX
NCBI GI	g1350720
BLAST score	183
E value	1.0e-13
Match length	44
% identity	84
NCBI Description	60S RIBOSOMAL PROTEIN L32
Seq. No.	163153
Seq. ID	LIB3177-057-P1-K1-C1
Method	BLASTX
NCBI GI	g1922244
BLAST score	360
E value	1.0e-34
Match length	74
% identity	96
NCBI Description	(Y10085) putative desication related protein LEA14 [Arabidopsis thaliana] >gi_2505882_emb_CAA73311_ (Y12776) LEA protein [Arabidopsis thaliana]
Seq. No.	163154
Seq. ID	LIB3177-057-P1-K1-C10
Method	BLASTN
NCBI GI	g3046854
BLAST score	155
E value	1.0e-81
Match length	392
% identity	99
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:

MRG7, complete sequence [Arabidopsis thaliana]

Seq. No.	163155
Seq. ID	LIB3177-057-P1-K1-C11
Method	BLASTX
NCBI GI	g3201613
BLAST score	645
E value	1.0e-67
Match length	122
% identity	100
NCBI Description	(AC004669) glutathione S-transferase [Arabidopsis thaliana]

Seq. No.	163156
Seq. ID	LIB3177-057-P1-K1-C12
Method	BLASTX
NCBI GI	g4689386
BLAST score	290
E value	4.0e-26
Match length	124
% identity	52
NCBI Description	(AF139468) photosystem I reaction center subunit III [Vigna radiata]

Seq. No.	163157
Seq. ID	LIB3177-057-P1-K1-C2
Method	BLASTX
NCBI GI	g1046225
BLAST score	457
E value	1.0e-45
Match length	88
% identity	99
NCBI Description	(U21952) ethylene response sensor [Arabidopsis thaliana] >gi_2623308 (AC002409) ethylene response sensor (ERS) [Arabidopsis thaliana] >gi_1584365_prf__2122405A ERS gene [Arabidopsis thaliana]

Seq. No.	163158
Seq. ID	LIB3177-057-P1-K1-C3
Method	BLASTX
NCBI GI	g115783
BLAST score	655
E value	8.0e-69
Match length	126
% identity	98
NCBI Description	CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR (CAB-140) (LHCP) >gi_16376_emb_CAA27543_ (X03909) chlorophyll a/b binding protein (LHCP AB 140) [Arabidopsis thaliana]

Seq. No.	163159
Seq. ID	LIB3177-057-P1-K1-C5
Method	BLASTX
NCBI GI	g4586249
BLAST score	564
E value	4.0e-58
Match length	110
% identity	100

NCBI Description	(AL049640) putative pollen surface protein [Arabidopsis thaliana]
Seq. No.	163160
Seq. ID	LIB3177-057-P1-K1-C7
Method	BLASTN
NCBI GI	g413731
BLAST score	286
E value	1.0e-160
Match length	319
% identity	97
NCBI Description	Arabidopsis thaliana phytoene synthase mRNA, complete cds
Seq. No.	163161
Seq. ID	LIB3177-057-P1-K1-C8
Method	BLASTX
NCBI GI	g115767
BLAST score	675
E value	3.0e-71
Match length	130
% identity	99
NCBI Description	CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR (CAB-165/180) (LHCP) >gi_81603_pir__A29280 chlorophyll a/b-binding protein ab165 - Arabidopsis thaliana >gi_16368_emb_CAA27540_ (X03907) chlorophyll a/b binding protein (LHCP AB 65) [Arabidopsis thaliana] >gi_16372_emb_CAA27541_ (X03908) chlorophyll a/b binding protein (LHCP AB 180) [Arabidopsis thaliana]
Seq. No.	163162
Seq. ID	LIB3177-057-P1-K1-C9
Method	BLASTX
NCBI GI	g1063415
BLAST score	366
E value	3.0e-52
Match length	122
% identity	88
NCBI Description	(L40948) K+ channel protein [Arabidopsis thaliana]
Seq. No.	163163
Seq. ID	LIB3177-057-P1-K1-D1
Method	BLASTX
NCBI GI	g1732570
BLAST score	407
E value	7.0e-40
Match length	75
% identity	100
NCBI Description	(U72153) beta-glucosidase [Arabidopsis thaliana]
Seq. No.	163164
Seq. ID	LIB3177-057-P1-K1-D10
Method	BLASTN
NCBI GI	g2245031
BLAST score	253
E value	1.0e-140
Match length	274
% identity	97

NCBI Description	Arabidopsis thaliana DNA chromosome 4, ESSA I contig fragment No
Seq. No.	163165
Seq. ID	LIB3177-057-P1-K1-D11
Method	BLASTX
NCBI GI	g3877951
BLAST score	167
E value	8.0e-12
Match length	64
% identity	28
NCBI Description	(Z81555) predicted using Genefinder [Caenorhabditis elegans]
Seq. No.	163166
Seq. ID	LIB3177-057-P1-K1-D2
Method	BLASTX
NCBI GI	g99696
BLAST score	629
E value	9.0e-66
Match length	141
% identity	87
NCBI Description	glutamate--ammonia ligase (EC 6.3.1.2) precursor, chloroplast (clone lambdaAtgsl1) - Arabidopsis thaliana >gi_240070_bbs_69728 (S69727) light-regulated glutamine synthetase isoenzyme [Arabidopsis thaliana, Peptide, 430 aa] [Arabidopsis thaliana] >gi_228453_prf__1804333A Gln synthetase [Arabidopsis thaliana]
Seq. No.	163167
Seq. ID	LIB3177-057-P1-K1-D3
Method	BLASTX
NCBI GI	g16374
BLAST score	725
E value	4.0e-77
Match length	142
% identity	97
NCBI Description	(X03908) chlorophyll a/b binding protein (LHCP AB 180) [Arabidopsis thaliana]
Seq. No.	163168
Seq. ID	LIB3177-057-P1-K1-D4
Method	BLASTX
NCBI GI	g3024022
BLAST score	588
E value	6.0e-61
Match length	130
% identity	85
NCBI Description	INITIATION FACTOR 5A-5 (EIF-5A) (EIF-4D) >gi_2225885_dbj_BAA20879_ (AB004826) eukaryotic initiation factor 5A5 [Solanum tuberosum]
Seq. No.	163169
Seq. ID	LIB3177-057-P1-K1-D5
Method	BLASTX
NCBI GI	g115783
BLAST score	660

E value	2.0e-69
Match length	125
% identity	99
NCBI Description	CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR (CAB-140) (LHCP) >gi_16376_emb_CAA27543_ (X03909) chlorophyll a/b binding protein (LHCP AB 140) [Arabidopsis thaliana]

Seq. No.	163170
Seq. ID	LIB3177-057-P1-K1-D6
Method	BLASTN
NCBI GI	g2352827
BLAST score	140
E value	5.0e-73
Match length	208
% identity	92
NCBI Description	Arabidopsis thaliana NaCl-inducible Ca2+-binding protein (ACP1) mRNA, complete cds

Seq. No.	163171
Seq. ID	LIB3177-057-P1-K1-D7
Method	BLASTN
NCBI GI	g2352827
BLAST score	278
E value	1.0e-155
Match length	302
% identity	98
NCBI Description	Arabidopsis thaliana NaCl-inducible Ca2+-binding protein (ACP1) mRNA, complete cds

Seq. No.	163172
Seq. ID	LIB3177-057-P1-K1-D9
Method	BLASTX
NCBI GI	g1063415
BLAST score	447
E value	2.0e-44
Match length	88
% identity	97
NCBI Description	(L40948) K+ channel protein [Arabidopsis thaliana]

Seq. No.	163173
Seq. ID	LIB3177-057-P1-K1-E1
Method	BLASTX
NCBI GI	g2506443
BLAST score	551
E value	1.0e-56
Match length	135
% identity	79
NCBI Description	GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE A PRECURSOR, CHLOROPLAST >gi_2117520_pir__JQ1285 glyceraldehyde-3-phosphate dehydrogenase (NADP+) (phosphorylating) (EC 1.2.1.13) A precursor, chloroplast - Arabidopsis thaliana >gi_166704 (M64117) glyceraldehyde 3-phosphate dehydrogenase [Arabidopsis thaliana] >gi_1402885_emb_CAA66816_ (X98130) glyceraldehyde-3-phosphate dehydrogenase (NADP+) (phosphorylating) [Arabidopsis thaliana]

Seq. No.	163174
Seq. ID	LIB3177-057-P1-K1-E11
Method	BLASTX
NCBI GI	g2495209
BLAST score	379
E value	2.0e-36
Match length	108
% identity	61
NCBI Description	HYPOTHETICAL 12.9 KD PROTEIN SLR1417 >gi_1651819_dbj_BAA16746_ (D90900) hypothetical protein [Synechocystis sp.]

Seq. No.	163175
Seq. ID	LIB3177-057-P1-K1-E12
Method	BLASTX
NCBI GI	g4741940
BLAST score	567
E value	1.0e-58
Match length	103
% identity	66
NCBI Description	(AF134120) Lhca2 protein [Arabidopsis thaliana]

Seq. No.	163176
Seq. ID	LIB3177-057-P1-K1-E2
Method	BLASTX
NCBI GI	g3608412
BLAST score	631
E value	5.0e-66
Match length	152
% identity	78
NCBI Description	(AF079355) protein phosphatase-2c [Mesembryanthemum crystallinum]

Seq. No.	163177
Seq. ID	LIB3177-057-P1-K1-E3
Method	BLASTX
NCBI GI	g3287944
BLAST score	137
E value	1.0e-08
Match length	44
% identity	61
NCBI Description	HYPOTHETICAL 16.2 KD PROTEIN C3D6.08C IN CHROMOSOME II >gi_2117304_emb_CAB09117.1_ (Z95620) hypothetical protein [Schizosaccharomyces pombe]

Seq. No.	163178
Seq. ID	LIB3177-057-P1-K1-E4
Method	BLASTX
NCBI GI	g3176668
BLAST score	766
E value	7.0e-82
Match length	151
% identity	97
NCBI Description	(AC004393) Similar to ribosomal protein L17 gb_X62724 from Hordeum vulgare. ESTs gb_Z34728, gb_F19974, gb_T75677 and gb_Z33937 come from this gene. [Arabidopsis thaliana]

Seq. No.	163179
Seq. ID	LIB3177-057-P1-K1-E5
Method	BLASTX
NCBI GI	g4539408
BLAST score	278
E value	3.0e-27
Match length	126
% identity	61
NCBI Description	(AL049524) putative alpha NAC [Arabidopsis thaliana]

Seq. No.	163180
Seq. ID	LIB3177-057-P1-K1-E6
Method	BLASTN
NCBI GI	g2341023
BLAST score	349
E value	0.0e+00
Match length	377
% identity	98
NCBI Description	Sequence of BAC F19P19 from Arabidopsis thaliana chromosome 1, complete sequence [Arabidopsis thaliana]

Seq. No.	163181
Seq. ID	LIB3177-057-P1-K1-E7
Method	BLASTN
NCBI GI	g2828184
BLAST score	174
E value	3.0e-93
Match length	294
% identity	90
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MSN9, complete sequence [Arabidopsis thaliana]

Seq. No.	163182
Seq. ID	LIB3177-057-P1-K1-E8
Method	BLASTX
NCBI GI	g1175010
BLAST score	302
E value	1.0e-27
Match length	75
% identity	83
NCBI Description	PLASMA MEMBRANE INTRINSIC PROTEIN 1A >gi_629540_pir__S44082 plasma membrane intrinsic protein 1a - Arabidopsis thaliana >gi_472873_emb_CAA53475_ (X75881) plasma membrane intrinsic protein 1a [Arabidopsis thaliana]

Seq. No.	163183
Seq. ID	LIB3177-057-P1-K1-F10
Method	BLASTX
NCBI GI	g115385
BLAST score	637
E value	1.0e-66
Match length	123
% identity	100
NCBI Description	CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR (CAB-4) (LHCP) >gi_166646 (M63931) light-harvesting chlorophyll a/b binding protein [Arabidopsis thaliana]

Seq. No.	163184
Seq. ID	LIB3177-057-P1-K1-F11
Method	BLASTX
NCBI GI	g2146746
BLAST score	792
E value	7.0e-85
Match length	154
% identity	99
NCBI Description	protein kinase (EC 2.7.1.-) - Arabidopsis thaliana >gi_166819 (L05562) protein kinase [Arabidopsis thaliana]

Seq. No.	163185
Seq. ID	LIB3177-057-P1-K1-F12
Method	BLASTN
NCBI GI	g3241925
BLAST score	348
E value	0.0e+00
Match length	348
% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MOK9, complete sequence [Arabidopsis thaliana]

Seq. No.	163186
Seq. ID	LIB3177-057-P1-K1-F2
Method	BLASTN
NCBI GI	g4165340
BLAST score	99
E value	2.0e-48
Match length	151
% identity	92
NCBI Description	Arabidopsis thaliana chromosome I BAC F11M15 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	163187
Seq. ID	LIB3177-057-P1-K1-F3
Method	BLASTN
NCBI GI	g769742
BLAST score	290
E value	1.0e-162
Match length	310
% identity	98
NCBI Description	A.thaliana mRNA for phosphoinositide-specific phospholipase C

Seq. No.	163188
Seq. ID	LIB3177-057-P1-K1-F4
Method	BLASTN
NCBI GI	g3413696
BLAST score	339
E value	0.0e+00
Match length	343
% identity	100
NCBI Description	Arabidopsis thaliana chromosome II BAC T19L18 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	163189

Seq. ID	LIB3177-057-P1-K1-F5
Method	BLASTX
NCBI GI	g3128180
BLAST score	94
E value	2.0e-53
Match length	112
% identity	92
NCBI Description	(AC004521) citrate synthetase [Arabidopsis thaliana]

Seq. No.	163190
Seq. ID	LIB3177-057-P1-K1-F6
Method	BLASTX
NCBI GI	g4741960
BLAST score	583
E value	2.0e-60
Match length	129
% identity	86
NCBI Description	(AF134130) Lhcb6 protein [Arabidopsis thaliana]

Seq. No.	163191
Seq. ID	LIB3177-057-P1-K1-F7
Method	BLASTX
NCBI GI	g2326359
BLAST score	186
E value	7.0e-14
Match length	45
% identity	87
NCBI Description	(Y11190) hypothetical protein [Arabidopsis thaliana]

Seq. No.	163192
Seq. ID	LIB3177-057-P1-K1-F8
Method	BLASTX
NCBI GI	g3746059
BLAST score	411
E value	3.0e-40
Match length	118
% identity	64
NCBI Description	(AC005311) putative cysteinyl-tRNA synthetase [Arabidopsis thaliana] >gi_4432812_gb_AAD20662_ (AC006593) putative cysteinyl-tRNA synthetase [Arabidopsis thaliana]

Seq. No.	163193
Seq. ID	LIB3177-057-P1-K1-F9
Method	BLASTX
NCBI GI	g2956690
BLAST score	503
E value	5.0e-51
Match length	134
% identity	61
NCBI Description	(AJ223306) PSBY [Arabidopsis thaliana] >gi_3414928 (AF079800) PsbY precursor [Arabidopsis thaliana]

Seq. No.	163194
Seq. ID	LIB3177-057-P1-K1-G1
Method	BLASTN
NCBI GI	g4589430
BLAST score	344

E value	0.0e+00
Match length	449
% identity	99
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MLD14, complete sequence

Seq. No.	163195
Seq. ID	LIB3177-057-P1-K1-G11
Method	BLASTN
NCBI GI	g2191126
BLAST score	374
E value	0.0e+00
Match length	434
% identity	100
NCBI Description	Arabidopsis thaliana BAC IG002N01

Seq. No.	163196
Seq. ID	LIB3177-057-P1-K1-G12
Method	BLASTN
NCBI GI	g2656028
BLAST score	357
E value	0.0e+00
Match length	385
% identity	98
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MNF13

Seq. No.	163197
Seq. ID	LIB3177-057-P1-K1-G2
Method	BLASTN
NCBI GI	g4490717
BLAST score	352
E value	0.0e+00
Match length	392
% identity	97
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone (ESSA project)

Seq. No.	163198
Seq. ID	LIB3177-057-P1-K1-G3
Method	BLASTN
NCBI GI	g3650026
BLAST score	229
E value	1.0e-126
Match length	461
% identity	98
NCBI Description	Arabidopsis thaliana chromosome II BAC T26I20 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	163199
Seq. ID	LIB3177-057-P1-K1-G6
Method	BLASTX
NCBI GI	g1353352
BLAST score	379
E value	2.0e-36
Match length	111
% identity	70

NCBI Description	(U31975) alanine aminotransferase [Chlamydomonas reinhardtii]

Seq. No.	163200
Seq. ID	LIB3177-057-P1-K1-G7
Method	BLASTX
NCBI GI	g1170089
BLAST score	736
E value	3.0e-78
Match length	147
% identity	99
NCBI Description	GLUTATHIONE S-TRANSFERASE ERD13 (CLASS PHI) >gi_481822_pir__S39542 probable glutathione transferase (EC 2.5.1.18) (clone ERD13) - Arabidopsis thaliana >gi_497789_dbj_BAA04554_ (D17673) glutathione S-transferase [Arabidopsis thaliana] >gi_3201614 (AC004669) glutathione S-transferase [Arabidopsis thaliana]

Seq. No.	163201
Seq. ID	LIB3177-057-P1-K1-G8
Method	BLASTN
NCBI GI	g3176701
BLAST score	79
E value	2.0e-36
Match length	115
% identity	92
NCBI Description	Arabidopsis thaliana chromosome II BAC T20K24 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	163202
Seq. ID	LIB3177-057-P1-K1-G9
Method	BLASTN
NCBI GI	g2618601
BLAST score	149
E value	4.0e-78
Match length	402
% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MHJ24, complete sequence [Arabidopsis thaliana]

Seq. No.	163203
Seq. ID	LIB3177-057-P1-K1-H1
Method	BLASTX
NCBI GI	g585084
BLAST score	154
E value	3.0e-10
Match length	45
% identity	64
NCBI Description	ELONGATION FACTOR G, MITOCHONDRIAL PRECURSOR (MEF-G) >gi_543383_pir__S40780 translation elongation factor G, mitochondrial - rat >gi_310102 (L14684) elongation factor G [Rattus norvegicus]

Seq. No.	163204
Seq. ID	LIB3177-057-P1-K1-H10
Method	BLASTN
NCBI GI	g403417

BLAST score	221
E value	1.0e-121
Match length	221
% identity	100
NCBI Description	Arabidopsis thaliana Columbia bZIP protein GBF4 gene, complete cds

Seq. No.	163205
Seq. ID	LIB3177-057-P1-K1-H11
Method	BLASTX
NCBI GI	g1946362
BLAST score	203
E value	3.0e-16
Match length	37
% identity	100
NCBI Description	(U93215) photosystem II reaction center 6.1KD protein [Arabidopsis thaliana]

Seq. No.	163206
Seq. ID	LIB3177-057-P1-K1-H2
Method	BLASTX
NCBI GI	g115783
BLAST score	653
E value	1.0e-68
Match length	125
% identity	98
NCBI Description	CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR (CAB-140) (LHCP) >gi_16376_emb_CAA27543_ (X03909) chlorophyll a/b binding protein (LHCP AB 140) [Arabidopsis thaliana]

Seq. No.	163207
Seq. ID	LIB3177-057-P1-K1-H3
Method	BLASTN
NCBI GI	g3241926
BLAST score	162
E value	4.0e-86
Match length	232
% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MSG15, complete sequence [Arabidopsis thaliana]

Seq. No.	163208
Seq. ID	LIB3177-057-P1-K1-H5
Method	BLASTN
NCBI GI	g1946354
BLAST score	70
E value	4.0e-31
Match length	74
% identity	99
NCBI Description	Arabidopsis thaliana chromosome II BAC T06B20 genomic sequence, complete sequence

Seq. No.	163209
Seq. ID	LIB3177-057-P1-K1-H6
Method	BLASTX
NCBI GI	g2497541

BLAST score	327
E value	7.0e-31
Match length	65
% identity	92
NCBI Description	PYRUVATE KINASE, CHLOROPLAST ISOZYME A PRECURSOR >gi_482936_emb_CAA82222_ (Z28373) pyruvate kinase; plastid isozyme [Nicotiana tabacum]

Seq. No.	163210
Seq. ID	LIB3177-057-P1-K1-H7
Method	BLASTX
NCBI GI	g399942
BLAST score	701
E value	3.0e-74
Match length	147
% identity	94
NCBI Description	CHLOROPLAST STROMA 70 KD HEAT SHOCK-RELATED PROTEIN PRECURSOR >gi_421881_pir__S32818 heat shock protein, 70K, chloroplast - garden pea >gi_169023 (L03299) 70 kDa heat shock protein [Pisum sativum] >gi_871515_emb_CAA49147_ (X69213) Psst70 (stress 70 protein) [Pisum sativum]

Seq. No.	163211
Seq. ID	LIB3177-059-P1-K1-A1
Method	BLASTN
NCBI GI	g4079614
BLAST score	270
E value	1.0e-150
Match length	372
% identity	100
NCBI Description	Arabidopsis thaliana chromosome I BAC F21M11 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	163212
Seq. ID	LIB3177-059-P1-K1-A10
Method	BLASTN
NCBI GI	g3128136
BLAST score	118
E value	3.0e-60
Match length	118
% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K1F13, complete sequence [Arabidopsis thaliana]

Seq. No.	163213
Seq. ID	LIB3177-059-P1-K1-A11
Method	BLASTX
NCBI GI	g2956690
BLAST score	390
E value	9.0e-38
Match length	108
% identity	54
NCBI Description	(AJ223306) PSBY [Arabidopsis thaliana] >gi_3414928 (AF079800) PsbY precursor [Arabidopsis thaliana]

Seq. No.	163214
Seq. ID	LIB3177-059-P1-K1-A12

Method	BLASTX
NCBI GI	g114532
BLAST score	287
E value	1.0e-25
Match length	69
% identity	80
NCBI Description	ATP SYNTHASE ALPHA CHAIN >gi_67824_pir__PWNTA H+-transporting ATP synthase (EC 3.6.1.34) alpha chain - common tobacco chloroplast >gi_11769_emb_CAA23471_ (V00162) alpha subunit of ATPase [Nicotiana tabacum] >gi_11811_emb_CAA77341_ (Z00044) ATPase alpha subunit [Nicotiana tabacum] >gi_225270_prf__1211235E ATPase alpha [Nicotiana tabacum]

Seq. No.	163215
Seq. ID	LIB3177-059-P1-K1-A2
Method	BLASTX
NCBI GI	g115783
BLAST score	567
E value	1.0e-58
Match length	106
% identity	100
NCBI Description	CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR (CAB-140) (LHCP) >gi_16376_emb_CAA27543_ (X03909) chlorophyll a/b binding protein (LHCP AB 140) [Arabidopsis thaliana]

Seq. No.	163216
Seq. ID	LIB3177-059-P1-K1-A3
Method	BLASTX
NCBI GI	g2388561
BLAST score	747
E value	1.0e-79
Match length	143
% identity	99
NCBI Description	(AC000098) Similar to Arabidopsis hypothetical protein PID:e326839 (gb_Z97337). [Arabidopsis thaliana]

Seq. No.	163217
Seq. ID	LIB3177-059-P1-K1-A4
Method	BLASTN
NCBI GI	g4204173
BLAST score	291
E value	1.0e-163
Match length	450
% identity	100
NCBI Description	Arabidopsis thaliana chromosome 1 BAC T2K10 sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	163218
Seq. ID	LIB3177-059-P1-K1-A6
Method	BLASTX
NCBI GI	g3043529
BLAST score	141
E value	1.0e-08
Match length	73
% identity	36

NCBI Description	(AJ002204) polyamine oxidase [Zea mays]

Seq. No.	163219
Seq. ID	LIB3177-059-P1-K1-A8
Method	BLASTX
NCBI GI	g2129559
BLAST score	322
E value	6.0e-30
Match length	75
% identity	83
NCBI Description	cellulase homolog OR16pep - Arabidopsis thaliana >gi_1022807 (U37702) cellulase [Arabidopsis thaliana] >gi_3493633 (AF074092) cellulase [Arabidopsis thaliana] >gi_3598956 (AF074375) cellulase [Arabidopsis thaliana] >gi_3978258 (AF073875) endo-1,4-beta-D-glucanase KORRIGAN [Arabidopsis thaliana]

Seq. No.	163220
Seq. ID	LIB3177-059-P1-K1-A9
Method	BLASTN
NCBI GI	g3449323
BLAST score	356
E value	0.0e+00
Match length	419
% identity	96
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MZA15, complete sequence [Arabidopsis thaliana]

Seq. No.	163221
Seq. ID	LIB3177-059-P1-K1-B1
Method	BLASTX
NCBI GI	g267069
BLAST score	604
E value	6.0e-63
Match length	130
% identity	88
NCBI Description	TUBULIN ALPHA-2/ALPHA-4 CHAIN >gi_320183_pir__JQ1594 tubulin alpha chain - Arabidopsis thaliana >gi_166914 (M84696) apha-2 tubulin [Arabidopsis thaliana] >gi_166916 (M84697) alpha-4 tubulin [Arabidopsis thaliana]

Seq. No.	163222
Seq. ID	LIB3177-059-P1-K1-B10
Method	BLASTX
NCBI GI	g4689386
BLAST score	333
E value	3.0e-31
Match length	79
% identity	78
NCBI Description	(AF139468) photosystem I reaction center subunit III [Vigna radiata]

Seq. No.	163223
Seq. ID	LIB3177-059-P1-K1-B11
Method	BLASTN
NCBI GI	g2182286
BLAST score	279

E value	1.0e-156
Match length	287
% identity	99
NCBI Description	Sequence of BAC F20P5 from Arabidopsis thaliana chromosome 1, complete sequence [Arabidopsis thaliana]

Seq. No.	163224
Seq. ID	LIB3177-059-P1-K1-B2
Method	BLASTX
NCBI GI	g464986
BLAST score	559
E value	1.0e-57
Match length	110
% identity	95
NCBI Description	UBIQUITIN-CONJUGATING ENZYME E2-17 KD 9 (UBIQUITIN-PROTEIN LIGASE 9) (UBIQUITIN CARRIER PROTEIN 9) (UBCAT4B) >gi_421857_pir__S32674 ubiquitin--protein ligase (EC 6.3.2.19) UBC9 - Arabidopsis thaliana >gi_297884_emb_CAA78714_ (Z14990) ubiquitin conjugating enzyme homolog [Arabidopsis thaliana] >gi_349211 (L00639) ubiquitin conjugating enzyme [Arabidopsis thaliana] >gi_600391_emb_CAA51201_ (X72626) ubiquitin conjugating enzyme E2 [Arabidopsis thaliana] >gi_4455355_emb_CAB36765.1_ (AL035524) ubiquitin-protein ligase UBC9 [Arabidopsis thaliana]

Seq. No.	163225
Seq. ID	LIB3177-059-P1-K1-B3
Method	BLASTX
NCBI GI	g3023216
BLAST score	696
E value	1.0e-73
Match length	139
% identity	100
NCBI Description	14-3-3-LIKE PROTEIN GF14 MU >gi_1531629 (U60444) GF14 mu [Arabidopsis thaliana]

Seq. No.	163226
Seq. ID	LIB3177-059-P1-K1-B6
Method	BLASTX
NCBI GI	g266463
BLAST score	692
E value	2.0e-73
Match length	147
% identity	97
NCBI Description	3-ISOPROPYLMALATE DEHYDROGENASE PRECURSOR (BETA-IPM DEHYDROGENASE) (IMDH) (3-IPM-DH) >gi_82259_pir__S25670 3-isopropylmalate dehydrogenase (EC 1.1.1.85) precursor - potato >gi_22643_emb_CAA47720_ (X67310) 3-isopropylmalate dehydrogenase [Solanum tuberosum] >gi_445064_prf__1908380A beta isopropylmalate dehydrogenase [Solanum tuberosum]

Seq. No.	163227
Seq. ID	LIB3177-059-P1-K1-B9
Method	BLASTN
NCBI GI	g4455168
BLAST score	159

E value	3.0e-84
Match length	296
% identity	94
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F10M10 (ESSAII project)

Seq. No.	163228
Seq. ID	LIB3177-059-P1-K1-C1
Method	BLASTN
NCBI GI	g3242700
BLAST score	306
E value	1.0e-172
Match length	330
% identity	98
NCBI Description	Arabidopsis thaliana chromosome II BAC F26B6 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	163229
Seq. ID	LIB3177-059-P1-K1-C10
Method	BLASTX
NCBI GI	g115783
BLAST score	623
E value	6.0e-67
Match length	129
% identity	99
NCBI Description	CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR (CAB-140) (LHCP) >gi_16376_emb_CAA27543_ (X03909) chlorophyll a/b binding protein (LHCP AB 140) [Arabidopsis thaliana]

Seq. No.	163230
Seq. ID	LIB3177-059-P1-K1-C11
Method	BLASTX
NCBI GI	g2388578
BLAST score	638
E value	6.0e-67
Match length	131
% identity	98
NCBI Description	(AC000098) Similar to Mycobacterium RlpF (gb_Z84395). ESTs gb_T75785,gb_R30580,gb_T04698 come from this gene. [Arabidopsis thaliana]

Seq. No.	163231
Seq. ID	LIB3177-059-P1-K1-C12
Method	BLASTX
NCBI GI	g4102703
BLAST score	484
E value	8.0e-49
Match length	95
% identity	100
NCBI Description	(AF015274) ribulose-5-phosphate-3-epimerase [Arabidopsis thaliana]

Seq. No.	163232
Seq. ID	LIB3177-059-P1-K1-C2
Method	BLASTX
NCBI GI	g2864602

BLAST score	190
E value	2.0e-14
Match length	112
% identity	52
NCBI Description	(Y12071) thylakoid lumen rotamase [Spinacia oleracea]

Seq. No.	163233
Seq. ID	LIB3177-059-P1-K1-C3
Method	BLASTX
NCBI GI	g4753651
BLAST score	465
E value	8.0e-47
Match length	96
% identity	93
NCBI Description	(AL049751) ribosomal protein L13a like protein [Arabidopsis thaliana]

Seq. No.	163234
Seq. ID	LIB3177-059-P1-K1-C4
Method	BLASTN
NCBI GI	g2245031
BLAST score	389
E value	0.0e+00
Match length	410
% identity	98
NCBI Description	Arabidopsis thaliana DNA chromosome 4, ESSA I contig fragment No

Seq. No.	163235
Seq. ID	LIB3177-059-P1-K1-C5
Method	BLASTX
NCBI GI	g282865
BLAST score	293
E value	2.0e-42
Match length	111
% identity	81
NCBI Description	chlorophyll a/b-binding protein - Arabidopsis thaliana >gi_16207_emb_CAA39534_ (X56062) chlorophyll A/B-binding protein [Arabidopsis thaliana] >gi_166644 (M85150) chlorophyll a/b-binding protein [Arabidopsis thaliana] >gi_4678304_emb_CAB41095.1_ (AL049655) chlorophyll a/b-binding protein [Arabidopsis thaliana]

Seq. No.	163236
Seq. ID	LIB3177-059-P1-K1-C6
Method	BLASTX
NCBI GI	g464662
BLAST score	257
E value	3.0e-22
Match length	117
% identity	50
NCBI Description	CHLOROPLAST 31 KD RIBONUCLEOPROTEIN PRECURSOR (RNA-BINDING PROTEIN RNP-T) (RNA-BINDING PROTEIN 1) >gi_282884_pir__S28057 RNA-binding protein RNP-T - Arabidopsis thaliana >gi_16490_emb_CAA46347_ (X65255) RNA-binding protein [Arabidopsis thaliana] >gi_387569 (M94554) 31 kDa RNA binding protein [Arabidopsis thaliana]

	>gi_475718 (U08467) RNA-binding protein 1 [Arabidopsis thaliana] >gi_4220513_emb_CAA22986_ (AL035356) RNA-binding protein RNP-T precursor [Arabidopsis thaliana] >gi_737169_prf__1921382A RNA-binding protein [Arabidopsis thaliana]
Seq. No.	163237
Seq. ID	LIB3177-059-P1-K1-C7
Method	BLASTX
NCBI GI	g4454056
BLAST score	318
E value	2.0e-29
Match length	85
% identity	82
NCBI Description	(AJ000930) ClpP [Arabidopsis thaliana]
Seq. No.	163238
Seq. ID	LIB3177-059-P1-K1-C8
Method	BLASTX
NCBI GI	g115767
BLAST score	681
E value	6.0e-72
Match length	130
% identity	100
NCBI Description	CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR (CAB-165/180) (LHCP) >gi_81603_pir__A29280 chlorophyll a/b-binding protein ab165 - Arabidopsis thaliana >gi_16368_emb_CAA27540_ (X03907) chlorophyll a/b binding protein (LHCP AB 65) [Arabidopsis thaliana] >gi_16372_emb_CAA27541_ (X03908) chlorophyll a/b binding protein (LHCP AB 180) [Arabidopsis thaliana]
Seq. No.	163239
Seq. ID	LIB3177-059-P1-K1-C9
Method	BLASTX
NCBI GI	g166834
BLAST score	574
E value	3.0e-71
Match length	137
% identity	90
NCBI Description	(M86720) ribulose bisphosphate carboxylase/oxygenase activase [Arabidopsis thaliana] >gi_2642155 (AC003000) Rubisco activase [Arabidopsis thaliana]
Seq. No.	163240
Seq. ID	LIB3177-059-P1-K1-D1
Method	BLASTX
NCBI GI	g2369714
BLAST score	452
E value	3.0e-45
Match length	117
% identity	76
NCBI Description	(Z97178) elongation factor 2 [Beta vulgaris]
Seq. No.	163241
Seq. ID	LIB3177-059-P1-K1-D11
Method	BLASTX

NCBI GI	g132074
BLAST score	618
E value	1.0e-64
Match length	112
% identity	100
NCBI Description	RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN 1A PRECURSOR (RUBISCO SMALL SUBUNIT 1A) >gi_68063_pir__RKMUA1 ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain A1 precursor - Arabidopsis thaliana

Seq. No.	163242
Seq. ID	LIB3177-059-P1-K1-D12
Method	BLASTX
NCBI GI	g3914658
BLAST score	604
E value	7.0e-63
Match length	138
% identity	86
NCBI Description	50S RIBOSOMAL PROTEIN L24, CHLOROPLAST PRECURSOR >gi_1694974_emb_CAA70851_ (Y09635) plastid ribosomal protein [Arabidopsis thaliana]

Seq. No.	163243
Seq. ID	LIB3177-059-P1-K1-D2
Method	BLASTX
NCBI GI	g1565225
BLAST score	548
E value	3.0e-56
Match length	104
% identity	98
NCBI Description	(X95572) salt-tolerance protein [Arabidopsis thaliana]

Seq. No.	163244
Seq. ID	LIB3177-059-P1-K1-D3
Method	BLASTX
NCBI GI	g4049350
BLAST score	526
E value	8.0e-54
Match length	102
% identity	99
NCBI Description	(AL034567) putative protein [Arabidopsis thaliana]

Seq. No.	163245
Seq. ID	LIB3177-059-P1-K1-D4
Method	BLASTX
NCBI GI	g4454036
BLAST score	386
E value	7.0e-70
Match length	131
% identity	94
NCBI Description	(AL035394) putative major latex protein [Arabidopsis thaliana]

Seq. No.	163246
Seq. ID	LIB3177-059-P1-K1-D6
Method	BLASTX
NCBI GI	g4586256

BLAST score	554
E value	5.0e-57
Match length	128
% identity	85
NCBI Description	(AL049640) probable photosystem I chain XI precursor [Arabidopsis thaliana]

Seq. No.	163247
Seq. ID	LIB3177-059-P1-K1-D7
Method	BLASTX
NCBI GI	g4033838
BLAST score	585
E value	2.0e-75
Match length	149
% identity	99
NCBI Description	(Y18550) sigma-like factor [Arabidopsis thaliana]

Seq. No.	163248
Seq. ID	LIB3177-059-P1-K1-D8
Method	BLASTX
NCBI GI	g1732570
BLAST score	659
E value	2.0e-69
Match length	131
% identity	96
NCBI Description	(U72153) beta-glucosidase [Arabidopsis thaliana]

Seq. No.	163249
Seq. ID	LIB3177-059-P1-K1-E1
Method	BLASTX
NCBI GI	g2506443
BLAST score	542
E value	1.0e-55
Match length	142
% identity	81
NCBI Description	GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE A PRECURSOR, CHLOROPLAST >gi_2117520_pir__JQ1285 glyceraldehyde-3-phosphate dehydrogenase (NADP+) (phosphorylating) (EC 1.2.1.13) A precursor, chloroplast - Arabidopsis thaliana >gi_166704 (M64117) glyceraldehyde 3-phosphate dehydrogenase [Arabidopsis thaliana] >gi_1402885_emb_CAA66816_ (X98130) glyceraldehyde-3-phosphate dehydrogenase (NADP+) (phosphorylating) [Arabidopsis thaliana]

Seq. No.	163250
Seq. ID	LIB3177-059-P1-K1-E10
Method	BLASTN
NCBI GI	g2980787
BLAST score	70
E value	3.0e-31
Match length	263
% identity	85
NCBI Description	Arabidopsis thaliana DNA chromosome 4, P1 clone M7J2 (ESSAII project)

Seq. No.	163251

Seq. ID	LIB3177-059-P1-K1-E11
Method	BLASTN
NCBI GI	g2351061
BLAST score	161
E value	2.0e-85
Match length	161
% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MAF19, complete sequence [Arabidopsis thaliana]

Seq. No.	163252
Seq. ID	LIB3177-059-P1-K1-E12
Method	BLASTX
NCBI GI	g4759288
BLAST score	272
E value	5.0e-24
Match length	130
% identity	47
NCBI Description	homolog of yeast (S. cerevisiae) ufd2 >gi_2495703_sp_Q14139_Y126_HUMAN HYPOTHETICAL PROTEIN KIAA0126 >gi_1469175_dbj_BAA09475_ (D50916) The KIAA0126 gene is partially related to a yeast gene. [Homo sapiens]

Seq. No.	163253
Seq. ID	LIB3177-059-P1-K1-E2
Method	BLASTX
NCBI GI	g2623302
BLAST score	641
E value	3.0e-67
Match length	125
% identity	99
NCBI Description	(AC002409) putative cysteine proteinase inhibitor [Arabidopsis thaliana]

Seq. No.	163254
Seq. ID	LIB3177-059-P1-K1-E3
Method	BLASTX
NCBI GI	g2119846
BLAST score	635
E value	1.0e-66
Match length	125
% identity	97
NCBI Description	chlorophyll a/b-binding protein type I precursor Lhb1B2 - Arabidopsis thaliana >gi_16364_emb_CAA45790_ (X64460) photosystem II type I chlorophyll a /b binding protein [Arabidopsis thaliana] >gi_3128230 (AC004077) photosystem II type I chlorophyll a/b binding protein [Arabidopsis thaliana] >gi_3337371 (AC004481) photosystem II type I chlorophyll a/b binding protein [Arabidopsis thaliana]

Seq. No.	163255
Seq. ID	LIB3177-059-P1-K1-E4
Method	BLASTX
NCBI GI	g3075394
BLAST score	647
E value	6.0e-68
Match length	127

% identity	99
NCBI Description	(AC004484) putative beta-ketoacyl-CoA synthase [Arabidopsis thaliana] >gi_3559809_emb_CAA09311_ (AJ010713) fiddlehead protein [Arabidopsis thaliana]

Seq. No.	163256
Seq. ID	LIB3177-059-P1-K1-E6
Method	BLASTX
NCBI GI	g542200
BLAST score	388
E value	2.0e-37
Match length	136
% identity	52
NCBI Description	hypothetical protein - garden asparagus >gi_452714_emb_CAA54526_ (X77320) unknown [Asparagus officinalis]

Seq. No.	163257
Seq. ID	LIB3177-059-P1-K1-E7
Method	BLASTN
NCBI GI	g2864607
BLAST score	335
E value	0.0e+00
Match length	347
% identity	99
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F10M6 (ESSAII project)

Seq. No.	163258
Seq. ID	LIB3177-059-P1-K1-E8
Method	BLASTX
NCBI GI	g3212877
BLAST score	724
E value	6.0e-77
Match length	140
% identity	56
NCBI Description	(AC004005) Lea-like protein [Arabidopsis thaliana]

Seq. No.	163259
Seq. ID	LIB3177-059-P1-K1-E9
Method	BLASTX
NCBI GI	g16374
BLAST score	770
E value	2.0e-82
Match length	147
% identity	99
NCBI Description	(X03908) chlorophyll a/b binding protein (LHCP AB 180) [Arabidopsis thaliana]

Seq. No.	163260
Seq. ID	LIB3177-059-P1-K1-F1
Method	BLASTN
NCBI GI	g790582
BLAST score	417
E value	0.0e+00
Match length	424
% identity	100

NCBI Description	Arabidopsis thaliana putative pathogenesis-related protein (ATOZI1) mRNA, complete cds
Seq. No.	163261
Seq. ID	LIB3177-059-P1-K1-F10
Method	BLASTN
NCBI GI	g4309683
BLAST score	250
E value	1.0e-138
Match length	270
% identity	98
NCBI Description	Arabidopsis thaliana chromosome 1 BAC T31J12 sequence, complete sequence [Arabidopsis thaliana]
Seq. No.	163262
Seq. ID	LIB3177-059-P1-K1-F11
Method	BLASTX
NCBI GI	g2104957
BLAST score	508
E value	1.0e-51
Match length	112
% identity	88
NCBI Description	(U96924) immunophilin [Arabidopsis thaliana]
Seq. No.	163263
Seq. ID	LIB3177-059-P1-K1-F12
Method	BLASTX
NCBI GI	g2088649
BLAST score	425
E value	6.0e-42
Match length	85
% identity	100
NCBI Description	(AF002109) unknown protein [Arabidopsis thaliana]
Seq. No.	163264
Seq. ID	LIB3177-059-P1-K1-F2
Method	BLASTX
NCBI GI	g2129767
BLAST score	449
E value	9.0e-45
Match length	85
% identity	99
NCBI Description	vacuolar processing enzyme (EC 3.4.22.-) isozyme beta precursor - Arabidopsis thaliana >gi_1805364_dbj_BAA09615_ (D61394) beta-VPE [Arabidopsis thaliana]
Seq. No.	163265
Seq. ID	LIB3177-059-P1-K1-F3
Method	BLASTX
NCBI GI	g4741185
BLAST score	601
E value	2.0e-62
Match length	112
% identity	100
NCBI Description	(AL049746) hypothetical protein [Arabidopsis thaliana]
Seq. No.	163266

Seq. ID	LIB3177-059-P1-K1-F5
Method	BLASTX
NCBI GI	g1806140
BLAST score	711
E value	2.0e-75
Match length	147
% identity	85
NCBI Description	(X97314) cdc2MsC [Medicago sativa]

Seq. No.	163267
Seq. ID	LIB3177-059-P1-K1-F7
Method	BLASTN
NCBI GI	g4586098
BLAST score	58
E value	1.0e-24
Match length	58
% identity	100
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F16J13 (ESSA project)

Seq. No.	163268
Seq. ID	LIB3177-059-P1-K1-F8
Method	BLASTX
NCBI GI	g131398
BLAST score	519
E value	7.0e-53
Match length	120
% identity	88
NCBI Description	PHOTOSYSTEM II 10 KD POLYPEPTIDE PRECURSOR >gi_72714_pir__F2MU10 photosystem II 10K protein precursor - Arabidopsis thaliana >gi_16447_emb_CAA39441_ (X55970) photosystem II 10 kDa polypeptide [Arabidopsis thaliana] >gi_3152571 (AC002986) Match to photosystem II 10kDa polypeptide gb_X55970. ESTs gb_Z17693, gb_N37616, gb_T41858, gb_T88021, gb_R37531, gb_T04679, gb_N37520, gb_N64965, gb_Z17592 and gb_N65338, gb_N37466 and gb_T45400 come from this gene. [Arabidopsis

Seq. No.	163269
Seq. ID	LIB3177-059-P1-K1-G1
Method	BLASTX
NCBI GI	g3193301
BLAST score	501
E value	8.0e-51
Match length	138
% identity	77
NCBI Description	(AF069298) Arabidopsis putative chloroplast outer envelope 86-like protein T10P11.19 (GB: AC002330) [Arabidopsis thaliana]

Seq. No.	163270
Seq. ID	LIB3177-059-P1-K1-G10
Method	BLASTX
NCBI GI	g4741952
BLAST score	576
E value	1.0e-59
Match length	108

% identity	74
NCBI Description	(AF134126) Lhcb3 protein [Arabidopsis thaliana]

Seq. No.	163271
Seq. ID	LIB3177-059-P1-K1-G11
Method	BLASTX
NCBI GI	g132102
BLAST score	787
E value	2.0e-84
Match length	148
% identity	99
NCBI Description	RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN 2B PRECURSOR (RUBISCO SMALL SUBUNIT 2B) >gi_68061_pir__RKMUB2 ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain B2 precursor - Arabidopsis thaliana >gi_16194_emb_CAA32701_ (X14564) ribulose bisphosphate carboxylase [Arabidopsis thaliana]

Seq. No.	163272
Seq. ID	LIB3177-059-P1-K1-G12
Method	BLASTX
NCBI GI	g1946690
BLAST score	691
E value	4.0e-73
Match length	131
% identity	100
NCBI Description	(U94495) glutathione peroxidase [Arabidopsis thaliana] >gi_4582452_gb_AAD24836.1_AC007071_8 (AC007071) putative glutathione peroxidase [Arabidopsis thaliana]

Seq. No.	163273
Seq. ID	LIB3177-059-P1-K1-G2
Method	BLASTX
NCBI GI	g4539316
BLAST score	671
E value	1.0e-70
Match length	141
% identity	99
NCBI Description	(AL035679) putative fructose-bisphosphate aldolase [Arabidopsis thaliana]

Seq. No.	163274
Seq. ID	LIB3177-059-P1-K1-G3
Method	BLASTN
NCBI GI	g4521999
BLAST score	76
E value	7.0e-35
Match length	219
% identity	100
NCBI Description	Arabidopsis thaliana chromosome II BAC F2G1 genomic sequence, complete sequence

Seq. No.	163275
Seq. ID	LIB3177-059-P1-K1-G4
Method	BLASTX
NCBI GI	g3080442
BLAST score	760

E value	4.0e-81
Match length	145
% identity	97
NCBI Description	(AL022605) putative protein [Arabidopsis thaliana]

Seq. No.	163276
Seq. ID	LIB3177-059-P1-K1-G5
Method	BLASTX
NCBI GI	g4567232
BLAST score	354
E value	1.0e-33
Match length	72
% identity	100
NCBI Description	(AC007119) putative 40S ribosomal protein S25 [Arabidopsis thaliana]

Seq. No.	163277
Seq. ID	LIB3177-059-P1-K1-G6
Method	BLASTX
NCBI GI	g4262232
BLAST score	628
E value	1.0e-65
Match length	149
% identity	87
NCBI Description	(AC006200) putative ribosomal protein L7 [Arabidopsis thaliana]

Seq. No.	163278
Seq. ID	LIB3177-059-P1-K1-G7
Method	BLASTX
NCBI GI	g4835226
BLAST score	262
E value	9.0e-23
Match length	85
% identity	58
NCBI Description	(AL049862) putative protein [Arabidopsis thaliana]

Seq. No.	163279
Seq. ID	LIB3177-059-P1-K1-G8
Method	BLASTX
NCBI GI	g2129672
BLAST score	301
E value	2.0e-27
Match length	119
% identity	55
NCBI Description	photosystem II reaction center protein, 6.1K - Arabidopsis thaliana >gi_950023_emb_CAA62296_ (X90769) component of 6.1 kDa polypeptide of photosystem II reaction center [Arabidopsis thaliana]

Seq. No.	163280
Seq. ID	LIB3177-059-P1-K1-G9
Method	BLASTX
NCBI GI	g115767
BLAST score	723
E value	7.0e-77
Match length	136

% identity	99
NCBI Description	CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR (CAB-165/180) (LHCP) >gi_81603_pir__A29280 chlorophyll a/b-binding protein ab165 - Arabidopsis thaliana >gi_16368_emb_CAA27540_ (X03907) chlorophyll a/b binding protein (LHCP AB 65) [Arabidopsis thaliana] >gi_16372_emb_CAA27541_ (X03908) chlorophyll a/b binding protein (LHCP AB 180) [Arabidopsis thaliana]

Seq. No.	163281
Seq. ID	LIB3177-059-P1-K1-H1
Method	BLASTN
NCBI GI	g2246379
BLAST score	380
E value	0.0e+00
Match length	408
% identity	99
NCBI Description	A.thaliana mRNA for peptidyl-prolyl cis-trans isomerase

Seq. No.	163282
Seq. ID	LIB3177-059-P1-K1-H10
Method	BLASTX
NCBI GI	g1169201
BLAST score	549
E value	2.0e-56
Match length	136
% identity	83
NCBI Description	DNA-DAMAGE-REPAIR/TOLERATION PROTEIN DRT112 PRECURSOR >gi_421830_pir__S33707 DRT112 protein - Arabidopsis thaliana >gi_166696 (M98456) DRT112 [Arabidopsis thaliana]

Seq. No.	163283
Seq. ID	LIB3177-059-P1-K1-H11
Method	BLASTX
NCBI GI	g4741950
BLAST score	606
E value	3.0e-63
Match length	116
% identity	97
NCBI Description	(AF134125) Lhcb2 protein [Arabidopsis thaliana]

Seq. No.	163284
Seq. ID	LIB3177-059-P1-K1-H12
Method	BLASTX
NCBI GI	g4741940
BLAST score	572
E value	4.0e-59
Match length	104
% identity	66
NCBI Description	(AF134120) Lhca2 protein [Arabidopsis thaliana]

Seq. No.	163285
Seq. ID	LIB3177-059-P1-K1-H3
Method	BLASTX
NCBI GI	g1363489
BLAST score	734
E value	4.0e-78

Match length	150
% identity	91
NCBI Description	thioglucosidase (EC 3.2.3.1) 3D precursor - Arabidopsis thaliana >gi_984052_emb_CAA61592_ (X89413) thioglucoside glucohydrolase [Arabidopsis thaliana]

Seq. No.	163286
Seq. ID	LIB3177-059-P1-K1-H4
Method	BLASTX
NCBI GI	g132110
BLAST score	315
E value	3.0e-29
Match length	92
% identity	74
NCBI Description	RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN 3B PRECURSOR (RUBISCO SMALL SUBUNIT 3B) >gi_68060_pir__RKMUB3 ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain B3 precursor - Arabidopsis thaliana >gi_16195_emb_CAA32702_ (X14564) ribulose bisphosphate carboxylase [Arabidopsis thaliana]

Seq. No.	163287
Seq. ID	LIB3177-059-P1-K1-H5
Method	BLASTN
NCBI GI	g2252823
BLAST score	35
E value	3.0e-10
Match length	173
% identity	93
NCBI Description	Arabidopsis thaliana BAC IG005I10

Seq. No.	163288
Seq. ID	LIB3177-059-P1-K1-H6
Method	BLASTX
NCBI GI	g2459417
BLAST score	113
E value	9.0e-37
Match length	96
% identity	90
NCBI Description	(AC002332) putative pre-mRNA splicing factor PRP19 [Arabidopsis thaliana]

Seq. No.	163289
Seq. ID	LIB3177-059-P1-K1-H7
Method	BLASTN
NCBI GI	g4454447
BLAST score	353
E value	0.0e+00
Match length	450
% identity	100
NCBI Description	Arabidopsis thaliana chromosome II BAC F5H14 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	163290
Seq. ID	LIB3177-059-P1-K1-H8
Method	BLASTX
NCBI GI	g131398

BLAST score	545
E value	6.0e-56
Match length	138
% identity	81
NCBI Description	PHOTOSYSTEM II 10 KD POLYPEPTIDE PRECURSOR >gi_72714_pir__F2MU10 photosystem II 10K protein precursor - Arabidopsis thaliana >gi_16447_emb_CAA39441_ (X55970) photosystem II 10 kDa polypeptide [Arabidopsis thaliana] >gi_3152571 (AC002986) Match to photosystem II 10kDa polypeptide gb_X55970. ESTs gb_Z17693, gb_N37616, gb_T41858, gb_T88021, gb_R37531, gb_T04679, gb_N37520, gb_N64965, gb_Z17592 and gb_N65338, gb_N37466 and gb_T45400 come from this gene. [Arabidopsis

Seq. No.	163291
Seq. ID	LIB3177-059-P1-K1-H9
Method	BLASTN
NCBI GI	g3510247
BLAST score	84
E value	2.0e-39
Match length	201
% identity	89
NCBI Description	Arabidopsis thaliana chromosome II BAC F19D11 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	163292
Seq. ID	LIB3177-060-P1-K1-A11
Method	BLASTX
NCBI GI	g2129562
BLAST score	309
E value	8.0e-29
Match length	62
% identity	95
NCBI Description	class III ADH, glutathione-dependent formaldehyde dehydrogenase. - Arabidopsis thaliana >gi_1143388_emb_CAA57973_ (X82647) class III ADH, glutathione-dependent formaldehyde dehydrogenase. [Arabidopsis thaliana]

Seq. No.	163293
Seq. ID	LIB3177-060-P1-K1-A12
Method	BLASTX
NCBI GI	g1345655
BLAST score	221
E value	2.0e-18
Match length	59
% identity	76
NCBI Description	CINNAMYL-ALCOHOL DEHYDROGENASE 2 (CAD) >gi_757535_emb_CAA83508_ (Z31715) cinnamyl alcohol dehydrogenase [Arabidopsis thaliana]

Seq. No.	163294
Seq. ID	LIB3177-060-P1-K1-A3
Method	BLASTN
NCBI GI	g3883125
BLAST score	269
E value	1.0e-150

Match length	317
% identity	96
NCBI Description	Arabidopsis thaliana arabinogalactan-protein (AGP4) mRNA, complete cds

Seq. No.	163295
Seq. ID	LIB3177-060-P1-K1-A5
Method	BLASTX
NCBI GI	g2911085
BLAST score	353
E value	4.0e-53
Match length	129
% identity	85
NCBI Description	(AL021960) photosystem II oxygen-evolving complex protein 3-like [Arabidopsis thaliana] >gi_3402748_emb_CAA20194.1_ (AL031187) photosystem II oxygen-evolving complex protein 3 - like [Arabidopsis thaliana]

Seq. No.	163296
Seq. ID	LIB3177-060-P1-K1-A6
Method	BLASTN
NCBI GI	g3702731
BLAST score	302
E value	1.0e-169
Match length	310
% identity	99
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MFC19, complete sequence [Arabidopsis thaliana]

Seq. No.	163297
Seq. ID	LIB3177-060-P1-K1-A9
Method	BLASTN
NCBI GI	g4325216
BLAST score	219
E value	1.0e-120
Match length	219
% identity	100
NCBI Description	Arabidopsis thaliana hydrophobic protein (RCI2A) mRNA, complete cds

Seq. No.	163298
Seq. ID	LIB3177-060-P1-K1-B10
Method	BLASTN
NCBI GI	g2642152
BLAST score	250
E value	1.0e-138
Match length	250
% identity	100
NCBI Description	Arabidopsis thaliana chromosome II BAC T5I7 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	163299
Seq. ID	LIB3177-060-P1-K1-B11
Method	BLASTX
NCBI GI	g2119846
BLAST score	266
E value	7.0e-24

Match length	60
% identity	90
NCBI Description	chlorophyll a/b-binding protein type I precursor Lhb1B2 - Arabidopsis thaliana >gi_16364_emb_CAA45790_ (X64460) photosystem II type I chlorophyll a /b binding protein [Arabidopsis thaliana] >gi_3128230 (AC004077) photosystem II type I chlorophyll a/b binding protein [Arabidopsis thaliana] >gi_3337371 (AC004481) photosystem II type I chlorophyll a/b binding protein [Arabidopsis thaliana]

Seq. No.	163300
Seq. ID	LIB3177-060-P1-K1-B12
Method	BLASTX
NCBI GI	g2781354
BLAST score	253
E value	1.0e-30
Match length	71
% identity	87
NCBI Description	(AC003113) F24O1.10 [Arabidopsis thaliana]

Seq. No.	163301
Seq. ID	LIB3177-060-P1-K1-B2
Method	BLASTX
NCBI GI	g3980405
BLAST score	400
E value	5.0e-39
Match length	83
% identity	98
NCBI Description	(AC004561) putative tropinone reductase [Arabidopsis thaliana]

Seq. No.	163302
Seq. ID	LIB3177-060-P1-K1-B3
Method	BLASTX
NCBI GI	g4679028
BLAST score	168
E value	3.0e-12
Match length	77
% identity	47
NCBI Description	(AF077207) HSPC021 [Homo sapiens]

Seq. No.	163303
Seq. ID	LIB3177-060-P1-K1-B5
Method	BLASTN
NCBI GI	g2760168
BLAST score	58
E value	4.0e-24
Match length	165
% identity	91
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MEE6, complete sequence [Arabidopsis thaliana]

Seq. No.	163304
Seq. ID	LIB3177-060-P1-K1-B6
Method	BLASTX
NCBI GI	g135406
BLAST score	343

E value	1.0e-68
Match length	150
% identity	88
NCBI Description	TUBULIN ALPHA-3/ALPHA-5 CHAIN >gi_99768_pir__A32712 tubulin alpha-5 chain - Arabidopsis thaliana >gi_166912 (M17189) alpha-tubulin [Arabidopsis thaliana] >gi_166918 (M84698) alpha-5 tubulin [Arabidopsis thaliana]

Seq. No.	163305
Seq. ID	LIB3177-060-P1-K1-B9
Method	BLASTN
NCBI GI	g2264314
BLAST score	40
E value	4.0e-13
Match length	356
% identity	58
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MQK4, complete sequence [Arabidopsis thaliana]

Seq. No.	163306
Seq. ID	LIB3177-060-P1-K1-C1
Method	BLASTX
NCBI GI	g2239083
BLAST score	133
E value	8.0e-12
Match length	83
% identity	49
NCBI Description	(Z84383) anthranilate N-hydroxycinnamoyl/benzoyltransferase [Dianthus caryophyllus] >gi_2239087_emb_CAB06429_ (Z84385) anthranilate N-hydroxycinnamoyl/benzoyltransferase [Dianthus caryophyllus]

Seq. No.	163307
Seq. ID	LIB3177-060-P1-K1-C10
Method	BLASTX
NCBI GI	g2213622
BLAST score	213
E value	3.0e-17
Match length	43
% identity	100
NCBI Description	(AC000103) F21J9.25 [Arabidopsis thaliana]

Seq. No.	163308
Seq. ID	LIB3177-060-P1-K1-C12
Method	BLASTN
NCBI GI	g2760168
BLAST score	44
E value	2.0e-15
Match length	59
% identity	95
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MEE6, complete sequence [Arabidopsis thaliana]

Seq. No.	163309
Seq. ID	LIB3177-060-P1-K1-C3
Method	BLASTX
NCBI GI	g4006934

BLAST score	346
E value	5.0e-33
Match length	71
% identity	94
NCBI Description	(AJ012571) glutathione transferase [Arabidopsis thaliana]

Seq. No.	163310
Seq. ID	LIB3177-060-P1-K1-C7
Method	BLASTX
NCBI GI	g1172806
BLAST score	245
E value	2.0e-21
Match length	46
% identity	96
NCBI Description	60S RIBOSOMAL PROTEIN L10 (WILM'S TUMOR SUPPRESSOR PROTEIN HOMOLOG) >gi_478401_pir__JQ2244 ribosomal protein L10.e, cytosolic - Arabidopsis thaliana >gi_17682_emb_CAA78856_ (Z15157) Wilm's tumor suppressor homologue [Arabidopsis thaliana]

Seq. No.	163311
Seq. ID	LIB3177-060-P1-K1-C8
Method	BLASTX
NCBI GI	g166708
BLAST score	573
E value	2.0e-59
Match length	114
% identity	100
NCBI Description	(M64118) glyceraldehyde-3-phosphate dehydrogenase [Arabidopsis thaliana]

Seq. No.	163312
Seq. ID	LIB3177-060-P1-K1-D10
Method	BLASTX
NCBI GI	g2275217
BLAST score	308
E value	2.0e-28
Match length	83
% identity	76
NCBI Description	(AC002337) chloroplast protein CP12 isolog [Arabidopsis thaliana]

Seq. No.	163313
Seq. ID	LIB3177-060-P1-K1-D12
Method	BLASTX
NCBI GI	g4512705
BLAST score	340
E value	3.0e-32
Match length	94
% identity	74
NCBI Description	(AC006569) putative serine/threonine protein kinase [Arabidopsis thaliana]

Seq. No.	163314
Seq. ID	LIB3177-060-P1-K1-D3
Method	BLASTX
NCBI GI	g2894565

BLAST score	478
E value	2.0e-48
Match length	96
% identity	96
NCBI Description	(AL021890) heat shock protein - like [Arabidopsis thaliana]

Seq. No.	163315
Seq. ID	LIB3177-060-P1-K1-D4
Method	BLASTX
NCBI GI	g3927830
BLAST score	142
E value	4.0e-09
Match length	51
% identity	59
NCBI Description	(AC005727) hypothetical protein [Arabidopsis thaliana]

Seq. No.	163316
Seq. ID	LIB3177-060-P1-K1-D5
Method	BLASTX
NCBI GI	g4510345
BLAST score	137
E value	2.0e-11
Match length	40
% identity	67
NCBI Description	(AC006921) unknown protein [Arabidopsis thaliana]

Seq. No.	163317
Seq. ID	LIB3177-060-P1-K1-D6
Method	BLASTN
NCBI GI	g4584841
BLAST score	59
E value	4.0e-25
Match length	76
% identity	95
NCBI Description	Genomic sequence for Arabidopsis thaliana BAC T23E23, complete sequence

Seq. No.	163318
Seq. ID	LIB3177-060-P1-K1-D7
Method	BLASTN
NCBI GI	g4584351
BLAST score	320
E value	1.0e-180
Match length	324
% identity	100
NCBI Description	Arabidopsis thaliana chromosome II BAC T12H3 genomic sequence, complete sequence

Seq. No.	163319
Seq. ID	LIB3177-060-P1-K1-D9
Method	BLASTX
NCBI GI	g1709825
BLAST score	701
E value	3.0e-74
Match length	141
% identity	100
NCBI Description	PHOTOSYSTEM I REACTION CENTRE SUBUNIT PSAN PRECURSOR

(PSI-N) >gi_1237124 (U32176) PSI-N [Arabidopsis thaliana]

Seq. No.	163320
Seq. ID	LIB3177-060-P1-K1-E1
Method	BLASTX
NCBI GI	g4678312
BLAST score	495
E value	3.0e-50
Match length	107
% identity	85
NCBI Description	(AL049655) putative protein [Arabidopsis thaliana]

Seq. No.	163321
Seq. ID	LIB3177-060-P1-K1-E10
Method	BLASTX
NCBI GI	g400923
BLAST score	420
E value	2.0e-41
Match length	83
% identity	99
NCBI Description	RAS-RELATED PROTEIN RAB7 >gi_485497_pir__S33531 GTP-binding protein rab - garden pea >gi_20756_emb_CAA46600_ (X65650) RAS-related GTP-binding protein [Pisum sativum]

Seq. No.	163322
Seq. ID	LIB3177-060-P1-K1-E3
Method	BLASTN
NCBI GI	g2584827
BLAST score	137
E value	3.0e-71
Match length	229
% identity	88
NCBI Description	Arabidopsis thaliana chromosome 1 BAC F12F1 sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	163323
Seq. ID	LIB3177-060-P1-K1-E4
Method	BLASTN
NCBI GI	g2351064
BLAST score	348
E value	0.0e+00
Match length	363
% identity	99
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MDJ22, complete sequence [Arabidopsis thaliana]

Seq. No.	163324
Seq. ID	LIB3177-060-P1-K1-E5
Method	BLASTN
NCBI GI	g2618601
BLAST score	203
E value	1.0e-110
Match length	211
% identity	99
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MHJ24, complete sequence [Arabidopsis thaliana]

Seq. No.	163325
Seq. ID	LIB3177-060-P1-K1-E7
Method	BLASTX
NCBI GI	g4689034
BLAST score	164
E value	2.0e-11
Match length	39
% identity	82
NCBI Description	(AJ133751) chloroplast ribosome recycling factor protein [Spinacia oleracea]

Seq. No.	163326
Seq. ID	LIB3177-060-P1-K1-E9
Method	BLASTX
NCBI GI	g4586264
BLAST score	609
E value	2.0e-63
Match length	118
% identity	97
NCBI Description	(AL049640) blue copper-binding protein, 15K (lamin) [Arabidopsis thaliana]

Seq. No.	163327
Seq. ID	LIB3177-060-P1-K1-F1
Method	BLASTX
NCBI GI	g4584110
BLAST score	268
E value	1.0e-23
Match length	102
% identity	52
NCBI Description	(AJ133639) SAH7 protein [Arabidopsis thaliana]

Seq. No.	163328
Seq. ID	LIB3177-060-P1-K1-F10
Method	BLASTX
NCBI GI	g4314392
BLAST score	452
E value	3.0e-45
Match length	92
% identity	100
NCBI Description	(AC006232) putative ferredoxin [Arabidopsis thaliana]

Seq. No.	163329
Seq. ID	LIB3177-060-P1-K1-F11
Method	BLASTX
NCBI GI	g2119846
BLAST score	634
E value	1.0e-66
Match length	115
% identity	100
NCBI Description	chlorophyll a/b-binding protein type I precursor Lhb1B2 - Arabidopsis thaliana >gi_16364_emb_CAA45790_ (X64460) photosystem II type I chlorophyll a /b binding protein [Arabidopsis thaliana] >gi_3128230 (AC004077) photosystem II type I chlorophyll a/b binding protein [Arabidopsis thaliana] >gi_3337371 (AC004481) photosystem II type I chlorophyll a/b binding protein [Arabidopsis thaliana]

Seq. No.	163330
Seq. ID	LIB3177-060-P1-K1-F12
Method	BLASTX
NCBI GI	g3914442
BLAST score	184
E value	3.0e-14
Match length	48
% identity	81
NCBI Description	PHOTOSYSTEM I REACTION CENTRE SUBUNIT VI PRECURSOR (LIGHT-HARVESTING COMPLEX I 11 KD PROTEIN) (PSI-H) >gi_1916350 (U92504) PSI-H subunit [Brassica rapa]

Seq. No.	163331
Seq. ID	LIB3177-060-P1-K1-F4
Method	BLASTX
NCBI GI	g3142289
BLAST score	358
E value	1.0e-34
Match length	69
% identity	99
NCBI Description	(AC002411) Strong similarity to beta-keto-Coa synthase gb_U37088 from Simmondsia chinensis. [Arabidopsis thaliana]

Seq. No.	163332
Seq. ID	LIB3177-060-P1-K1-F5
Method	BLASTX
NCBI GI	g2119846
BLAST score	553
E value	5.0e-57
Match length	104
% identity	100
NCBI Description	chlorophyll a/b-binding protein type I precursor Lhb1B2 - Arabidopsis thaliana >gi_16364_emb_CAA45790_ (X64460) photosystem II type I chlorophyll a /b binding protein [Arabidopsis thaliana] >gi_3128230 (AC004077) photosystem II type I chlorophyll a/b binding protein [Arabidopsis thaliana] >gi_3337371 (AC004481) photosystem II type I chlorophyll a/b binding protein [Arabidopsis thaliana]

Seq. No.	163333
Seq. ID	LIB3177-060-P1-K1-F7
Method	BLASTN
NCBI GI	g4589445
BLAST score	62
E value	2.0e-26
Match length	182
% identity	59
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MWL2, complete sequence

Seq. No.	163334
Seq. ID	LIB3177-060-P1-K1-F8
Method	BLASTN
NCBI GI	g2264317
BLAST score	53
E value	1.0e-21

Match length	53
% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MUG13, complete sequence [Arabidopsis thaliana]
Seq. No.	163335
Seq. ID	LIB3177-060-P1-K1-F9
Method	BLASTX
NCBI GI	g1769905
BLAST score	175
E value	8.0e-26
Match length	105
% identity	63
NCBI Description	(X98108) 23 kDa polypeptide of oxygen-evolving comlex (OEC) [Arabidopsis thaliana]
Seq. No.	163336
Seq. ID	LIB3177-060-P1-K1-G1
Method	BLASTX
NCBI GI	g3121825
BLAST score	67
E value	3.0e-20
Match length	101
% identity	57
NCBI Description	2-CYS PEROXIREDOXIN BAS1 PRECURSOR (THIOL-SPECIFIC ANTIOXIDANT PROTEIN) >gi_1498247_emb_CAA63910_ (X94219) bas1 protein [Spinacia oleracea]
Seq. No.	163337
Seq. ID	LIB3177-060-P1-K1-G10
Method	BLASTX
NCBI GI	g2583134
BLAST score	441
E value	8.0e-44
Match length	82
% identity	100
NCBI Description	(AC002387) putative proline-rich protein [Arabidopsis thaliana]
Seq. No.	163338
Seq. ID	LIB3177-060-P1-K1-G11
Method	BLASTX
NCBI GI	g115767
BLAST score	613
E value	5.0e-64
Match length	116
% identity	100
NCBI Description	CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR (CAB-165/180) (LHCP) >gi_81603_pir__A29280 chlorophyll a/b-binding protein ab165 - Arabidopsis thaliana >gi_16368_emb_CAA27540_ (X03907) chlorophyll a/b binding protein (LHCP AB 65) [Arabidopsis thaliana] >gi_16372_emb_CAA27541_ (X03908) chlorophyll a/b binding protein (LHCP AB 180) [Arabidopsis thaliana]
Seq. No.	163339
Seq. ID	LIB3177-060-P1-K1-G2

Method	BLASTN
NCBI GI	g4741945
BLAST score	73
E value	4.0e-33
Match length	177
% identity	85
NCBI Description	Arabidopsis thaliana Lhcb2 protein (Lhcb2.2) mRNA, complete cds

Seq. No.	163340
Seq. ID	LIB3177-060-P1-K1-G4
Method	BLASTN
NCBI GI	g3327922
BLAST score	314
E value	1.0e-176
Match length	337
% identity	99
NCBI Description	Arabidopsis thaliana chromosome II BAC T31E10 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	163341
Seq. ID	LIB3177-060-P1-K1-G5
Method	BLASTX
NCBI GI	g4580527
BLAST score	603
E value	8.0e-63
Match length	117
% identity	99
NCBI Description	(AF036307) scarecrow-like 11 [Arabidopsis thaliana]

Seq. No.	163342
Seq. ID	LIB3177-060-P1-K1-G6
Method	BLASTX
NCBI GI	g115767
BLAST score	413
E value	1.0e-40
Match length	84
% identity	95
NCBI Description	CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR (CAB-165/180) (LHCP) >gi_81603_pir__A29280 chlorophyll a/b-binding protein ab165 - Arabidopsis thaliana >gi_16368_emb_CAA27540_ (X03907) chlorophyll a/b binding protein (LHCP AB 65) [Arabidopsis thaliana] >gi_16372_emb_CAA27541_ (X03908) chlorophyll a/b binding protein (LHCP AB 180) [Arabidopsis thaliana]

Seq. No.	163343
Seq. ID	LIB3177-060-P1-K1-G7
Method	BLASTX
NCBI GI	g4725941
BLAST score	394
E value	3.0e-38
Match length	95
% identity	80
NCBI Description	(AL049730) putative pollen-specific protein [Arabidopsis thaliana]

Seq. No.	163344
Seq. ID	LIB3177-060-P1-K1-G8
Method	BLASTN
NCBI GI	g16316
BLAST score	238
E value	1.0e-131
Match length	258
% identity	98
NCBI Description	A.thaliana gene for histone H1-1

Seq. No.	163345
Seq. ID	LIB3177-060-P1-K1-G9
Method	BLASTX
NCBI GI	g115783
BLAST score	626
E value	2.0e-65
Match length	118
% identity	100
NCBI Description	CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR (CAB-140) (LHCP) >gi_16376_emb_CAA27543_ (X03909) chlorophyll a/b binding protein (LHCP AB 140) [Arabidopsis thaliana]

Seq. No.	163346
Seq. ID	LIB3177-060-P1-K1-H1
Method	BLASTX
NCBI GI	g132110
BLAST score	625
E value	2.0e-65
Match length	122
% identity	98
NCBI Description	RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN 3B PRECURSOR (RUBISCO SMALL SUBUNIT 3B) >gi_68060_pir__RKMUB3 ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain B3 precursor - Arabidopsis thaliana >gi_16195_emb_CAA32702_ (X14564) ribulose bisphosphate carboxylase [Arabidopsis thaliana]

Seq. No.	163347
Seq. ID	LIB3177-060-P1-K1-H10
Method	BLASTN
NCBI GI	g4558521
BLAST score	92
E value	3.0e-44
Match length	291
% identity	97
NCBI Description	Genomic sequence for Arabidopsis thaliana BAC T10O24, complete sequence

Seq. No.	163348
Seq. ID	LIB3177-060-P1-K1-H11
Method	BLASTX
NCBI GI	g3929651
BLAST score	653
E value	1.0e-68
Match length	135
% identity	97

NCBI Description	(AJ131206) microbody NAD-dependent malate dehydrogenase [Arabidopsis thaliana]
Seq. No.	163349
Seq. ID	LIB3177-060-P1-K1-H12
Method	BLASTX
NCBI GI	g1063400
BLAST score	471
E value	1.0e-47
Match length	99
% identity	97
NCBI Description	(X92888) glycolate oxidase [Lycopersicon esculentum]
Seq. No.	163350
Seq. ID	LIB3177-060-P1-K1-H4
Method	BLASTX
NCBI GI	g2119848
BLAST score	577
E value	9.0e-60
Match length	107
% identity	100
NCBI Description	chlorophyll a/b-binding protein type I precursor Lhb1B1 - Arabidopsis thaliana >gi_16366_emb_CAA45789_ (X64459) photosystem II type I chlorophyll a /b binding protein [Arabidopsis thaliana] >gi_3128229 (AC004077) putative photosystem II type I chlorophyll a/b binding protein [Arabidopsis thaliana] >gi_3337372 (AC004481) putative photosystem II type I chlorophyll a/b binding protein [Arabidopsis thaliana]
Seq. No.	163351
Seq. ID	LIB3177-060-P1-K1-H5
Method	BLASTX
NCBI GI	g4455295
BLAST score	557
E value	2.0e-57
Match length	116
% identity	91
NCBI Description	(AL035528) isoflavone reductase-like protein [Arabidopsis thaliana]
Seq. No.	163352
Seq. ID	LIB3177-060-P1-K1-H7
Method	BLASTN
NCBI GI	g3241923
BLAST score	288
E value	1.0e-161
Match length	320
% identity	98
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MMN10, complete sequence [Arabidopsis thaliana]
Seq. No.	163353
Seq. ID	LIB3177-060-P1-K1-H9
Method	BLASTX
NCBI GI	g1710521
BLAST score	242

E value	1.0e-20
Match length	58
% identity	81
NCBI Description	60S RIBOSOMAL PROTEIN L24 >gi_1154859_emb_CAA63960_ (X94296) L24 ribosomal protein [Hordeum vulgare]

Seq. No.	163354
Seq. ID	LIB3177-062-P1-K1-A10
Method	BLASTN
NCBI GI	g2760173
BLAST score	152
E value	7.0e-80
Match length	404
% identity	95
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MYH19, complete sequence [Arabidopsis thaliana]

Seq. No.	163355
Seq. ID	LIB3177-062-P1-K1-A11
Method	BLASTX
NCBI GI	g132074
BLAST score	427
E value	2.0e-42
Match length	81
% identity	100
NCBI Description	RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN 1A PRECURSOR (RUBISCO SMALL SUBUNIT 1A) >gi_68063_pir__RKMUA1 ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain A1 precursor - Arabidopsis thaliana

Seq. No.	163356
Seq. ID	LIB3177-062-P1-K1-A2
Method	BLASTN
NCBI GI	g3643588
BLAST score	117
E value	3.0e-59
Match length	224
% identity	85
NCBI Description	Arabidopsis thaliana chromosome II BAC F17H15 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	163357
Seq. ID	LIB3177-062-P1-K1-A3
Method	BLASTX
NCBI GI	g1052960
BLAST score	138
E value	8.0e-09
Match length	32
% identity	81
NCBI Description	(U37437) PNIL34 [Ipomoea nil]

Seq. No.	163358
Seq. ID	LIB3177-062-P1-K1-A4
Method	BLASTX
NCBI GI	g282865
BLAST score	259
E value	1.0e-22

Match length	59
% identity	83
NCBI Description	chlorophyll a/b-binding protein - Arabidopsis thaliana >gi_16207_emb_CAA39534_ (X56062) chlorophyll A/B-binding protein [Arabidopsis thaliana] >gi_166644 (M85150) chlorophyll a/b-binding protein [Arabidopsis thaliana] >gi_4678304_emb_CAB41095.1_ (AL049655) chlorophyll a/b-binding protein [Arabidopsis thaliana]

Seq. No.	163359
Seq. ID	LIB3177-062-P1-K1-A5
Method	BLASTX
NCBI GI	g132110
BLAST score	666
E value	4.0e-70
Match length	124
% identity	98
NCBI Description	RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN 3B PRECURSOR (RUBISCO SMALL SUBUNIT 3B) >gi_68060_pir__RKMUB3 ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain B3 precursor - Arabidopsis thaliana >gi_16195_emb_CAA32702_ (X14564) ribulose bisphosphate carboxylase [Arabidopsis thaliana]

Seq. No.	163360
Seq. ID	LIB3177-062-P1-K1-A6
Method	BLASTX
NCBI GI	g4415907
BLAST score	93
E value	6.0e-45
Match length	101
% identity	95
NCBI Description	(AC006282) 60S ribosomal protein L24 [Arabidopsis thaliana] >gi_4581159_gb_AAD24643.1_AC006919_21 (AC006919) putative 60S ribosomal protein L24 [Arabidopsis thaliana]

Seq. No.	163361
Seq. ID	LIB3177-062-P1-K1-A7
Method	BLASTN
NCBI GI	g4589436
BLAST score	241
E value	1.0e-133
Match length	265
% identity	98
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MPA22, complete sequence

Seq. No.	163362
Seq. ID	LIB3177-062-P1-K1-A8
Method	BLASTX
NCBI GI	g4689386
BLAST score	442
E value	8.0e-44
Match length	112
% identity	74
NCBI Description	(AF139468) photosystem I reaction center subunit III [Vigna radiata]

Seq. No.	163363
Seq. ID	LIB3177-062-P1-K1-A9
Method	BLASTX
NCBI GI	g3688799
BLAST score	592
E value	2.0e-61
Match length	127
% identity	94
NCBI Description	(AF057137) gamma tonoplast intrinsic protein 2 [Arabidopsis thaliana]

Seq. No.	163364
Seq. ID	LIB3177-062-P1-K1-B1
Method	BLASTN
NCBI GI	g4757662
BLAST score	263
E value	1.0e-146
Match length	303
% identity	100
NCBI Description	Genomic sequence for Arabidopsis thaliana BAC F10B6 from chromosome I, complete sequence

Seq. No.	163365
Seq. ID	LIB3177-062-P1-K1-B10
Method	BLASTN
NCBI GI	g2656028
BLAST score	283
E value	1.0e-158
Match length	298
% identity	99
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MNF13

Seq. No.	163366
Seq. ID	LIB3177-062-P1-K1-B11
Method	BLASTX
NCBI GI	g115385
BLAST score	450
E value	5.0e-45
Match length	89
% identity	99
NCBI Description	CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR (CAB-4) (LHCP) >gi_166646 (M63931) light-harvesting chlorophyll a/b binding protein [Arabidopsis thaliana]

Seq. No.	163367
Seq. ID	LIB3177-062-P1-K1-B12
Method	BLASTN
NCBI GI	g2564044
BLAST score	411
E value	0.0e+00
Match length	411
% identity	85
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K19P17, complete sequence [Arabidopsis thaliana]

Seq. No.	163368
Seq. ID	LIB3177-062-P1-K1-B2
Method	BLASTX
NCBI GI	g1546688
BLAST score	376
E value	3.0e-36
Match length	96
% identity	79
NCBI Description	(X98802) peroxidase ATP11a [Arabidopsis thaliana] >gi_2388572 (AC000098) Strong similarity to Arabidopsis peroxidase ATP11A (gb_X98802). [Arabidopsis thaliana] >gi_2388573 (AC000098) Strong similarity to Arabidopsis peroxidase ATP11A (gb_X98802). [Arabidopsis thaliana]

Seq. No.	163369
Seq. ID	LIB3177-062-P1-K1-B4
Method	BLASTX
NCBI GI	g4835234
BLAST score	464
E value	2.0e-46
Match length	124
% identity	82
NCBI Description	(AL049862) putative cold acclimation protein [Arabidopsis thaliana]

Seq. No.	163370
Seq. ID	LIB3177-062-P1-K1-B7
Method	BLASTX
NCBI GI	g123178
BLAST score	268
E value	8.0e-24
Match length	66
% identity	82
NCBI Description	HISTIDINOL DEHYDROGENASE, CHLOROPLAST PRECURSOR (HDH) >gi_99844_pir__A39358 histidinol dehydrogenase (EC 1.1.1.23) precursor, chloroplast - cabbage >gi_167142 (M60466) histidinol dehydrogenase [Brassica oleracea]

Seq. No.	163371
Seq. ID	LIB3177-062-P1-K1-B8
Method	BLASTX
NCBI GI	g2317905
BLAST score	313
E value	8.0e-29
Match length	71
% identity	83
NCBI Description	(U89959) bZIP-like protein [Arabidopsis thaliana]

Seq. No.	163372
Seq. ID	LIB3177-062-P1-K1-B9
Method	BLASTX
NCBI GI	g1652649
BLAST score	392
E value	4.0e-38
Match length	123
% identity	58
NCBI Description	(D90907) hypothetical protein [Synechocystis sp.]

Seq. No.	163373
Seq. ID	LIB3177-062-P1-K1-C1
Method	BLASTX
NCBI GI	g3885513
BLAST score	262
E value	8.0e-23
Match length	67
% identity	72
NCBI Description	(AF084201) similar to chloroplast 50S ribosomal protein L31 [Medicago sativa]

Seq. No.	163374
Seq. ID	LIB3177-062-P1-K1-C10
Method	BLASTX
NCBI GI	g4539430
BLAST score	150
E value	3.0e-10
Match length	46
% identity	61
NCBI Description	(AL049171) putative protein [Arabidopsis thaliana]

Seq. No.	163375
Seq. ID	LIB3177-062-P1-K1-C11
Method	BLASTX
NCBI GI	g2129550
BLAST score	364
E value	9.0e-35
Match length	135
% identity	57
NCBI Description	calcium-dependent protein kinase (EC 2.7.1.-) CDPK6 - Arabidopsis thaliana >gi_2129554_pir__S71901 calcium-dependent protein kinase 6 - Arabidopsis thaliana >gi_836940 (U20623) calcium-dependent protein kinase [Arabidopsis thaliana] >gi_836944 (U20625) calcium-dependent protein kinase [Arabidopsis thaliana] >gi_4454034_emb_CAA23031.1_ (AL035394) calcium-dependent protein kinase (CDPK6) [Arabidopsis thaliana]

Seq. No.	163376
Seq. ID	LIB3177-062-P1-K1-C12
Method	BLASTX
NCBI GI	g99735
BLAST score	740
E value	8.0e-79
Match length	141
% identity	98
NCBI Description	L-ascorbate peroxidase (EC 1.11.1.11) precursor - Arabidopsis thaliana (fragment)

Seq. No.	163377
Seq. ID	LIB3177-062-P1-K1-C2
Method	BLASTX
NCBI GI	g115783
BLAST score	542
E value	1.0e-55
Match length	106

% identity	96
NCBI Description	CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR (CAB-140) (LHCP) >gi_16376_emb_CAA27543_ (X03909) chlorophyll a/b binding protein (LHCP AB 140) [Arabidopsis thaliana]
Seq. No.	163378
Seq. ID	LIB3177-062-P1-K1-C3
Method	BLASTX
NCBI GI	g166834
BLAST score	560
E value	1.0e-57
Match length	131
% identity	86
NCBI Description	(M86720) ribulose bisphosphate carboxylase/oxygenase activase [Arabidopsis thaliana] >gi_2642155 (AC003000) Rubisco activase [Arabidopsis thaliana]
Seq. No.	163379
Seq. ID	LIB3177-062-P1-K1-C4
Method	BLASTX
NCBI GI	g4741960
BLAST score	300
E value	2.0e-27
Match length	94
% identity	55
NCBI Description	(AF134130) Lhcb6 protein [Arabidopsis thaliana]
Seq. No.	163380
Seq. ID	LIB3177-062-P1-K1-C5
Method	BLASTN
NCBI GI	g972924
BLAST score	195
E value	1.0e-105
Match length	244
% identity	99
NCBI Description	Arabidopsis thaliana IAA11 (IAA11) gene, complete cds
Seq. No.	163381
Seq. ID	LIB3177-062-P1-K1-C7
Method	BLASTX
NCBI GI	g166834
BLAST score	386
E value	2.0e-37
Match length	90
% identity	87
NCBI Description	(M86720) ribulose bisphosphate carboxylase/oxygenase activase [Arabidopsis thaliana] >gi_2642155 (AC003000) Rubisco activase [Arabidopsis thaliana]
Seq. No.	163382
Seq. ID	LIB3177-062-P1-K1-C8
Method	BLASTX
NCBI GI	g3169173
BLAST score	769
E value	3.0e-82
Match length	143

% identity	97
NCBI Description	(AC004401) putative serine carboxypeptidase I [Arabidopsis thaliana] >gi_3445215 (AC004786) putative serine carboxypeptidase I [Arabidopsis thaliana]

Seq. No.	163383
Seq. ID	LIB3177-062-P1-K1-C9
Method	BLASTX
NCBI GI	g1419390
BLAST score	322
E value	8.0e-30
Match length	67
% identity	94
NCBI Description	(X98926) thylakoid-bound ascorbate peroxidase [Arabidopsis thaliana]

Seq. No.	163384
Seq. ID	LIB3177-062-P1-K1-D1
Method	BLASTX
NCBI GI	g730645
BLAST score	619
E value	1.0e-64
Match length	135
% identity	91
NCBI Description	40S RIBOSOMAL PROTEIN S15 >gi_629556_pir__S43412 ribosomal protein S15 - Arabidopsis thaliana >gi_313152_emb_CAA80679_ (Z23161) ribosomal protein S15 [Arabidopsis thaliana] >gi_313188_emb_CAA80681_ (Z23162) ribosomal protein S15 [Arabidopsis thaliana] >gi_1903366_gb_AAB70449_ (AC000104) Strong similarity to Oryza 40S ribosomal protein S15. ESTs gb_R29788,gb_ATTS0365 come from this gene. [Arabidopsis thaliana]

Seq. No.	163385
Seq. ID	LIB3177-062-P1-K1-D10
Method	BLASTX
NCBI GI	g3236476
BLAST score	194
E value	5.0e-15
Match length	45
% identity	91
NCBI Description	(AF071195) 26S protease regulatory subunit [Gossypium hirsutum]

Seq. No.	163386
Seq. ID	LIB3177-062-P1-K1-D11
Method	BLASTX
NCBI GI	g4454481
BLAST score	366
E value	3.0e-35
Match length	97
% identity	78
NCBI Description	(AC006234) unknown protein [Arabidopsis thaliana] >gi_4512647_gb_AAD21702.1_ (AC007048) unknown protein [Arabidopsis thaliana]

Seq. No. 163387

Seq. ID	LIB3177-062-P1-K1-D12
Method	BLASTX
NCBI GI	g113026
BLAST score	480
E value	2.0e-48
Match length	109
% identity	85
NCBI Description	ISOCITRATE LYASE (ISOCITRASE) (ISOCITRATASE) (ICL) >gi_68211_pir__WZRPI isocitrate lyase (EC 4.1.3.1) - rape >gi_255220_bbs_112862 isocitrate lyase, threo-D S-isocitrate glyoxylate-lyase, IL (EC 4.1.3.1) [Brassica napus, seedlings, Peptide, 576 aa] >gi_167144 (L08482) isocitrate lyase [Brassica napus] >gi_447142_prf__1913424A isocitrate lyase [Brassica napus]

Seq. No.	163388
Seq. ID	LIB3177-062-P1-K1-D3
Method	BLASTX
NCBI GI	g131162
BLAST score	343
E value	9.0e-40
Match length	82
% identity	99
NCBI Description	PHOTOSYSTEM I IRON-SULFUR CENTER 1 (PHOTOSYSTEM I SUBUNIT VII-1) (9 KD POLYPEPTIDE 1) (PSI-C-1) >gi_131163_sp_P07136_PSAC_TOBAC PHOTOSYSTEM I IRON-SULFUR CENTER (PHOTOSYSTEM I SUBUNIT VII) (9 KD POLYPEPTIDE) (PSI-C) >gi_97657_pir__S14967 photosystem I iron-sulfur protein psaC - Synechocystis sp. (PCC 6803) >gi_100391_pir__S07170 photosystem I iron-sulfur protein psaC - common tobacco chloroplast >gi_11792_emb_CAA29304_ (X05881) 9kd polypeptide (psaC gene product, AA 1 - 81) [Nicotiana tabacum] >gi_47596_emb_CAA37836_ (X53842) 8.9kDa iron-sulfur containing subunit of Photosystem I [Synechocystis sp.] >gi_2924280_emb_CAA77433_ (Z00044) PSI 9kD protein [Nicotiana tabacum]

Seq. No.	163389
Seq. ID	LIB3177-062-P1-K1-D4
Method	BLASTX
NCBI GI	g1769895
BLAST score	583
E value	2.0e-60
Match length	134
% identity	87
NCBI Description	(X96598) CaLB protein [Arabidopsis thaliana]

Seq. No.	163390
Seq. ID	LIB3177-062-P1-K1-D5
Method	BLASTX
NCBI GI	g2119846
BLAST score	496
E value	3.0e-50
Match length	125
% identity	81
NCBI Description	chlorophyll a/b-binding protein type I precursor Lhb1B2 - Arabidopsis thaliana >gi_16364_emb_CAA45790_ (X64460)

	photosystem II type I chlorophyll a /b binding protein [Arabidopsis thaliana] >gi_3128230 (AC004077) photosystem II type I chlorophyll a/b binding protein [Arabidopsis thaliana] >gi_3337371 (AC004481) photosystem II type I chlorophyll a/b binding protein [Arabidopsis thaliana]
Seq. No.	163391
Seq. ID	LIB3177-062-P1-K1-D6
Method	BLASTX
NCBI GI	g3386620
BLAST score	174
E value	4.0e-13
Match length	64
% identity	41
NCBI Description	(AC004665) hypothetical protein [Arabidopsis thaliana]
Seq. No.	163392
Seq. ID	LIB3177-062-P1-K1-D7
Method	BLASTN
NCBI GI	g2088638
BLAST score	147
E value	4.0e-77
Match length	321
% identity	100
NCBI Description	Arabidopsis thaliana chromosome II BAC T28M21 genomic sequence, complete sequence [Arabidopsis thaliana]
Seq. No.	163393
Seq. ID	LIB3177-062-P1-K1-D9
Method	BLASTX
NCBI GI	g2129672
BLAST score	170
E value	1.0e-12
Match length	57
% identity	63
NCBI Description	photosystem II reaction center protein, 6.1K - Arabidopsis thaliana >gi_950023_emb_CAA62296_ (X90769) component of 6.1 kDa polypeptide of photosystem II reaction center [Arabidopsis thaliana]
Seq. No.	163394
Seq. ID	LIB3177-062-P1-K1-E1
Method	BLASTX
NCBI GI	g132102
BLAST score	765
E value	1.0e-81
Match length	145
% identity	99
NCBI Description	RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN 2B PRECURSOR (RUBISCO SMALL SUBUNIT 2B) >gi_68061_pir__RKMUB2 ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain B2 precursor - Arabidopsis thaliana >gi_16194_emb_CAA32701_ (X14564) ribulose bisphosphate carboxylase [Arabidopsis thaliana]
Seq. No.	163395
Seq. ID	LIB3177-062-P1-K1-E10

Method	BLASTX
NCBI GI	g3914442
BLAST score	419
E value	2.0e-41
Match length	105
% identity	79
NCBI Description	PHOTOSYSTEM I REACTION CENTRE SUBUNIT VI PRECURSOR (LIGHT-HARVESTING COMPLEX I 11 KD PROTEIN) (PSI-H) >gi_1916350 (U92504) PSI-H subunit [Brassica rapa]

Seq. No.	163396
Seq. ID	LIB3177-062-P1-K1-E11
Method	BLASTX
NCBI GI	g3136033
BLAST score	183
E value	2.0e-13
Match length	87
% identity	44
NCBI Description	(AL023590) putative metallopeptidase [Schizosaccharomyces pombe]

Seq. No.	163397
Seq. ID	LIB3177-062-P1-K1-E12
Method	BLASTX
NCBI GI	g3915823
BLAST score	300
E value	1.0e-27
Match length	57
% identity	100
NCBI Description	[Segment 1 of 2] 60S RIBOSOMAL PROTEIN L5

Seq. No.	163398
Seq. ID	LIB3177-062-P1-K1-E2
Method	BLASTX
NCBI GI	g2493144
BLAST score	191
E value	1.0e-14
Match length	58
% identity	71
NCBI Description	VACUOLAR ATP SYNTHASE 16 KD PROTEOLIPID SUBUNIT (V-ATPASE 16 KD PROTEOLIPID SUBUNIT) >gi_2118221_pir__S60132 H+-transporting ATPase (EC 3.6.1.35), vacuolar, 16K chain (clone AVA-P2) - Arabidopsis thaliana >gi_926937 (L44585) vacuolar H+-pumping ATPase 16 kDa proteolipid [Arabidopsis thaliana]

Seq. No.	163399
Seq. ID	LIB3177-062-P1-K1-E3
Method	BLASTX
NCBI GI	g4512685
BLAST score	469
E value	9.0e-64
Match length	155
% identity	79
NCBI Description	(AC006931) hypothetical protein [Arabidopsis thaliana] >gi_4559325_gb_AAD22987.1_AC007087_6 (AC007087) hypothetical protein [Arabidopsis thaliana]

Seq. No.	163400
Seq. ID	LIB3177-062-P1-K1-E4
Method	BLASTN
NCBI GI	g2264311
BLAST score	210
E value	1.0e-114
Match length	251
% identity	96
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MLN1, complete sequence [Arabidopsis thaliana]

Seq. No.	163401
Seq. ID	LIB3177-062-P1-K1-E5
Method	BLASTX
NCBI GI	g544425
BLAST score	429
E value	2.0e-42
Match length	83
% identity	100
NCBI Description	GLYCINE-RICH RNA-BINDING PROTEIN 8 (CCR1 PROTEIN) >gi_419756_pir__S30148 glycine-rich protein (clone AtGRP8) - Arabidopsis thaliana >gi_16305_emb_CAA78712_ (Z14988) glycine rich protein [Arabidopsis thaliana] >gi_166658 (L04171) ORF [Arabidopsis thaliana] >gi_166839 (L00649) RNA-binding protein [Arabidopsis thaliana]

Seq. No.	163402
Seq. ID	LIB3177-062-P1-K1-E6
Method	BLASTX
NCBI GI	g4741952
BLAST score	278
E value	1.0e-24
Match length	60
% identity	90
NCBI Description	(AF134126) Lhcb3 protein [Arabidopsis thaliana]

Seq. No.	163403
Seq. ID	LIB3177-062-P1-K1-E7
Method	BLASTX
NCBI GI	g1477480
BLAST score	704
E value	1.0e-74
Match length	145
% identity	99
NCBI Description	(U40341) carbamoyl phosphate synthetase large chain [Arabidopsis thaliana]

Seq. No.	163404
Seq. ID	LIB3177-062-P1-K1-E8
Method	BLASTX
NCBI GI	g1871577
BLAST score	188
E value	2.0e-14
Match length	52
% identity	65
NCBI Description	(Y11553) putative 21kD protein precursor [Medicago sativa]

Seq. No.	163405
Seq. ID	LIB3177-062-P1-K1-F1
Method	BLASTX
NCBI GI	g2252828
BLAST score	455
E value	2.0e-45
Match length	121
% identity	80
NCBI Description	(AF013293) No definition line found [Arabidopsis thaliana]

Seq. No.	163406
Seq. ID	LIB3177-062-P1-K1-F10
Method	BLASTX
NCBI GI	g3128217
BLAST score	473
E value	2.0e-47
Match length	110
% identity	87
NCBI Description	(AC004077) hypothetical protein [Arabidopsis thaliana] >gi_3337374 (AC004481) hypothetical protein [Arabidopsis thaliana]

Seq. No.	163407
Seq. ID	LIB3177-062-P1-K1-F11
Method	BLASTX
NCBI GI	g1773014
BLAST score	300
E value	2.0e-27
Match length	89
% identity	70
NCBI Description	(Y10338) chloride channel Stclc1 [Solanum tuberosum]

Seq. No.	163408
Seq. ID	LIB3177-062-P1-K1-F12
Method	BLASTX
NCBI GI	g2062161
BLAST score	678
E value	2.0e-71
Match length	140
% identity	50
NCBI Description	(AC001645) jasmonate inducible protein isolog [Arabidopsis thaliana]

Seq. No.	163409
Seq. ID	LIB3177-062-P1-K1-F2
Method	BLASTX
NCBI GI	g3885511
BLAST score	366
E value	4.0e-35
Match length	95
% identity	79
NCBI Description	(AF084200) similar to PSI-K subunit of photosystem I from barley [Medicago sativa]

Seq. No.	163410
Seq. ID	LIB3177-062-P1-K1-F4